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(21) International Application Number: PCT/US00/08621 (22) International Filing Date: 31 March 2000 (31.03.00) (30) Priority Data: <table><tr><td>60/127,607</td><td>31 March 1999 (31.03.99)</td><td>US</td></tr><tr><td>60/127,636</td><td>2 April 1999 (02.04.99)</td><td>US</td></tr><tr><td>60/127,728</td><td>5 April 1999 (05.04.99)</td><td>US</td></tr><tr><td>09/540,763</td><td>30 March 2000 (30.03.00)</td><td>US</td></tr></table> (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications <table><tr><td>US</td><td>60/127,607 (CIP)</td></tr><tr><td>Filed on</td><td>31 March 1999 (31.03.99)</td></tr><tr><td>US</td><td>60/127,636 (CIP)</td></tr><tr><td>Filed on</td><td>2 April 1999 (02.04.99)</td></tr><tr><td>US</td><td>60/127,728 (CIP)</td></tr><tr><td>Filed on</td><td>5 April 1999 (05.04.99)</td></tr><tr><td>US</td><td>09/540,763 (CIP)</td></tr><tr><td>Filed on</td><td>30 March 2000 (30.03.00)</td></tr></table> (71) Applicant (for all designated States except US): CURAGEN CORPORATION [US/US]; 555 Long Wharf Drive, 11th Floor, New Haven, CT 06511 (US).		60/127,607	31 March 1999 (31.03.99)	US	60/127,636	2 April 1999 (02.04.99)	US	60/127,728	5 April 1999 (05.04.99)	US	09/540,763	30 March 2000 (30.03.00)	US	US	60/127,607 (CIP)	Filed on	31 March 1999 (31.03.99)	US	60/127,636 (CIP)	Filed on	2 April 1999 (02.04.99)	US	60/127,728 (CIP)	Filed on	5 April 1999 (05.04.99)	US	09/540,763 (CIP)	Filed on	30 March 2000 (30.03.00)	(72) Inventors; and (75) Inventors/Applicants (for US only): SHIMKETS, Richard, A. [US/US]; 191 Leete Street, West Haven, CT 06516 (US). LEACH, Martin [GB/US]; 884 School Street, Webster, MA 01570 (US). (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin; Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>	
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(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"																															
(57) Abstract <p>The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.</p>																															

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NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2 n -1, wherein n is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2 n , wherein n is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic
15 acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

The invention is also directed to methods of identifying an ORFX polypeptide or nucleic
20 acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

In a another aspect, the invention provides a method of determining the presence of or
30 predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF n according to the invention (wherein n is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2 n -1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2 n . For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected. Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu/>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of '7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

Amylases

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

5 **Amyloid**

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. 10
15 Amyloid deposition is also associated with type II diabetes mellitus.

Angiopoeitin

Members of the angiopoeitin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an 20 essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

25 **Apoptosis-related proteins**

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

5 **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form
10 of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in
15 hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a
20 membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent
25 cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia
5 areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes
10 may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the
15 proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by
20 interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and
25 dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

10	Abbrev:	Title:
	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotinddep	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_ma_bind	DNA/RNA binding protein/factor
	dna_ma_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein

	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
	glucoamylase	glucoamylase
10	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase PIR	phosphorylase PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase potassium_channel prostaglandin protease proteaseinhib reductase	polymerase potassium channel protein prostaglandin protease protease inhibitor reductase
10	ribosomalprot RTR	ribosomal associated protein EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
15	SIM SPTR	similar EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
20	struct sulfotransferase SWP	structural associated protein sulfotransferase SWISS-PROT DATABASE (release 18-OCT-1998)
25	SWPN synthase tgf tgfreceptor thioesterase thiolase tm7	SWISS-PROT Update (release 11-NOV-98) synthase transforming growth factor transforming growth factor receptor thioesterase thiolase seven transmembrane domain G-protein coupled receptor
30	tnf traffic tnfreceptor TRN	necrosis factor receptor tumor necrosis factor tumor trafficking associated protein EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor transferase transport tubulin ubiquitin	transcription factor transferase transport protein tubulin ubiquitin
40	unclassified water channel	Protein not categorized into one of the aforementioned protein families water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

ORFX nucleic acids, and their encoded polypeptides, according to the invention are useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

ORFX nucleic acids and polypeptides according to the invention can also be used to identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

ORFX Nucleic Acids

The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2*n*, wherein *n* = 1 to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . . , 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof, any of whose bases may be changed from the disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), including fragments, derivatives,

analog and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as
5 polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is
10 double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and
15 much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic
20 acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism
25 from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular
30 material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby forming a stable duplex.

5 As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect.

10 Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the
15 nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively,
20 and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but
25 differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or
30 analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified

oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4.

ORFX variants

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, e.g., Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (e.g., as employed for cross-species hybridizations). See, e.g., Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative mutations

In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2 n (wherein $n = 1$ to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2 n -1 for the corresponding n , such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (*v*), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (*v*), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

Ribozymes and PNA moieties

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are

carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

- 5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
- 10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
- 15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

- Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
- 20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

- In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
- 25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
- 30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX-like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2n (wherein n = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2n (wherein n = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2n (wherein n = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2n (wherein n = 1 to 3161).

Determining homology between two or more sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (i.e., as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch 1970 J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2n-1 (wherein n = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

Chimeric and fusion proteins

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

5 For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

10 In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

15 In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

20 In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX
25 cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of
30 ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

ORFX agonists and antagonists

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one

embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477.

Polypeptide libraries

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the proteins of the invention.

An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in any of SEQ ID NO:2*n* (wherein $n = 1$ to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6 contiguous amino acids of any of SEQ ID NO:2*n* (wherein $n = 1$ to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2*n* (wherein $n = 1$ to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)_2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND
5 CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*,
10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by
15 techniques known in the art including, but not limited to: (i) an F_{(ab)₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized
20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent
25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J.*
30 *Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

ORFX Recombinant Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can
10 be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are
15 replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the
20 invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the
25 recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation
30 system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews--Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

5 Transgenic animals

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene (*e.g.*, SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmot *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

Pharmaceutical Compositions

The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Additional Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5 This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

Screening Assays

 The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides,
10 peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

 In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained
15 using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are
20 applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

 Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993)
25 *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

 Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409),
30 plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can be of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) Cell 72:223-232; Madura *et al.* (1993) J Biol Chem 268:12046-12054; Bartel *et al.* (1993) Biotechniques 14:920-924; Iwabuchi *et al.* (1993) Oncogene 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

Use of Partial ORFX Sequences in Forensic Biology

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, *e.g.*, hair or skin, or body fluids, *e.g.*, blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs: __ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5 Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

10 Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

15 Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

20 An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

25 The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be

30 administered in which an antibody specifically binding the ORFX-like proteins of the invention

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX nucleic acids of SEQ ID NO:2n-1 (wherein $n = 1$ to 3161) may be used to detect DNA containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene, or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue, as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (e.g., mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID NO:2n-1 (wherein $n = 1$ to 3161), or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable probes for use in the diagnostic assays of the invention are described herein.

An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity in, e.g., proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, e.g., U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, e.g., Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in ORFX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS* 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA

heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, e.g., Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, e.g., Myers *et al.* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, e.g., Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, e.g., Saiki *et al.* (1986) *Nature* 324:163; Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, e.g., Gasparini *et al.* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5 The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10 Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

15 Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be
20 considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate
25 dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30 Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

Determination of the Biological Effect of a Therapeutic

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Malignancies

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,

but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models, in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein. Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination); benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

Neurodegenerative disorders

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

Disorders related to organ transplantation

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

Cardiovascular Disease

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5 A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),
10 transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein
15 (Frostegard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for
20 example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

 Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be
25 treated or prevented by administration of a Therapeutic that modulates activity.

Cytokine and Cell Proliferation/Differentiation Activity

 A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons, Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immunol* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by vital, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the

immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be
5 capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a
10 subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression
15 of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells.
20 In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on
25 the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a
30 B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without
5 limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981;
10 Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which
15 will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins
20 that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by
25 dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J*
30 *Exp Med* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al.* *Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell.*
10 *Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al.*,
15 *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *et al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp.
20 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for
25 wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation
30 employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

Activin/Inhibin Activity

5 A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

20 Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

25 A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example,

30

attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*,
15 eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those
30 described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor
5 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and
ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and
their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell
interactions and their ligands (including without limitation, cellular adhesion molecules (such as
10 selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation,
antigen recognition and development of cellular and humoral immune responses). Receptors and
ligands are also useful for screening of potential peptide or small molecule inhibitors of the
relevant receptor/ligand interaction. A protein of the present invention (including, without
limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of
receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the
following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:
CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and
Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions
20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp.*
Med. 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*,
J Immunol Methods 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The
25 anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the
inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example,
cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory
process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
of other factors which more directly inhibit or promote an inflammatory response. Proteins
30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

10 EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gij4691395jemb CAB41562.1 - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	264636
2	80248091 (3, 4)	Novel Protein sim. GBank gij2829505 sp P71559 SUCC_MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264689, 264638, 264587
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264905, 264636, 264691, 264907, 264692, 264629
4	82018837 (7, 8)			UNCLASSIFIED	264908, 264909, 264760, 264628, 264635
5	79970035 (9, 10)			UNCLASSIFIED	22279002, 264563
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	264908
7	85515576 (13, 14)	Novel Protein sim. GBank gij4415925 gb AAD20157 - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	20281099, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 265009, 264910, 264595, 264596, 264758, 264603, 264604, 264760, 264762, 264683, 264766, 264767, 264689, 35695917, 264690, 264692, 264693, 33657109, 264628, 264629, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264488
8	56924278 (15, 16)	Novel Protein sim. GBank gij585562 sp Q06458 NIRB_KLEPN - NITRITE REDUCTASE (NAD(P)H) LARGE SUBUNIT		reductase	264907
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79556459 (19, 20)			UNCLASSIFIED	264906
11	20414027 (21, 22)				264605
12	94141210 (23, 24)	Novel Protein sim. GBank gij3878145 emb CAA9987.1 - (Z75543) similar to potassium channel protein [Caenorhabditis elegans]		misc_channel	264259, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264564
14	95105114 (27, 28)	Novel Protein sim. GBank gij2832781 emb CAA12645 - (AJ225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Ank repeat	potassium_channel	35696286, 35696052, 264510, 35695917, 264691, 264628, 35696423, 264555, 264558, 264559, 83373044
15	20458307 (29, 30)	Novel Protein sim. GBank gij1710791 sp Q10234 RT05_SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264604
16	20760356 (31, 32)				264555

17	20282744 (33, 34)	Novel Protein sim. GBank gij1174884[sp]P44391[URE1_HAEN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE) Novel Protein sim. GBank gij2281102 (AC002333) - SF16 isolob [Arabidopsis thaliana]	Contains protein domain (PF00449) - Urease		264600
18	80246804 (35, 36)				26331827, 264555, 264557, 264638, 264558
19	80076624 (37, 38)				22278998, 264907, 264910, 264600, 264693
20	20724558 (39, 40)	Novel Protein sim. GBank gij2506112[sp]P43672[UUP_ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP Novel Protein sim. GBank gij1730203[sp]P50442[GATM_RAT - GLYCINE AMINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMINOTRANSFERASE) (TRANSAMIDINASE) (AT)	UNCLASSIFIED transport		264602
21	80417554 (41, 42)				22278995, 264906, 265008, 265010, 265011, 264602, 264605, 264766, 264688, 21908764, 264691, 18108376, 264636, 18108387, 264486
22	11705858 (43, 44)				264685
23	80419176 (45, 46)	Novel Protein sim. GBank gij1877329[emb]CAB07077] - (Z92771) fadE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - dehydrogenase Acyl-CoA dehydrogenase		264488, 264907, 264809, 264600, 264602, 264603, 264605, 264682, 264766, 3283386, 264636, 264486
24	20291697 (47, 48)				264600
25	80253774 (49, 50)				264593
26	80255394 (51, 52)				22278996, 56182435, 265018, 264566
27	80235785 (53, 54)	Novel Protein sim. GBank gij4808369[emb]CAB42783.1] - (AL049841) putative 30S ribosomal protein S14 [Sireptomycetes coelicolor]	UNCLASSIFIED ribosomal prot		18108370, 35696423, 264635, 264555
28	78483561 (55, 56)				264638
29	82448765 (57, 58)	Novel Protein sim. GBank gij3122290[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)	UNCLASSIFIED kinase		264601, 264762, 264766, 264768, 264638
30	78189333 (59, 60)				264908, 265019, 264687, 21908764,
31	19848158 (61, 62)				21906766
32	82448495 (63, 64)	Novel Protein sim. GBank gij3560504 (AF027770) - unknown [Mycobacterium smegmatis]	UNCLASSIFIED		264534
33	78582628 (65, 66)	Novel Protein sim. GBank gij2129003[pir][G64507 - hypothetical protein MJ1685 - Methanococcus jannaschii	UNCLASSIFIED		264905, 264605, 264762, 264766, 264687, 264689
34	87467657 (67, 68)				264687
35	95005170 (69, 70)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		60432289, 264600, 264602, 264760,
36	18642042 (71, 72)	Novel Protein sim. GBank gij3287739[sp]P73538[BIOB_SYNY3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)	UNCLASSIFIED		18108357, 264768, 265020, 264691
37	20369215 (73, 74)	Novel Protein sim. GBank gij2313134[gb]AAD07126.1] - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26695]	UNCLASSIFIED synthase		264600, 264687, 264558, 264639
			dehydrogenase		264566
					264603

38	20466334 (75, 76)	Novel Protein sim. GBank gij3805970[emb]CAA06231] - (AJ004933) periplasmic nitrate reductase, large subunit [Rhodospseudomonas sp.]			264605
39	94300715 (77, 78)	Novel Protein sim. GBank gij1929449 (L63543) - endodermin [Xenopus laevis]	Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	264905, 264906, 264907, 66712502, 264908, 264909, 264511, 265009, 264910, 55812038, 264758, 265011, 264782, 264882, 264763, 264784, 264766, 265022, 264693, 264628, 264631, 264634, 264635, 264555, 264638, 18108381, 264558, 18108385, 264482
40	20635625 (78, 80)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	264592
41	80023287 (81, 82)	Novel Protein sim. GBank gij3820584 (AF086791) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]		UNCLASSIFIED	264591, 35695917
42	20724566 (83, 84)	Novel Protein sim. GBank gij3820584 (AF086791) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]		synthase	264602
43	20467069 (85, 86)	Novel Protein sim. GBank gij3820584 (AF086791) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]			264605
44	13085287 (87, 88)	Novel Protein sim. GBank gij2494764[sp]Q50729[GUA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)]	Contains protein domain (PF00958) - GMP synthase C terminal domain	synthase	264769, 264636
45	39384711 (89, 90)	Novel Protein sim. GBank gij1881738 (U89688) - myosin-I binding protein Acan125 [Acanthamoeba castellanii]		UNCLASSIFIED	264769, 264510, 264508
46	95003398 (91, 92)			ngf	264566
47	11698624 (93, 94)			UNCLASSIFIED	264689
48	79407218 (95, 96)				18108385, 264635, 264828
49	21659844 (97, 98)			UNCLASSIFIED	264603
50	80503996 (99, 100)				264508, 264603, 264769, 264689, 264636, 264558, 264486
51	80255569 (101, 102)	Novel Protein sim. GBank gij3411177 (AF076240) - MccC [Rhizobium leguminosarum bv. viciae]		UNCLASSIFIED	264593, 18108387
52	78208528 (103, 104)	Novel Protein sim. GBank gij3914892[sp]Q26284[ISM41_HEMPU - 41 KD SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)]		strud	264634
53	36996970 (105, 106)	Novel Protein sim. GBank gij3880411 (AC004581) - putative proline-rich protein [Arabidopsis thaliana]		UNCLASSIFIED	264782
54	79570897 (107, 108)	Novel Protein sim. GBank gij1633572 (U52084) - Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]		UNCLASSIFIED	264630, 264909, 264766
55	80202703 (109, 110)	Novel Protein sim. GBank gij4321580[gijAAD15785] - (AF050114) alginatase [Pseudomonas sp. W7]			29331824, 264102, 265018, 18108376
56	8758408 (111, 112)				264604
57	11223386 (113, 114)		Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264557

58	91227508 (115, 116)	Novel Protein sim. GBank gij15616074 gb AAD45616.1 AF06194 - (AF061943) protease- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	56182575, 264259, 60432049, 35896052, 66712502, 264909, 265008, 265010, 265011, 264681, 29148784, 35695917, 60170615, 264691, 264692, 264693, 18108374, 35696423, 56182323, 60432113 264600, 264689, 264638
59	80077371 (117, 118)	Novel Protein sim. GBank gij1172920 sp P45830 JFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGLUCOSAMINYLTRANSFERASE	Contains protein domain (PF00953) - Glycosyl transferase	transferase	
60	12958341 (119, 120)				264689
61	80426808 (121, 122)	Novel Protein sim. GBank gij11710216 (U79260) - unknown [Homo sapiens]		glycoprotein	264766
62	13504866 (123, 124)				264630
63	16474553 (125, 126)			UNCLASSIFIED	265019
64	20724578 (127, 128)	Novel Protein sim. GBank gij420945 pir JA47041 - transposase homolog (insertion element [SAE1]) - Alcaligenes eutrophus		UNCLASSIFIED	264602
65	79326308 (129, 130)	Novel Protein sim. GBank gij3122312 sp O06134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	kinase	264563
66	46854384 (131, 132)	Novel Protein sim. GBank gij3928723 emb CAA22218 - (AL034355) putative ABC transporter (Streptomyces coelicolor)		transport	22278996, 264558
67	78952543 (133, 134)	Novel Protein sim. GBank gij231985 sp P30234 DHA_MYCTU - ALANINE DEHYDROGENASE (40 KD ANTIGEN)		dehydrogenase	265021
68	79817382 (135, 136)				264909
69	79841764 (137, 138)			UNCLASSIFIED	264908
70	79871329 (139, 140)				264906, 264908
71	65897458 (141, 142)			UNCLASSIFIED	264602, 265021
72	87734977 (143, 144)	Novel Protein sim. GBank gij4415926 gb AAD20157 - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264511, 265008, 264910, 264758, 87168474, 264682, 264766, 264686, 264689, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 264629, 264631, 264639, 22279000
73	80025241 (145, 146)			UNCLASSIFIED	60424179, 264508, 264908, 265007, 264603, 264687, 264689, 264692, 18108387
74	20377410 (147, 148)			UNCLASSIFIED	264605
75	11819032 (149, 150)	Novel Protein sim. GBank gij2853098 emb CAA16914 - (AL021767) vacuolar protein sorting [Schizosaccharomyces pombe]		UNCLASSIFIED	264689
76	95105303 (151, 152)	Novel Protein sim. GBank gij446881 emb CAB38212 - (AL035601) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	83373044, 264906, 264557
77	10144718 (153, 154)	Novel Protein sim. GBank gij854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264563
78	87582558 (155, 156)			UNCLASSIFIED	264604

79	94140180 (157, 158)	Novel Protein sim. GBank gjl5689453[dbjBAA83010.1] - (AB028981) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain		35696286, 22278998, 29331822, 29331824, 29331825, 29331827, 264905, 264906, 264907, 66712502, 264908, 264908, 265008, 265009, 264910, 60170831, 55812038, 33109954, 265017, 265018, 264288, 264768, 56181562, 21906765, 21906769, 29148784, 265020, 264690, 264691, 264692, 264693, 60431528, 35696423, 264631, 264632, 264634, 264636, 264639, 83373044, 264564, 264566, 264567
80	82314840 (159, 160)		UNCLASSIFIED		264769, 264501, 265006, 264910, 264604, 264605, 264634, 264635, 264905, 264762, 264637, 264592, 264628, 264907, 264691, 264908, 264567, 264909, 264766
81	20467247 (161, 162)	Novel Protein sim. GBank gjl1723442[spQ10258]YD2A_SCHPO - HYPOTHETICAL 69.0 KD PROTEIN C56F8.10 IN CHROMOSOME 1	reductase		264605
82	16331388 (163, 164)	Novel Protein sim. GBank gjl2895866 (AF045770) - methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]	dehydrogenase		264567
83	94741180 (165, 166)	Novel Protein sim. GBank gjl3402673 (AC004697) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED		264488, 264508, 264509, 264905, 264908, 264909, 264511, 264591, 264593, 264594, 264595, 264596, 264758, 264603, 264760, 264681, 18108351, 264762, 264682, 264764, 264684, 264766, 264686, 264632, 264637, 264557, 264638, 264639, 18108385, 264556
84	80355375 (167, 168)	Novel Protein sim. GBank gjl173364[spP45380]SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTIporter)	transport		264508, 264908, 264907, 264908, 264909, 264910, 264760, 264763, 264764, 264766, 264768, 264769, 35695855, 264636, 264637
85	80498600 (169, 170)	Novel Protein sim. GBank gjl2120998[pirJ]S70682 - glycosyltransferase homolog - Bordetella pertussis	transferase		264605, 264762, 264687, 264769, 18108374, 264636, 264486
86	39559043 (171, 172)	Novel Protein sim. GBank gjl3256023[emb]CAA17228.11 - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]			264910
87	13856808 (173, 174)		UNCLASSIFIED		264093

88	95344718 (175, 176)	Novel Protein sim. GBank gjl559703[dbj BAA07552] - (D38549) ha1025 is new [Homo sapiens]		52644507, 52646365, 18108398, 65274572, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 264094, 264095, 264259, 29331822, 29331824, 56182181, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 264105, 264508, 264905, 264806, 264907, 264908, 29331830, 66712502, 52644045, 56182435, 285007, 265009, 264810, 60170831, 264592, 60431735, 60433358, 33657402, 264757, 60433438, 55812038, 264758, 21906754, 52646317, 33109954, 52644298, 87168474, 265011, 87168559, 264601, 265017, 265018, 264604, 265019, 264448, 264369, 264288, 264766, 52644229, 21906768, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 60170615, 52644150, 33657023, 65274620, 33657109, 27486261, 27486264, 33657349, 35695763, 264628, 263972, 18108374, 55810764, 35698423, 55811576, 65274791, 35695855, 60431850, 264636, 52644332, 56182323, 60170394, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264564, 264486
89	80077389 (177, 178)	Novel Protein sim. GBank gjl1710383[sp P4632 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX		264600
90	82115999 (178, 180)	Novel Protein sim. GBank gjl2499891[sp P76403 YEGQ_ECOLI - PUTATIVE PROTEASE IN BAER-OGRK INTERGENIC REGION	UNCLASSIFIED protease	264760 265006
92	78554871 (183, 184)	Novel Protein sim. GBank gjl3367754[emb CAA20079] - (AL031155) hypothetical protein SC3A7.16c [Streptomyces coelicolor]	UNCLASSIFIED	264691
93	80496778 (185, 186)	Novel Protein sim. GBank gjl2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]	ATPase_associated	264907, 264908, 264910, 265009, 264605, 264769
94	78646649 (187, 188)	Novel Protein sim. GBank gjl171919[sp P46920 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUA	Contains protein domain (PF00571) - CBS domain	264906
95	11090238 (189, 190)			264594

98	94322125 (191, 192)	Novel Protein sim. GBank gi 4589560 dbj BAA76802.1 - (AB023175) KIAA0958 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 264259, 29331822, 29331826, 35696052, 28146499, 284509, 284906, 284907, 264908, 284909, 265007, 285008, 284910, 265009, 284593, 265010, 265017, 264604, 265019, 18108351, 264288, 264768, 264768, 264768, 21906765, 21906767, 21905769, 265020, 264692, 33657182, 35695763, 264628, 264629, 18108379, 284631, 284636, 18108381, 264559, 18108382, 83373044, 22278002, 284508
97	79605200 (193, 194)	Novel Protein sim. GBank gi 4583559 emb CAB40388.1 - (AJ005255) OxyR [Erwinia chrysanthemi]		UNCLASSIFIED	
96	79427000 (195, 196)	Novel Protein sim. GBank gi 1001693 dbj BAA10430 - (D64002) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	264909
99	20466324 (197, 198)	Novel Protein sim. GBank gi 1169479 sp P43925 EFG_HAEIN - ELONGATION FACTOR G (EF-G)		UNCLASSIFIED	264605
100	79840113 (199, 200)	Novel Protein sim. GBank gi 480897 pir J37485 - gene		UNCLASSIFIED	264693
101	80203298 (201, 202)	msg1 protein - mouse		UNCLASSIFIED	265020, 264102, 263972
102	20467259 (203, 204)	Novel Protein sim. GBank gi 2894166 emb CAA11773.1 - (AJ223998) PCZA361.18 [Amycolopsis orientalis]		synthase	264605
103	20466368 (205, 206)	Novel Protein sim. GBank gi 1731040 sp P54509 YQH_H_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	264605
104	80247572 (207, 208)	Novel Protein sim. GBank gi 854085 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264591, 264595, 264602
105	79605206 (209, 210)	Novel Protein sim. GBank gi 1685117 (U70770) - furrowed [Drosophila melanogaster]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complement	264508
106	28382058 (211, 212)	Novel Protein sim. GBank gi 1705505 sp P54729 BS4 MOUSE - BS4 PROTEIN	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264511, 265009
107	80057791 (213, 214)	Novel Protein sim. GBank gi 4887229 gb AAD32244.1 AF150755 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]		ATPase-associated	29331824, 264591, 21906754, 265019
108	80237636 (215, 216)	Novel Protein sim. GBank gi 263577 emb CAB15264 - (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]	Contains protein domain (PF00005) - ABC transporter	transport	18108374, 35695917, 22278996, 264113, 284600, 264602, 264603, 285017, 264910, 264906, 264636, 264766
109	95194148 (217, 218)	Novel Protein sim. GBank gi 233079 emb CAB11265 - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	284758, 264603, 264630, 264636, 264637
110	79582823 (219, 220)				264687
111	39565458 (221, 222)				264564
112	79856038 (223, 224)			UNCLASSIFIED	284908
113	17959439 (225, 226)			UNCLASSIFIED	265007
114	80502101 (227, 228)			UNCLASSIFIED	264769

115	80251003 (229, 230)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52645156, 52645080, 33656970, 264592, 21908754, 27486264, 18108379, 35696423, 264635, 52644332, 18108382
116	81286689 (231, 232)				264905, 284906, 264907, 284908, 284909, 284910, 264758, 285010, 264763, 284682, 264764, 264766, 284885, 264686, 264768, 264769, 33657023, 264693, 33657109, 284628, 18108374, 284631, 264632, 264634, 264636, 264637, 264638, 264639, 56528486, 264585, 264586
117	78636695 (233, 234)			UNCLASSIFIED	264639, 284693
118	80222170 (235, 236)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263974
119	91013071 (237, 238)	Novel Protein sim. GBank gij732526 (U22327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278996, 29331824, 60432289, 265007, 60433438, 264603, 284605, 18108351, 264769, 284689, 265020, 264534, 27486261, 264558, 83373044, 18108385, 264564
120	8756481 (239, 240)	Novel Protein sim. GBank gij2131219 [pir] [S50157] - cyclin-dependent kinase chain SRB10 - yeast [Saccharomyces cerevisiae]		kinase	284603
121	80026153 (241, 242)				284595
122	20457620 (243, 244)	Novel Protein sim. GBank gij2052147 [emb] [CAB08137] - (Z94752) ksgA [Mycobacterium tuberculosis]	Contains protein domain (PF00398) - Ribosomal RNA adenine dimethylases	transferase	264605
123	8758278 (245, 246)				264604
124	79104017 (247, 248)	Novel Protein sim. GBank gij2833385 [sp] [Q43134] [UGST_SORBI - GRANULE-BOUND GLYCOPROTEIN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 265006, 265007, 265008, 265010, 265011, 18108355, 18108379, 18108380, 18108384
125	87797988 (249, 250)	Novel Protein sim. GBank gij475542 (U08255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	264508, 264906, 265009, 264596, 22278002
126	56701283 (251, 252)	Novel Protein sim. GBank gij5102785 [emb] [CAB45200.1] - (AL078308) putative transcriptional regulator [Streptomyces coelicolor]			264511
127	20467267 (253, 254)			UNCLASSIFIED	264605
128	80248473 (255, 256)	Novel Protein sim. GBank gij130120 [sp] [P23620] [PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264907, 264909, 264910, 264600, 264601, 264603, 264605, 18108351, 264693, 264557
129	95280543 (257, 258)	Novel Protein sim. GBank gij2508493 [sp] [P38036] [YGC_B_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35696423, 35695855, 264600, 264602, 284603, 264604, 264605, 264508, 284906, 264564, 284628, 284682, 264555, 264683
130	80085583 (259, 260)	Novel Protein sim. GBank gij854065 [emb] [CAA58337] - (X83413) U88 [Human herpesvirus 6]			264634
131	94895022 (261, 262)	Novel Protein sim. GBank gij1076038 [pir] [S54860 - ABC transporter PstC-2 chain - Mycobacterium tuberculosis]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108376, 264769, 29331826, 264689, 22278996, 265021, 264600, 264511, 264601, 264602, 264605, 284905, 264636

132	10887692 (263, 264)	Novel Protein sim. GBank gii187340[emb]CAB07068] - (Z92771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) Carbamoyl-phosphate synthase (CPSase)	carboxylase	264636
133	94630883 (265, 266)	Novel Protein sim. GBank gii4585838[emb]CAB40932.1] - (AL049630) putative NADH dehydrogenase [Streptomyces coelicolor]		dehydrogenase	264905, 264605, 265021
134	79834860 (267, 268)	Novel Protein sim. GBank gii1460074[emb]CAB01049] - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]			264634
135	19885057 (269, 270)	Novel Protein sim. GBank gii2125896[emb]CAA73511] - (Y13070) polyphosphatase synthase [Streptomyces coelicolor]		synthase	264508
136	79846083 (271, 272)				
137	79819770 (273, 274)				264683, 264685, 264686, 264691, 264692, 264693
138	79635971 (275, 276)	Novel Protein sim. GBank gii5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108374, 18108385, 33657109, 33657182, 265010, 22278998, 265006, 265007, 265008, 265009, 264693
139	86688076 (277, 278)	Novel Protein sim. GBank gii5689912[emb]CAB52075.1] - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01817) Chorismate mutase	dehydrogenase	22278996, 265007, 264910, 60433356, 265010, 264602, 264605, 264766, 264688, 264769, 264693, 32833986, 18108374, 18108387
140	79825759 (279, 280)			UNCLASSIFIED	264908
141	20700094 (281, 282)				264600
142	80028104 (283, 284)	Novel Protein sim. GBank gii3581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]		nuclease	264602, 265017
143	11072274 (285, 286)				
144	95009102 (287, 288)	Novel Protein sim. GBank gii3334127[sp]P97303[BAC2_MOUSE - TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)]		UNCLASSIFIED	264600
145	80027058 (289, 290)	Novel Protein sim. GBank gii3757569[emb]CAA21315] - (AL031863) 1-evidence-predicted by content; 1-method=genefinder.084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster]			263978, 264600, 264910, 264632, 264508, 264563, 264564, 264591, 264556, 264908, 264629, 264639
146	13085662 (291, 292)	Novel Protein sim. GBank gii140807[sp]P24536[Y121_BURCE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN]	Contains protein domain (PF01675) Transposase		22278996, 264602
147	94320366 (293, 294)	Novel Protein sim. GBank gii2827608[emb]CAA16663] - (AL021646) uvrD2 [Mycobacterium tuberculosis]		helicase	264905, 264906, 264809, 264510, 265009, 60433356, 264600, 264601, 264604, 264605, 264687, 264769, 18108365, 65274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank gii2916947[emb]CAA17585] - (AL021999) hypothetical protein Rv0986 [Mycobacterium tuberculosis]		transport	265009, 265010, 264600, 264602, 264603, 264604, 264605, 264693, 33657109, 264636

149	80249373 (297, 298)	Novel Protein sim. GBank gij1723073 sp Q11040 Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01	Contains protein domain (PF00005) - transport ABC transporter	265010, 264600, 264601, 264603, 264604, 27486285, 264636
150	20284748 (289, 300)	Novel Protein sim. GBank gij3724125 emb CAA11905 - (AJ224340) maltose phosphorylase [Lactobacillus sanfrancisco]		264600
151	20726398 (301, 302)	Novel Protein sim. GBank gij729312 sp P07651 DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - Metalloenzyme superfamily	264602
152	95002877 (303, 304)	Novel Protein sim. GBank gij2497952 sp P55667 Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM	peptidase	264602
153	80256665 (305, 306)	Novel Protein sim. GBank gij3123021 sp Q90508 VIT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))	UNCLASSIFIED	264593
154	82305866 (307, 308)	Novel Protein sim. GBank gij418697 pir JN0443 - transcription initiation factor sigma homolog hdb - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	264910, 264762, 264691, 264634 264605
155	20428859 (309, 310)	Novel Protein sim. GBank gij628710 pir JSA1739 - hypothetical protein - Escherichia coli	UNCLASSIFIED	264585
156	39564742 (311, 312)	Novel Protein sim. GBank gij3695013 (AF052586) - CIRA (Pseudomonas aeruginosa)	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/HnfC family	264691
157	10358887 (313, 314)	Novel Protein sim. GBank gij1073072 pir JCS5543 - cmaU protein - Pseudomonas syringae pv. syringae	UNCLASSIFIED	264805
158	79761938 (315, 316)	Novel Protein sim. GBank gij1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00400) - WD domain, G-beta repeat	265008 264605
159	78890376 (317, 318)	Novel Protein sim. GBank gij5304869 emb CAB46028.1 - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00327) - Ribosomal protein L30pL7e	22278996, 264600, 264603, 35695917, 32833986, 35696423, 264636
160	11075119 (319, 320)	Novel Protein sim. GBank gij76177 pir JQCECT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	264112, 264532, 22278002
161	80055007 (321, 322)	Novel Protein sim. GBank gij2661691 emb CAA15795 - (AL009204) putative protease [Streptomyces coelicolor]	UNCLASSIFIED	264639
162	80016371 (323, 324)	Novel Protein sim. GBank gij4416478 gb AA020378 - (AF125999) transposase [Mycobacterium avium]	UNCLASSIFIED	264905, 264907, 264600
163	11692308 (325, 326)	Novel Protein sim. GBank gij76177 pir JQCECT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli	UNCLASSIFIED	264691
164	80077902 (327, 328)	Novel Protein sim. GBank gij76177 pir JQCECT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli	UNCLASSIFIED	264605, 264486
165	10856067 (329, 330)	Novel Protein sim. GBank gij76177 pir JQCECT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli	UNCLASSIFIED	265010
166	88095003 (331, 332)	Novel Protein sim. GBank gij76177 pir JQCECT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli	UNCLASSIFIED	264600
167	16395460 (333, 334)	Novel Protein sim. GBank gij76177 pir JQCECT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli	UNCLASSIFIED	264556, 264557, 264558, 264559
168	80079362 (335, 336)	Novel Protein sim. GBank gij76177 pir JQCECT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli		
169	80239581 (337, 338)	Novel Protein sim. GBank gij76177 pir JQCECT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli		

170	78612364 (339, 340)	Novel Protein sim. GBank gi 140888 sp P27847 YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECQ-PLDB INTERGENIC REGION (F138)	Contains protein domain (PF01810) - LysE type translocator	264906	
171	95293073 (341, 342)			264595, 264604	
172	37797007 (343, 344)	Novel Protein sim. GBank gi 4210905 gb AAD12048.1 - (AF045609) AglG (Shorhizobium meliloti)	transport	264769	
173	57529660 (345, 346)	Novel Protein sim. GBank gi 132854 sp P02387 RL2_ECOLI - 50S RIBOSOMAL PROTEIN L2	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	264769	
174	95293078 (347, 348)	Novel Protein sim. GBank gi 1881350 gb BAA19371 - (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]	ribosomalprot	264769	
175	79758270 (349, 350)	Novel Protein sim. GBank gi 2072722 emb CAB08326 - (Z95121) manA [Mycobacterium tuberculosis]	transport	264510, 264593, 264602, 264603, 264605, 264762, 264693	
176	80066896 (351, 352)	Novel Protein sim. GBank gi 1055198 (U40187) - similar to PIR:A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen [Caenorhabditis elegans]	isomerase	264565	
177	86684852 (353, 354)	Novel Protein sim. GBank gi 2328739 emb CAB10952 - (Z98268) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	UNCLASSIFIED	264907, 264910, 264681, 264558	
178	78559526 (355, 356)	Novel Protein sim. GBank gi 1906596 (U81788) - kinesin-73 [Drosophila melanogaster]	Contains protein domain (PF01513) - Domain of unknown function	264768, 60424179, 264687, 264688, 264769, 29331826, 60432289, 18108376, 264689, 18108387, 32833986, 22278996, 265020, 264600, 264601, 264602, 264603, 264604, 264605, 264635, 264762, 264636, 264908, 264564, 264637, 264638, 264486, 60433356, 264786	
179	20263112 (357, 358)		struct	264693, 33657109, 264635	
180	80488958 (359, 360)	Novel Protein sim. GBank gi 1169387 sp P45256 DNAB_HAEIN - REPLICATIVE DNA HELICASE	UNCLASSIFIED	264563	
181	78585369 (361, 362)	Novel Protein sim. GBank gi 3170615 (AF059485) - DOC4 [Mus musculus]	helicase	264769	
182	80577899 (363, 364)		UNCLASSIFIED	21908767, 264635, 264639, 18108384	
183	11614017 (365, 366)	Novel Protein sim. GBank gi 1076627 pir J554172 - inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	UNCLASSIFIED	264259, 35696052, 56182435, 264511, 265018, 33657109, 264555, 264568	
184	10174167 (367, 368)	Novel Protein sim. GBank gi 4371280 gb AAD18138 - (AC006260) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	264690	
			UNCLASSIFIED	264510	

185	21660822 (369, 370)	Novel Protein sim. GBank gij3006176[emb]CAA18398.1] - (AL02304) putative mma transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	264604
186	80070329 (371, 372)	Novel Protein sim. GBank gij289802[sp]P94408[YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION]		transport	264595
187	80185611 (373, 374)	Novel Protein sim. GBank gij3150260[emb]CAA19179] - (AL023634) cyclin [Schizosaccharomyces pombe]		UNCLASSIFIED	264369
188	20464942 (375, 376)	Novel Protein sim. GBank gij2145853[pi]S72938 - hix protein - Mycobacterium leprae		kinase	264605
189	82338215 (377, 378)	Novel Protein sim. GBank gij1881244[db]BAA19271] - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE. [Bacillus subtilis]		UNCLASSIFIED	35896052, 264602, 264605, 264762, 264689, 35895917, 18108370, 18108372, 264636, 264565
190	80086821 (379, 380)	Novel Protein sim. GBank gij120226[sp]P28725[FKBP_STRCH - FK506-BINDING PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIPIASE) (ROTAMASE)]	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	synthase	284563
191	88095012 (381, 382)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	264508, 264604, 264605, 264769, 264555
192	16333378 (383, 384)	Novel Protein sim. GBank gij4980892[gb]AAD35474.1[AE00171] - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]			264567
193	78910127 (385, 386)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]			264908, 264693
194	20464949 (387, 388)	Novel Protein sim. GBank gij4980892[gb]AAD35474.1[AE00171] - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]			264605
195	13518389 (389, 390)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]		transport	264636
196	95005569 (391, 392)	Novel Protein sim. GBank gij3122305[sp]Q27778[K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)]	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	gaba	264600, 264689, 264638
197	80248665 (393, 394)	Novel Protein sim. GBank gij3122305[sp]Q27778[K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)]	Contains protein domain (PF00365) - Kinase	kinase	264602, 264882, 264692, 18108374
198	79163635 (395, 396)	Novel Protein sim. GBank gij1781203[emb]CAB06110] - (Z83859) gnd [Mycobacterium tuberculosis]			264636
199	78890715 (397, 398)	Novel Protein sim. GBank gij2642222 (AF030885) - telomere-associated recQ-like helicase [Usilago maydis]	Contains protein domain (PF00393) - 6-phosphogluconate dehydrogenases		265008
200	79413849 (399, 400)	Novel Protein sim. GBank gij2894379[emb]CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]		UNCLASSIFIED	264595, 264598
201	86945924 (401, 402)	Novel Protein sim. GBank gij2894379[emb]CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]		UNCLASSIFIED	29331826, 265007, 264512, 33657402, 264598, 265017, 18108351, 264682, 264683, 264767, 264629, 55810764, 264634, 264635, 56182323, 60432113, 22279000

202	79588046 (403, 404)	Novel Protein sim. GBank gi231772 sp P30598 CHS1_USTMA - CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)	Contains protein domain (PF01644) - synthase Chitin synthase	264600
203	79843927 (405, 406)	Novel Protein sim. GBank gi1504042 dbj BAA13220 - (D86984) similar to yeast adenylate cyclase (S56776) [Homo sapiens]		22278995, 29331822, 29331825, 29331827, 264906, 21908754, 264683, 21908766, 21908769, 35696423, 264558
204	79855186 (407, 408)		UNCLASSIFIED	264909
205	10090563 (409, 410)	Novel Protein sim. GBank gi2633808 emb CAB13310 - (Z89111) similar to hypothetical proteins [Bacillus subtilis]	transport	264909
206	8758473 (411, 412)		UNCLASSIFIED	264604
207	20754522 (413, 414)	Novel Protein sim. GBank gi2134381 pir IS0678 - polybromo 1 protein - chicken	UNCLASSIFIED	264556
208	20289261 (415, 416)			264605
209	80071069 (417, 418)	Novel Protein sim. GBank gi2501040 sp O05814 SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS)		264605, 264689
210	80168800 (419, 420)			264905, 264907, 264909, 264766, 264687, 264691, 264629, 18108374, 264638
211	80034539 (421, 422)			263978
212	82442474 (423, 424)	Novel Protein sim. GBank gi5031809 ref NP_005536.1 pISLR - immunoglobulin superfamily containing leucine-rich repeat	UNCLASSIFIED	264508, 264905, 264906, 264807, 264808, 264600, 264762, 264534, 264632, 264634, 264635, 264639, 264486
213	80248562 (425, 426)	Novel Protein sim. GBank gi3122359 sp O33123 LEU2_MYCLE - 3- ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)	Contains protein domain (PF00330) - aconitase family (aconitate hydratase)	22278996, 264508, 264600, 264602, 264603, 264605, 33657023, 264565, 264486
214	80079381 (427, 428)	Novel Protein sim. GBank gi116236 sp P19421 CH60_COXBU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)	Contains protein domain (PF00118) - eph TCP-1/cpn60 chaperonin family	264600, 264693
215	14973283 (429, 430)			
216	80177716 (431, 432)	Novel Protein sim. GBank gi2506924 sp P49754 VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)	UNCLASSIFIED	264629
217	79603634 (433, 434)	Novel Protein sim. GBank gi1173288 sp P38108 IRSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	Contains protein domain (PF00096) - dna_mn_bind	264448
218	80258475 (435, 436)	Novel Protein sim. GBank gi1173288 sp P38108 IRSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	Zinc finger, C2H2 type	264508
219	20438797 (437, 438)	Novel Protein sim. GBank gi1781097 emb CAB06231 - (Z83864) giB [Mycobacterium tuberculosis]	mapolymerase	264594
220	13489572 (439, 440)	Novel Protein sim. GBank gi2984703 (AF052427) - unknown [Trypanosoma cruzi]	synthase	264604
221	11287498 (441, 442)	Novel Protein sim. GBank gi4587313 dbj BAA76708.1 - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]	nucleosidase	264689
			UNCLASSIFIED	264555

222	78862802 (443, 444)	Novel Protein sim. GBank gij1877269[emb]CAB07049] - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 264769, 35696423
223	83053869 (445, 446)			UNCLASSIFIED	264908, 264907, 264603
224	79557920 (447, 448)			UNCLASSIFIED	264604, 264693
225	79559541 (448, 450)			UNCLASSIFIED	264692
226	78172397 (451, 452)	Novel Protein sim. GBank gij2274851[dbj]BAA21515] - (D64159) 3-7 gene product [Homo sapiens]		UNCLASSIFIED	22278998, 264112, 33657023, 263981
227	81777196 (453, 454)	Novel Protein sim. GBank gij868245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]		UNCLASSIFIED	35695917, 264636, 264907
228	79872285 (455, 456)			UNCLASSIFIED	264768, 264907, 264908, 264692, 264593, 264639
229	79838266 (457, 458)			UNCLASSIFIED	264908, 264910
230	11013209 (459, 460)			UNCLASSIFIED	264631
231	20822207 (461, 462)	Novel Protein sim. GBank gij1835114[emb]CAA71733] - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]		UNCLASSIFIED	264906, 264600, 264603, 264692
232	80055035 (463, 464)			UNCLASSIFIED	264600, 264603, 264605, 264687, 264769
233	80063054 (465, 466)	Novel Protein sim. GBank gij2642340 (AF032970) - imidazolone propionate hydrolase [Pseudomonas putida]	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	264604
234	7523998 (467, 468)	Novel Protein sim. GBank gij3510505 (AF030881) - polypeptide [Fugu rubripes]		UNCLASSIFIED	264369
235	80203671 (469, 470)	Novel Protein sim. GBank gij21046809[emb]CAB08605] - (Z95398) PckA [Mycobacterium leprae]		UNCLASSIFIED	264106
236	78940001 (471, 472)			UNCLASSIFIED	264905
237	11755273 (473, 474)			UNCLASSIFIED	264681
238	79461401 (475, 476)			UNCLASSIFIED	264639
239	82435190 (477, 478)	Novel Protein sim. GBank gij2495617[sp]Q57252[YDIJ_HAEIN - HYPOTHETICAL PROTEIN H11163]	Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron-sulfur cluster binding domains.	UNCLASSIFIED	264906, 265010, 264603, 264762, 264682, 264636, 264638, 264486
240	21635375 (479, 480)	Novel Protein sim. GBank gij3183458[sp]P75796[YLIA_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA]	transport	UNCLASSIFIED	264259, 264769
241	80377307 (481, 482)	Novel Protein sim. GBank gij3875920[emb]CAB0411] - (Z81503) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D68888 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264908, 264909, 264764, 264639
242	82148454 (483, 484)			UNCLASSIFIED	264489, 264907, 264908, 264511, 264760, 264764, 264692, 264635, 264637
243	79633207 (485, 486)			UNCLASSIFIED	264906
244	80248582 (487, 488)	Novel Protein sim. GBank gij2624302[emb]CAA15575] - (AL008967) ald [Mycobacterium tuberculosis]		UNCLASSIFIED	264600, 264602, 264605, 264769, 264689
245	79663543 (489, 490)	Novel Protein sim. GBank gij2920625 (AF044499) - vgrE protein [Escherichia coli]		UNCLASSIFIED	264907, 264758
246	79162929 (491, 492)	Novel Protein sim. GBank gij5420387[emb]CAB6679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01106) - NiU-like domain		264637, 18108381, 18108387, 264565

247	79873185 (493, 494)	Novel Protein sim. GBank gij1838006[emb] [CAB06648] - (Z85982) argB [Mycobacterium tuberculosis]		kinase	264909, 264691, 35696423, 18108387
248	80488883 (495, 496)	Novel Protein sim. GBank gij1168574[sp]P42464[ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35696286, 264907, 264511, 264602, 264768, 264688, 265021, 35695855, 18108385
249	78764845 (497, 498)			UNCLASSIFIED	264907, 264910, 265011, 264762, 264636
250	78619980 (499, 500)				21908768, 264692
251	84359489 (501, 502)			UNCLASSIFIED	52645156, 29331822, 29331824, 52644045, 265018, 21906765, 21906768, 265020, 27486261, 27486265, 35695763, 18108376, 264556, 264559, 264565
252	79737756 (503, 504)	Novel Protein sim. GBank gij3327166[dbj]BAA31651] - (AB014576) KIAA0676 protein [Homo sapiens]			264685, 264687, 264632
253	20443124 (505, 506)	Novel Protein sim. GBank gij3038880[emb] [CAA18513] - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	264604
254	80027421 (507, 508)	Novel Protein sim. GBank gij3915488[sp]O34961[YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION		UNCLASSIFIED	264508, 264906, 264602, 264687, 265021, 264486
255	11388315 (508, 510)	Novel Protein sim. GBank gij1665720[dbj]BAA04134] - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264593
256	80028158 (511, 512)	Novel Protein sim. GBank gij465787[sp]P34422[YL31_CAEEL - HYPOTHETICAL 86.0 KD PROTEIN F44B9.1 IN CHROMOSOME III	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	264602, 264692
257	20289282 (513, 514)	Novel Protein sim. GBank gij1172039[sp]P42315[SCOA_BACSU - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	264605
258	20459464 (515, 516)	Novel Protein sim. GBank gij3127836[emb] [CAA18902] - (AL023496) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264604
259	78910152 (517, 518)			collagen	264681, 264686, 264692
260	20378437 (519, 520)			UNCLASSIFIED	264692, 264556
261	20265883 (521, 522)	Novel Protein sim. GBank gij123761[sp]P24221[HUTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	264600
262	80189317 (523, 524)			UNCLASSIFIED	285017, 264369
263	88095045 (525, 528)	Novel Protein sim. GBank gij3924708[emb] [CAA84646] - (Z35597) Weak similarity with sea squirt nidogen precursor protein (bias score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...		UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 264758, 264596, 264804, 265019, 264805, 264760, 18108351, 264763, 264764, 264288, 264768, 264768, 264769, 264691, 264692, 264693, 264628, 264634, 264635, 264555, 264636, 264638, 264639
264	87370826 (527, 528)	Novel Protein sim. GBank gij3043734[dbj]BAA25531] - (AB011177) KIAA0605 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	264259, 264908, 21808754, 265018, 265019, 265020

265	95355646 (528, 530)	Novel Protein sim. GBank gij4509624[dj][BAA76834.1] - (AB023207) KIAA0990 protein [Homo sapiens]		kinase	264488, 35696286, 29331824, 56182181, 35696052, 264508, 264905, 264908, 264907, 66712502, 264908, 264909, 264511, 264512, 264910, 264592, 264595, 264758, 264598, 55811386, 264600, 265017, 264603, 264604, 264605, 264760, 18108351, 264762, 264681, 264764, 264288, 264766, 264768, 264769, 21906765, 21908767, 21908769, 265020, 264691, 33657023, 33657109, 33657182, 264628, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 83373044, 56526488, 87168518, 264564, 264566, 264488
266	79588075 (531, 532)			UNCLASSIFIED	264600
267	11362222 (533, 534)			UNCLASSIFIED	264878
268	79509568 (535, 536)			UNCLASSIFIED	264687, 264769, 264689
269	80025810 (537, 538)			UNCLASSIFIED	264602
270	84361144 (539, 540)	Novel Protein sim. GBank gij4507367[ref]NP_003182.1pTARS - threonyl-tRNA synthetase		UNCLASSIFIED	264693
271	79552301 (541, 542)	Novel Protein sim. GBank gij4980738[g]AAD35331.1(AE00170) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]		UNCLASSIFIED	264909, 264693
272	9674778 (543, 544)	Novel Protein sim. GBank gij1168224[sp]P44569[5]NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR		synthase	264908
273	12840694 (545, 546)	Novel Protein sim. GBank gij1168224[sp]P44569[5]NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR		UNCLASSIFIED	264688
274	39524246 (547, 548)	Novel Protein sim. GBank gij3253159 (AF005355) - Translation Initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264564
275	82787041 (549, 550)	Novel Protein sim. GBank gij1134920[sp]P21997[SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)]		UNCLASSIFIED	264807, 264908, 264909, 264766, 264768, 264691, 264632, 264636
276	86671073 (551, 552)	Novel Protein sim. GBank gij1134920[sp]P21997[SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)]			265008, 60432229
277	80079735 (553, 554)	Novel Protein sim. GBank gij128021[sp]P20964[OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN]		ribosomal prot	264600, 18108387
278	12866947 (555, 556)	Novel Protein sim. GBank gij128021[sp]P20964[OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN]		UNCLASSIFIED	264689
279	95292719 (557, 558)	Novel Protein sim. GBank gij128021[sp]P20964[OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN]		nuclease	264508, 264604, 21906764, 264638, 264557, 264404
280	5603617 (559, 560)	Novel Protein sim. GBank gij128021[sp]P20964[OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN]			264259
281	80249599 (561, 562)	Novel Protein sim. GBank gij128021[sp]P20964[OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN]			18108392, 264634, 264555, 264558, 264557, 264558
282	18598682 (563, 564)			UNCLASSIFIED	285019
283	20814211 (565, 566)			UNCLASSIFIED	264555

284	91212160 (567, 568)	Novel Protein sim. GBank gi 2429094 (U58632) - acetyl xylan esterase; AxeA [Thermotoga neapolitana]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696052, 29331828, 264508, 264905, 264600, 264602, 264605, 264682, 264764, 56181562, 21906764, 18108376, 264636, 264559, 18108387
285	8757940 (569, 570)	Novel Protein sim. GBank gi 2072674 (emb CAB08305) - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	264603
286	80503235 (571, 572)	Novel Protein sim. GBank gi 765323 (bbs 157676 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori]; silkworms. Peptide Partial, 633 aa] [Bombyx mori]		UNCLASSIFIED	35696052, 264769, 264638
287	12745521 (573, 574)	Novel Protein sim. GBank gi 765323 (bbs 157676 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori]; silkworms. Peptide Partial, 633 aa] [Bombyx mori]		UNCLASSIFIED	264689
288	20756502 (575, 576)	Novel Protein sim. GBank gi 1870009 (emb CAB06860) - (Z92539) hypothetical protein Rv1018 [Mycobacterium tuberculosis]	Contains protein domain (PF00440) - Bacterial regulatory proteins. telR family	UNCLASSIFIED	264557
289	80043804 (577, 578)	Novel Protein sim. GBank gi 1870009 (emb CAB06860) - (Z92539) hypothetical protein Rv1018 [Mycobacterium tuberculosis]			264593, 264600
290	80430175 (579, 580)	Novel Protein sim. GBank gi 2506684 (sp P40120) (YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264768
291	20747431 (581, 582)	Novel Protein sim. GBank gi 525182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	264601
292	80052555 (583, 584)	Novel Protein sim. GBank gi 525182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	264605
293	80082519 (585, 586)	Novel Protein sim. GBank gi 1718065 (sp P53528) (UVRD_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG	helicase		264909, 264605, 264687, 264689, 264692
294	79830303 (587, 588)	Novel Protein sim. GBank gi 117422 (sp P10040) (CRB_DROME - CRUMBS PROTEIN PRECURSOR (95F)	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696052, 264906, 265011, 264628, 55811576
295	79444180 (589, 590)	Novel Protein sim. GBank gi 1181619 (dbj BAA11565) - (D82364) a variant of TSC-22 [Gallus gallus]			52844507, 29331822, 264592, 265020, 264639
296	79607076 (591, 592)	Novel Protein sim. GBank gi 3649789 (dbj BAA33403) - (AB012228) SecA [Vibrio alginolyticus]		synthase	264508
297	79631287 (593, 594)	Novel Protein sim. GBank gi 5689967 (emb CAB52004.1) - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264905, 264687, 264638
298	80418898 (595, 596)			UNCLASSIFIED	264905, 264691, 264639, 264766

299	95283298 (597, 598)	Novel Protein sim. GBank gij220637(dbjBAA01477) - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264488, 263994, 56994075, 22278997, 22278998, 22278999, 20281099, 29331824, 29331825, 29331826, 80432289, 29331827, 29331828, 264905, 264906, 264907, 264908, 52844045, 264909, 264511, 265008, 264910, 264595, 264596, 264758, 33657084, 87168559, 265018, 265019, 264764, 264288, 264766, 264687, 56181582, 264769, 21906765, 21906768, 21906769, 33657023, 264692, 33637109, 27486281, 18108370, 264628, 264629, 55811576, 35695855, 264631, 264634, 264635, 264636, 264639, 83373044, 18108387, 87168518, 22279000, 22279002, 264585, 264586, 264587
300	20711340 (599, 600)	Novel Protein sim. GBank gij145922 (M20981) - iron	UNCLASSIFIED	264602
301	13511332 (601, 602)	Novel Protein sim. GBank gij145922 (M20981) - iron	transport	264687
302	9875260 (603, 604)	Novel Protein sim. GBank gij1174661spjP44594TGT_HAEIN - QUEUINE TRNA-RIBOSYL TRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)		264908
303	79574895 (605, 606)	Novel Protein sim. GBank gij67985spjHJNNAV - helicase		264689
304	20711344 (607, 608)	(EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus	helicase	264602
305	80412520 (609, 610)	Novel Protein sim. GBank gij728857spjP40602APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		264763
306	8515876 (611, 612)	Novel Protein sim. GBank gij16575541gbjAAB18082.1] - (U73857) hypothetical protein [Escherichia coli]	UNCLASSIFIED	263978
307	80222801 (613, 614)	Novel Protein sim. GBank gij1710612spjQ10793jRNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)	UNCLASSIFIED	265010, 21906768, 265020, 18108374, 263977
308	80064305 (615, 616)	Novel Protein sim. GBank gij1710612spjQ10793jRNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)	Contains protein domain (PF01351) - Ribonuclease HII	264910, 264600, 264605, 264687, 264689, 264638, 18108387
309	80504138 (617, 618)	Novel Protein sim. GBank gij54203871embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		264769
310	80053616 (619, 620)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]		264603
311	11090659 (621, 622)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]	synthase	264602
312	80054347 (623, 624)		UNCLASSIFIED	264566
313	80046168 (625, 626)		UNCLASSIFIED	264603, 264567

314	87645112 (627, 628)	Novel Protein sim. GBank gj13661583 (AF092175) - ikaros [Danio rerio]	Contains protein domain (PF00320) - GATA zinc finger	dna_rna_bind	264259, 60432289, 29331828, 264905, 264906, 264908, 264909, 265008, 264910, 60432229, 33657402, 60433438, 33109954, 265011, 265017, 264603, 265018, 264288, 264768, 264692, 35695763, 264628, 264629, 264639, 60170394, 22279002, 264568
315	82356091 (628, 630)	Novel Protein sim. GBank gj11652620(dbj)BAA17540(- (D90907) pyridine nucleotide transhydrogenase beta subunit [Synechocystis sp.]			264508, 264600, 264762, 264687, 264768, 52644229, 264769, 264689, 264635, 264636, 264638, 264486
316	78911071 (631, 632)			UNCLASSIFIED	264693
317	20466944 (633, 634)	Novel Protein sim. GBank gj118244(sp)P24176(DAPE, ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (SDAP)		UNCLASSIFIED	264605
318	94141838 (635, 636)	Novel Protein sim. GBank gj14680229(gb)AAD27583.1(AF118274) DNB-5 [Homo sapiens]	Contains protein domain (PF00526) Dictyostelium (slime mold) repeats	transport	264908, 264809, 264910, 264593, 264594, 264760, 264288, 264768, 264769, 21908769, 264691, 264693, 264628, 65274791, 264635, 264636, 264638, 83373044, 22279002, 264568
319	17289360 (637, 638)	Novel Protein sim. GBank gj1148693(emb)CAA60220(- (X86499) rbcC [Clostridium perfringens]		transport	265018
320	13527675 (639, 640)	Novel Protein sim. GBank gj2611033(sp)O05314(GLGC_MYCTU - GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)		synthase	264687
321	84134387 (641, 642)	Novel Protein sim. GBank gj11680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danio rerio]		cyto450	264509, 264906, 264907, 264908, 265009, 264596, 264764, 264628, 264634, 264635, 264638, 264639, 83373044, 264567
322	66489053 (643, 644)	Novel Protein sim. GBank gj1160355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	55811150, 264691, 60431528, 55810764
323	94653725 (645, 646)			UNCLASSIFIED	264488, 265009, 264593, 264628, 264635
324	78174383 (647, 648)				264687
325	78862691 (649, 650)			UNCLASSIFIED	264693
326	28774974 (651, 652)			UNCLASSIFIED	264288, 18108385
327	78776267 (653, 654)	Novel Protein sim. GBank gj1451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]			264488, 264805, 264509, 264910
328	80253202 (655, 656)			UNCLASSIFIED	264592
329	10173821 (657, 658)			UNCLASSIFIED	264510
330	86597767 (659, 660)			UNCLASSIFIED	264259, 264908
331	78754988 (661, 662)	Novel Protein sim. GBank gj14191358 (AF087825) - claudin-7 [Mus musculus]		transcriptfactor	264910, 264687, 264689, 264636, 264567
332	80071440 (663, 664)	Novel Protein sim. GBank gj114049(sp)P19480(AHPF_SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN)		reductase	35696423, 264636, 264638, 264565
333	13009555 (665, 666)				264687

334	80230771 (667, 668)	Novel Protein sim. GBank gij3222228pirij322227 - glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905, 264600, 264604, 264486
335	80057028 (668, 670)	Novel Protein sim. GBank gij2193938jembjCAB09602j - (Z96800) glpQ2 [Mycobacterium tuberculosis]		esterase	264907, 264603, 264693, 18108374, 264636, 18108387
336	80414319 (671, 672)			UNCLASSIFIED	265009, 264766, 264686
337	11090829 (673, 674)				264602
338	95413134 (675, 676)	Novel Protein sim. GBank gij5454074jrefjNP_006303.1pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	nuc1_recp	264569, 18108397, 22278998, 29331822, 29381099, 29331824, 58182181, 68714117, 29331825, 35696052, 29331828, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 265006, 265008, 264910, 265009, 264758, 55812038, 65274444, 265011, 87168559, 265017, 265018, 265019, 264760, 55811150, 264681, 264762, 18108351, 264682, 264764, 264766, 264685, 264686, 264768, 52644229, 264689, 55811957, 35695917, 264692, 264693, 264628, 18108370, 18108374, 55811576, 35696423, 35695855, 264635, 264555, 264636, 264556, 264637, 264557, 18108380, 264638, 264558, 264639, 18108381, 83373044, 18108385, 87168518, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank gij4001713jdbjBAA35087.1j - (AB015679) DnaK [Porphyrinomonas gingivalis]		eph	264593
340	80504149 (679, 680)	Novel Protein sim. GBank gij2842699jQ92333jUBPC SCHPO - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)		ubiquitin	264905, 265019, 264769, 18108374
341	11075198 (681, 682)	Novel Protein sim. GBank gij2688580 (AE001166) - conserved hypothetical protein [Borrelia burgdorferi]	Contains protein domain (PF00290) - Tryptophan synthase alpha chain	isomerase	264605
342	80054186 (683, 684)	Novel Protein sim. GBank gij1684738jembjCAA70601j - (Y09452) Yed J hypothetical protein [Pseudomonas syringae]			264603, 264604
343	20466792 (685, 686)				
344	80428870 (687, 688)	Novel Protein sim. GBank gij2117275jembjCAB09104j - (Z95618) hypothetical protein Rv0807 [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 264600, 264605, 264768, 18108370, 18108374, 35695855
345	80258853 (689, 690)	Novel Protein sim. GBank gij3023317jSpjQ48935jAPHA_MYCRA - ACETYL POLYAMINE AMINOHYDROLASE		histone	264593
346	78831058 (691, 692)	Novel Protein sim. GBank gij4239787jembjCAA75437j - (Y15166) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905

347	79158195 (693, 694)	Novel Protein sim. GBank glt731675[sp]P38795 YH4_YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION		UNCLASSIFIED	265006, 265008, 265010, 265018, 263967, 263981
348	80020208 (695, 696)	Novel Protein sim. GBank glt1073610[pi]S47672 - ugpB protein - Escherichia coli		transport	264602, 18108351, 18108387
349	17282112 (697, 698)	Novel Protein sim. GBank glt3261599[emb]CAB009171 - (Z77137) hypothetical protein Rv1277 [Mycobacterium tuberculosis]		nuclease	265007 265009, 264769, 264689, 18108370
350	80502370 (699, 700)	Novel Protein sim. GBank glt2959367[emb]CAA179211 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]		glycoprotein	264769, 264905, 264908
351	80501805 (701, 702)	Novel Protein sim. GBank glt4416302[gb]AAD203071 - (AF105716) copla-type pol polyprotein [Zea mays]		protease	264595
352	11611585 (703, 704)	Novel Protein sim. GBank glt1174887[sp]P42873 URE1_STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	264604
353	80061653 (705, 706)	Novel Protein sim. GBank glt115157[sp]P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		UNCLASSIFIED	264628
354	56826130 (707, 708)	Novel Protein sim. GBank glt115157[sp]P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED	264909, 264595, 264683, 22279002
355	80046344 (709, 710)	Novel Protein sim. GBank glt115157[sp]P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		oxidase	264605
356	80043835 (711, 712)	Novel Protein sim. GBank glt115157[sp]P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		UNCLASSIFIED	264768
357	80070566 (713, 714)	Novel Protein sim. GBank glt115157[sp]P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		UNCLASSIFIED	264604, 264769
358	37032756 (715, 716)	Novel Protein sim. GBank glt115157[sp]P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		UNCLASSIFIED	264594
359	80501488 (717, 718)	Novel Protein sim. GBank glt115157[sp]P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		transferase	22278996, 264259, 29331822, 29331824, 264605, 55811957, 265022
360	80026748 (719, 720)	Novel Protein sim. GBank glt115157[sp]P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		amylase	264688
361	80584075 (721, 722)	Novel Protein sim. GBank glt115157[sp]P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		UNCLASSIFIED	
362	13089485 (723, 724)	Novel Protein sim. GBank glt113784[sp]P25719 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		UNCLASSIFIED	
363	79750145 (725, 726)	Novel Protein sim. GBank glt113784[sp]P25719 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		UNCLASSIFIED	
364	82443593 (727, 728)	Novel Protein sim. GBank glt113784[sp]P25719 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)	Contains protein domain (PF00420) - NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	dehydrogenase	264586 264769, 264602, 264604, 264508, 264762, 264638, 264488

365	88040288 (728, 730)	Novel Protein sim. GBank gij4928268[gb AAD33924.1] - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	264488, 21906766, 21906767, 55811576, 21906769, 29148629, 22278995, 22278996, 265020, 265022, 264634, 264691, 264593, 33657023, 33657402, 264693, 264639, 264594, 29331824, 264758, 18108385, 29331827, 87168559, 265018, 22279000, 265019, 264482, 264761, 264681, 18108351, 265017, 264757
366	81821838 (731, 732)	Novel Protein sim. GBank gij4503843[ref NP_003908.1 pGZAD - UNKNOWN	Contains protein domain (PF01602) - Adaplin N terminal region	60424179, 65274572, 56182575, 22278994, 56994075, 22278998, 264259, 29331822, 29331824, 56182181, 60424269, 88714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264905, 264828, 56182435, 265008, 264512, 265008, 264591, 55812038, 55811386, 265010, 87168559, 265017, 265018, 264604, 265019, 55811150, 264448, 264369, 264288, 264686, 264768, 56181562, 21906769, 55811957, 336595917, 265022, 60170815, 33657023, 65274620, 18108365, 263967, 33657109, 33657349, 35695763, 264628, 18108376, 55811576, 65274791, 35695855, 56182323, 83373044, 60432113, 264563, 264564, 264567
367	95357471 (733, 734)	Novel Protein sim. GBank gij3913029[sp P94967 ALR_MYCSM - ALANINE RACEMASE	UNCLASSIFIED	264509, 264508, 264604, 264605, 264636
370	88090366 (739, 740)	Novel Protein sim. GBank gij3249559 (AF018261) - EH domain binding protein Epsin [Rattus norvegicus]	UNCLASSIFIED	264905, 264592, 264605, 264766, 264691
371	95292599 (741, 742)	Novel Protein sim. GBank gij2995299[emb CAA18328] - (AL022268) putative IRNA delta(2)-isopentenylpyrophosphate transferase [Streptomyces coelicolor]	Contains protein domain (PF01715) - IPP transferase	264905, 264906, 264510, 264600, 264601, 264602, 264603, 265018, 264604, 264605, 265021, 264692, 264636, 264564
372	80021107 (743, 744)	Novel Protein sim. GBank gij2506393[sp P31576 FIXX_ECOLI - FERREDOXIN LIKE PROTEIN	UNCLASSIFIED	264564
373	79863766 (745, 746)	Novel Protein sim. GBank gij3341640[emb CAA13164] - (AJ231122) z611 [Vibrio cholerae]	UNCLASSIFIED	264909, 264903, 264906
374	79847568 (747, 748)	Novel Protein sim. GBank gij5456934[gb AAD43716.1] - (AF152322) protocadherin gamma A2 [Homo sapiens]	cadherin	55274572, 264259, 29331826, 56182435, 60433356, 60433438, 264757, 55812038, 264758, 55811957, 264690, 33657023
375	91230181 (749, 750)	Novel Protein sim. GBank gij1805408[dbj BAA08970] - (D50453) homologues to nitrite hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	UNCLASSIFIED	264769
376	80505214 (751, 752)	Novel Protein sim. GBank gij1805408[dbj BAA08970] - (D50453) homologues to nitrite hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	UNCLASSIFIED	264769
377	10338083 (753, 754)			264906

378	80056153 (755, 756)	Novel Protein sim. GBank gjl1076013 pir A49930 - carb protein homolog - Mycobacterium bovis (strain BCG) (fragment)	Contains protein domain (PF00289) - synthase (CPSase)	UNCLASSIFIED	265008, 264555
379	80503437 (757, 758)	Novel Protein sim. GBank gjl216556 dbj BAA02174 - (D12651) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - dehydrogenase PQQ enzyme repeat		264769
380	80060937 (759, 760)	Novel Protein sim. GBank gjl3327136 dbj BAA31636 - (A8014561) KIAA0681 protein [Homo sapiens]		UNCLASSIFIED	264604
381	11769027 (761, 762)				264684
382	80054377 (763, 764)				264592
383	83258025 (765, 766)				264595, 265017, 265021, 264638, 87168518, 22279002
384	95314255 (767, 768)			UNCLASSIFIED	264259, 29331822, 60432288, 29331827, 264288, 264766, 263987, 85274791, 35695855, 263981, 83373044, 264557
385	10237678 (769, 770)				264692
386	79633434 (771, 772)	Novel Protein sim. GBank gjl1073456 pir S47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00465) - dehydrogenase Iron-containing alcohol		264806
387	17960637 (773, 774)	Novel Protein sim. GBank gjl1460074 emb CAB01049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741376 (775, 776)	Novel Protein sim. GBank gjl4240169 dbj BAA74863.1 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	homeobox	3569286, 264905, 66712502, 60432229, 264593, 60433358, 264686, 264688, 21906765, 264681, 22279000, 264482
389	79316971 (777, 778)			UNCLASSIFIED	18108394, 22278996, 264630, 264556, 22279002
390	80079949 (779, 780)	Novel Protein sim. GBank gjl854065 emb CAA56337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264600
391	7657302 (781, 782)				264482
392	79786056 (783, 784)			UNCLASSIFIED	264908
393	33206031 (785, 786)	Novel Protein sim. GBank gjl3378523 emb CAA08867 - (AJ009832) cyclomaltohexanase glucanotransferase [Thermoloba neapolitana]		synthase	264602, 21906764
394	10104463 (787, 788)				
395	80229010 (789, 790)			UNCLASSIFIED	264683
396	20436224 (791, 792)	Novel Protein sim. GBank gjl2677780 (U70327) - unknown [Pareitropus polyactis]	Contains protein domain (PF00047) - struct immunoglobulin domain	UNCLASSIFIED	264508, 264563
397	80417014 (793, 794)	Novel Protein sim. GBank gjl4507909 ref NP_000388.1 pWAS - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)			265007, 265009, 264508, 264556, 264629, 264766
398	91230517 (795, 796)	Novel Protein sim. GBank gjl1518458 (U45998) - mitochondrial solute carrier [Onchocerca volvulus]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	transport	18108398, 22278995, 22278996, 56994075, 22278999, 264259, 29331824, 29331826, 264905, 264908, 265007, 265008, 265009, 21906754, 33657084, 265017, 264448, 264288, 264766, 21908765, 21908768, 21908767, 265020, 265021, 33657023, 33657109, 264628, 35886423, 35695855, 264952, 18108380, 264587, 18108391

398	80055278 (797, 798)	Novel Protein sim. GBank gi 3358091 dbj BAA31995 - (AB015974) glycerol kinase [Pseudomonas tolaasii]	Contains protein domain (PF00370) - Kinase FGY family of carbohydrate kinases		264592, 264595
400	94117490 (789, 800)	Novel Protein sim. GBank gi 728835 sp P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII	Contains protein domain (PF00560) - cadherin Leucine Rich Repeat		18108394, 56182575, 22278995, 22278997, 22278998, 264259, 29331824, 265008, 265007, 265009, 60432229, 33657402, 21908754, 265010, 265017, 265018, 265019, 18108351, 18108357, 21908765, 265021, 265022, 264691, 264692, 33657023, 18108370, 65274791, 264634, 264636, 60170394, 56182323, 264594
401	11397481 (801, 802)	Novel Protein sim. GBank gi 428292 gb AA033527.1 AF13211 - (AF132117) FhuA [Staphylococcus aureus]		transport	
402	95420294 (803, 804)	Novel Protein sim. GBank gi 5689487 dbj BAA83027.1 - (AB028988) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - phosphatase Src homology domain 2		65274572, 56182575, 35696286, 22278996, 22278998, 264093, 264259, 29331822, 29331824, 29331825, 29331828, 60432289, 29331827, 29331828, 264908, 264907, 264909, 265008, 264511, 265007, 265008, 264910, 264591, 33657402, 60433356, 60433438, 264596, 21908754, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264881, 18108351, 264882, 264448, 264288, 264684, 264766, 264767, 264688, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 265020, 265021, 265022, 264690, 264693, 65274620, 35695763, 264628, 18108370, 264629, 18108379, 35696423, 55811576, 264635, 264636, 264557, 264639, 18108385, 22279002, 264563, 264564, 264565, 264568, 264768, 264632, 264639, 264563, 264682
403	80439913 (805, 806)			UNCLASSIFIED	
404	11809865 (807, 808)			polymerase	
405	79471280 (809, 810)	Novel Protein sim. GBank gi 2661649 emb CAA15755 - (AL009198) dnaE2 [Mycobacterium tuberculosis]			265009, 264682
406	78634172 (811, 812)		Contains protein domain (PF00159) - Pancreatic hormone peptides	UNCLASSIFIED	18108357, 264693
407	80478229 (813, 814)			UNCLASSIFIED	264769
408	80078958 (815, 816)			UNCLASSIFIED	264600
409	5840527 (817, 818)	Novel Protein sim. GBank gi 3047117 (AF058919) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]		helicase	264259

410	95357486 (819, 820)	Novel Protein sim. GBank gi 475016 dbj BAA06184 - (D29801) Unknown [Mus musculus]		UNCLASSIFIED	264489, 52646365, 52646842, 56181686, 35696286, 52645080, 29331822, 29331824, 56182181, 29331825, 60424269, 35696052, 33656970, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 265007, 264512, 265008, 264910, 33657402, 264758, 52646317, 55811386, 265010, 265011, 265017, 264604, 265018, 55811150, 264762, 264764, 264766, 264687, 264768, 264769, 52644229, 21906768, 265020, 265021, 264534, 52644150, 264692, 33657023, 65274620, 33657109, 33657182, 27488281, 35695783, 264628, 264629, 60431528, 18108376, 263978, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 56182323, 264559, 60432113, 22279002, 264563, 264565, 264486
411	80501670 (821, 822)			UNCLASSIFIED	264769
412	80241662 (823, 824)				264907, 264910, 263973, 22279002
413	11076446 (825, 826)	Novel Protein sim. GBank gi 3261784 emb CAB08997 - (Z95558) hpx [Mycobacterium tuberculosis]		eph	264605
414	82050554 (827, 828)	Novel Protein sim. GBank gi 179036 sp P20707 OD01_AZOVI - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)		dehydrogenase	18108374, 264760, 264769, 264602, 264638, 264603, 264909, 264605
415	84453144 (829, 830)	Novel Protein sim. GBank gi 4686350 gb AAD31273.1 AF13202 - (AF132025) rhophilin [Drosophila melanogaster]		UNCLASSIFIED	264908, 87168518
416	80402775 (831, 832)	Novel Protein sim. GBank gi 2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium etli]		kinase	264488, 264600, 264602, 264764, 264636
417	20153767 (833, 834)	Novel Protein sim. GBank gi 1709171 sp P52311 MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) (M.XORII)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase		264605
418	94125841 (835, 836)			UNCLASSIFIED	264689, 264693
419	95314273 (837, 838)			collagen	264908, 264910, 264764, 264639
420	37036349 (839, 840)	Novel Protein sim. GBank gi 3261659 emb CAB03751 - (Z81368) hypothetical protein Rv2419c [Mycobacterium tuberculosis]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	phosphatase	264769
421	95292942 (841, 842)	Novel Protein sim. GBank gi 2916942 emb CAA17580 - (AL021999) hypothetical protein Rv0981 [Mycobacterium tuberculosis]	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264908, 264600, 264601, 264603, 264604, 264760, 264769
422	79471293 (843, 844)	Novel Protein sim. GBank gi 231752 sp Q00767 CHB1_STRAL - 60 KD CHAPERONIN 1 (PROTEIN CPN60 1) (GROEL PROTEIN 1) (HSP58)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	22278996, 264682, 18108376, 18108387
423	79604948 (845, 846)			UNCLASSIFIED	264509

424	7896557 (847, 848)	Novel Protein sim. GBank gi 4826814 ref NP_004977.1 pKTN1 - kinesin receptor			265019	
425	80431450 (849, 850)	Novel Protein sim. GBank gi 1703701 bbs 178462 - KRP5=kinesin-related protein [rats, testes, Peptide Partial, 167 aa]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264909, 265007, 55811386, 264768, 55810764	
426	80064522 (851, 852)				264605, 264559	
427	80057232 (853, 854)	Novel Protein sim. GBank gi 231829 sp P29829 COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED	264603, 264636	
428	79487798 (855, 856)	Novel Protein sim. GBank gi 81286 p j S22697 - extensin - Volvox cartter (fragment)		UNCLASSIFIED	264683	
429	80091252 (857, 858)	Novel Protein sim. GBank gi 1806154 emb CAB06451 - (284395) hypothetical protein Rv0888 [Mycobacterium tuberculosis]		UNCLASSIFIED	35698423, 35695763, 35695855, 265017, 264584, 264762	
430	80504192 (859, 860)	Novel Protein sim. GBank gi 1806154 emb CAB06451 - (284395) hypothetical protein Rv0888 [Mycobacterium tuberculosis]		reductase	264508, 264905, 264509, 264908, 264909, 265008, 264600, 264687, 264769, 264689, 264636, 264638, 18108385, 264488	
431	20624249 (861, 862)				264568	
432	16525372 (863, 864)	Novel Protein sim. GBank gi 3123552 emb CAA18609 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	265020	
433	81494303 (865, 866)	Novel Protein sim. GBank gi 2495272 sp Q89626 CDX2_HUMAN - HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	264907, 264908, 264909, 264910, 264592, 264595, 264758, 264604, 264760, 264762, 264763, 264636, 264637, 22279002	
434	94326323 (867, 868)	Novel Protein sim. GBank gi 114105 sp P08532 ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH		UNCLASSIFIED	55812038, 56182181, 56181562, 29331828, 35896052, 55810764, 55811576, 65274791, 35695855, 60432113, 55811150, 264636, 264766	
435	80502738 (869, 870)	Novel Protein sim. GBank gi 114105 sp P08532 ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH		transport	264595, 264769	
436	41085953 (871, 872)			UNCLASSIFIED	265020, 22279002	
437	11399291 (873, 874)			UNCLASSIFIED	264593	
438	11773835 (875, 876)			UNCLASSIFIED	264686	
439	80018495 (877, 878)	Novel Protein sim. GBank gi 3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]			264905, 264600, 264602, 264604	
440	79841062 (879, 880)	Novel Protein sim. GBank gi 2291232 gb AA865351.1 - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA), Score=268.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)		35696052, 264905, 264908, 264909, 265011, 35698423	
441	20396935 (881, 882)	Novel Protein sim. GBank gi 5639946 gb AAD45904.1 AF16132 - (AF161328) histidine kinase CstS [Corynebacterium diphtheriae]			264605	
442	85281058 (883, 884)	Novel Protein sim. GBank gi 1184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909	
443	82456427 (885, 886)	Novel Protein sim. GBank gi 568993 emb CAB52056.1 - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	35696052, 264508, 264906, 264512, 264604, 264762, 264769, 264689, 264636	
444	11395897 (887, 888)	Novel Protein sim. GBank gi 1763249 dbj BAA11726 - (D83026) homologous to citrate-sodium symport (citrate transporters); hypothetical [Bacillus subtilis]		UNCLASSIFIED	264591	

445	79552709 (889, 890)	Novel Protein sim. GBank gij5531272[emb]CAB50897.1] - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	264693
446	78810937 (891, 892)	Novel Protein sim. GBank gij538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcript factor	264509
447	80438888 (893, 894)	Novel Protein sim. GBank gij1542914[emb]CAB02185] - (Z80108) fnt [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - Formyl transferase	dehydrogenase	264768, 55811576
448	80238110 (895, 896)	Novel Protein sim. GBank gij118794[sp]P10443[DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264508, 264600, 264603, 264605, 264682, 264769, 18108362, 264634, 18108387
449	20460834 (897, 898)	Novel Protein sim. GBank gij118794[sp]P10443[DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN			264605, 264559
450	94631210 (899, 900)	Novel Protein sim. GBank gij4589508[dbj]BAA76775.1] - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481) - Protein phosphatase 2C	phosphatase	55274572, 22278998, 29331824, 29331826, 264906, 264910, 264592, 52646317, 265017, 21908767, 55811957, 56528486, 22279002
451	21433609 (901, 902)	Novel Protein sim. GBank gij2650814 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	264486
452	10267278 (903, 904)	Novel Protein sim. GBank gij2493000[sp]Q09450[SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)]		UNCLASSIFIED	264692
453	52560098 (905, 906)	Novel Protein sim. GBank gij2493000[sp]Q09450[SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)]		UNCLASSIFIED	264907, 264600
454	39523922 (907, 908)	Novel Protein sim. GBank gij2493000[sp]Q09450[SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)]		transferase	264603
455	13089692 (909, 910)	Novel Protein sim. GBank gij4468699[emb]CAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	264687
456	79563081 (911, 912)	Novel Protein sim. GBank gij3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	kinase	264691
457	79831273 (913, 914)	Novel Protein sim. GBank gij4468699[emb]CAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	264905
458	79561227 (915, 916)	Novel Protein sim. GBank gij4468699[emb]CAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	kinase	55812038, 265010, 265018, 264681
459	80567359 (917, 918)	Novel Protein sim. GBank gij4508075[ref]NP_002733.1[prkC - protein kinase C, mu	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	22278997, 264259, 29331826, 265018, 264448, 264369, 21906765, 35696423
460	79245890 (919, 920)	Novel Protein sim. GBank gij113158[sp]P25516[ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)]		UNCLASSIFIED	264906
461	95287618 (921, 922)	Novel Protein sim. GBank gij1168574[sp]P42464[ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	264602, 264605, 264768, 264769, 265021, 33857023, 264559

462	78060589 (923, 924)	Novel Protein sim. GBank gil1348891 sp P45597 PTF1_XANCP - MULTIPHOSPHORYL TRANSFER PROTEIN (MTP) (CONTAINS: PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ...	Contains protein domain (PF00381) - PEP-utilizing enzymes	UNCLASSIFIED	264807
463	79786417 (925, 926)	Novel Protein sim. GBank gil854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264905, 264906, 264908, 264909, 264910, 264591, 264595, 265011, 264632, 264635, 264638, 264637, 264638, 264639 264634
464	82340151 (927, 928)	Novel Protein sim. GBank gil5689776 emb CA852137.1 - (AJ242832) calpain [Homo sapiens]	Contains protein domain (PF00848) - Calpain family cysteine protease	UNCLASSIFIED	265017, 21906764, 265020
465	83005730 (929, 930)	Novel Protein sim. GBank gil1806175 emb CA806470 - (Z84395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.	UNCLASSIFIED	264605, 264559
466	20460845 (931, 932)	Novel Protein sim. GBank gil548705 sp P36949 RBSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	264764
467	80408035 (933, 934)	Novel Protein sim. GBank gil114921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN		UNCLASSIFIED	264692 264488
468	52562208 (935, 936)	Novel Protein sim. GBank gil2114024 emb CA808957 - (Z95558) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	264602, 264769
469	18520527 (937, 938)	Novel Protein sim. GBank gil2809459 emb CAA17347 - (AL021929) cobQ [Mycobacterium tuberculosis]		UNCLASSIFIED	265019
470	80502756 (939, 940)	Novel Protein sim. GBank gil114921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN		UNCLASSIFIED	264596, 264685, 264557 264369
471	17937351 (941, 942)	Novel Protein sim. GBank gil114921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN		UNCLASSIFIED	22278997, 264692, 264288 264907, 264908, 264511, 265009, 264762, 264448, 264636, 264638
472	80047458 (943, 944)	Novel Protein sim. GBank gil862343 (L10908) - Gcap1 gene product [Mus musculus]		UNCLASSIFIED	65274572, 60432049, 264259, 264508, 52644045, 55812038, 264758, 265011, 264288, 264686, 52844229, 65274791, 264638, 264586 264638
473	20558793 (945, 946)	Novel Protein sim. GBank gil5453656 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264690, 264693 264686, 35695855, 265008, 264631, 264910, 264632, 264638, 265018, 264369, 264909 264369
474	80593365 (947, 948)	Novel Protein sim. GBank gil5453656 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	264693
475	82454685 (949, 950)	Novel Protein sim. GBank gil1127551 (U18939) - orf2 [Batrachocottus baikalensis]		UNCLASSIFIED	264909, 264686, 264768, 264693, 55811576, 56182323, 18108385
476	94143857 (951, 952)	Novel Protein sim. GBank gil5453656 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	
477	79175833 (953, 954)	Novel Protein sim. GBank gil1127551 (U18939) - orf2 [Batrachocottus baikalensis]		UNCLASSIFIED	
478	79633483 (955, 956)	Novel Protein sim. GBank gil1127551 (U18939) - orf2 [Batrachocottus baikalensis]		UNCLASSIFIED	
479	80189746 (957, 958)	Novel Protein sim. GBank gil1127551 (U18939) - orf2 [Batrachocottus baikalensis]		UNCLASSIFIED	
480	79390729 (959, 960)	Novel Protein sim. GBank gil1127551 (U18939) - orf2 [Batrachocottus baikalensis]		UNCLASSIFIED	
481	79624578 (961, 962)	Novel Protein sim. GBank gil1127551 (U18939) - orf2 [Batrachocottus baikalensis]		UNCLASSIFIED	
482	83050611 (963, 964)	Novel Protein sim. GBank gil1127551 (U18939) - orf2 [Batrachocottus baikalensis]		UNCLASSIFIED	

483	20293306 (965, 966)	Novel Protein sim. GBank gij2104303[emb]CAB08632] - (Z95387) hypothetical protein RV2610c [Mycobacterium tuberculosis]	Contains protein domain (PF00534) - Glycosyl transferases group 1	264600	
484	11618046 (867, 868)	Novel Protein sim. GBank gij3450883 (AF083334) - fibroin [Antheraea pernyi]	UNCLASSIFIED	264594	
485	80191234 (969, 970)	Novel Protein sim. GBank gij5042272[emb]CAB44526.1] - (AL078618) nuoF. NADH dehydrogenase subunit [Streptomyces coelicolor]	UNCLASSIFIED	264369, 21906765, 22279000, 22279002	
486	80059042 (871, 872)		dehydrogenase	264604	
487	11813339 (973, 974)			264638	
488	91222383 (975, 976)	Novel Protein sim. GBank gij5724778[gb]AAC53522.2] - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00620) - RhoGAP domain	264686, 66714117, 264768, 18108385, 55811576, 265008, 265008, 265009, 265019, 22279002, 264259, 18108370, 264907, 264784, 56182323, 264288, 264693	
489	10867710 (977, 978)	Novel Protein sim. GBank gij3882223[dbj]BAA34471.1] - (AB018294) KIAA0751 protein [Homo sapiens]	kinase	264639	
490	95361124 (979, 980)	Novel Protein sim. GBank gij82091[pir]J25494 - hydroxyproline-rich glycoprotein - tomato (fragment)	collagen	22278996, 29331822, 29331828, 264107, 264909, 264110, 265009, 264592, 264593, 80433358, 264288, 264693, 263974, 263976, 20281071, 60432113	
491	80496412 (981, 982)	Novel Protein sim. GBank gij2894206[emb]CAA17072] - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis]	UNCLASSIFIED	264769	
492	87421264 (983, 984)			264600	
493	11692842 (985, 986)		UNCLASSIFIED	264638	
494	87726604 (887, 888)	Novel Protein sim. GBank gij5262605[emb]CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264489, 35696286, 60432289, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 33657402, 264762, 264764, 264768, 264769, 264688, 21906765, 21906769, 35695917, 265020, 264693, 33657109, 264629, 35696423, 35695855, 284634, 264638	
495	80026599 (989, 990)	Novel Protein sim. GBank gij2791517[emb]CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]	Contains protein domain (PF00005) - ABC transporter	264602, 264682, 264638	
496	78985624 (991, 992)	Novel Protein sim. GBank gij230281[dbj]R669] - 434 Repressor (Amino-Terminal Domain) (R1-69)	Contains protein domain (PF01381) - Helix-turn-helix	264601, 265021	
497	78949661 (993, 994)	Novel Protein sim. GBank gij129736[sp]P28225[PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)]	oxidase	265006	

498	88095488 (895, 896)	Novel Protein sim. GBank gij1145789 (U41662) - neuroigin 2 (Rattus norvegicus)	Contains protein domain (PF00135) - Carboxylesterases	esterase	264259, 29331826, 35698052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264591, 33857402, 264758, 265010, 265011, 264600, 264601, 264605, 264683, 264764, 264768, 264767, 264768, 264687, 264769, 21908767, 33657023, 284693, 264628, 284629, 35698423, 264630, 264632, 264634, 284635, 284637, 264638, 264558, 264639, 18108385, 264563, 284564, 284565, 264566, 264587
499	20438222 (897, 998)	Novel Protein sim. GBank gij97480(pir)S19739 - integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	264605
500	11076810 (899, 1000)				264605
501	13418034 (1001, 1002)	Novel Protein sim. GBank gij5708250(emb)CAB52363.1] - (AL109747) putative integral membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264688
502	80021176 (1003, 1004)	Novel Protein sim. GBank gij4468678(emb)CAB38132.1] - (AL035591) glucose-6-phosphate isomerase [Streptomyces coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	isomerase	22278996, 265011, 264602, 264605, 264635
503	20264483 (1005, 1006)			UNCLASSIFIED	264584
504	10887321 (1007, 1008)			UNCLASSIFIED	264687
505	95003068 (1009, 1010)			UNCLASSIFIED	264369
506	16454292 (1011, 1012)	Novel Protein sim. GBank gij4033509(sp)P02598(CALM TETPY - CALMODULIN	Contains protein domain (PF00036) - EF hand	struct	265010
507	20451598 (1013, 1014)	Novel Protein sim. GBank gij2501069(sp)Q46127(SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS)		UNCLASSIFIED	264604
508	79841424 (1015, 1016)	Novel Protein sim. GBank gij466088(sp)P34618(YO82, CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN CHROMOSOME III		UNCLASSIFIED	264908
509	11776386 (1017, 1018)				264638
510	83373465 (1019, 1020)			UNCLASSIFIED	284687, 284639
511	16525578 (1021, 1022)				265007
512	20399484 (1023, 1024)	Novel Protein sim. GBank gij2497419(sp)P55635(Y4RB, RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB		UNCLASSIFIED	264565
513	79457404 (1025, 1026)	Novel Protein sim. GBank gij1276897 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - cyclin	cyclin	284683, 264689, 35698423, 264639
514	79813805 (1027, 1028)	Novel Protein sim. GBank gij1184790 (U46066) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
515	79462591 (1029, 1030)				22278999, 264690
516	8862020 (1031, 1032)	Novel Protein sim. GBank gij2127400(pir)S65770 - maltotriose trehalose trehalohydrolase - Arthrobacter sp. (strain Q36)		amylase	264910

517	95292894 (1033, 1034)	Novel Protein sim. GBank gi 2983605 (AE000725) - ribose 5 phosphate isomerase B [Aquifex aeolicus]		isomerase	265018, 264605, 264764, 264766, 264687, 264891, 264585
518	8491831 (1035, 1036)	Novel Protein sim. GBank gi 854065 (emb CAA58337) - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264487
519	91677886 (1037, 1038)	Novel Protein sim. GBank gi 5689355 (dbj BAA83073.1) - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	dna_rna_bind	52644507, 22278997, 22278998, 60432049, 264259, 52645090, 29331824, 66714117, 60424269, 29331826, 35696052, 264905, 29331830, 66712502, 264511, 265007, 264591, 60432229, 33657402, 60433438, 21906754, 33109954, 52644296, 87168474, 87168559, 265017, 265018, 264604, 265019, 264681, 264448, 264369, 264288, 264685, 21906765, 21906766, 21906767, 21906769, 265021, 60170615, 33657023, 264692, 52645129, 33657109, 27486262, 27486264, 35895763, 18108370, 264629, 52644332, 56182323, 264639, 83373044, 18108385, 56526486, 60432113
520	79859188 (1039, 1040)				264769
521	11076821 (1041, 1042)	Novel Protein sim. GBank gi 169126 (sp P46839) CTPA_MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A	transport		264605
522	80435060 (1043, 1044)	Novel Protein sim. GBank gi 1172869 (sp P44331) RBKS_HAEIN - RIBOKINASE	Contains protein domain (PF00294) - pfkB family carbohydrate kinase	kinase	284905, 264768
523	18356013 (1045, 1046)	Novel Protein sim. GBank gi 2132243 (pir S61028) - hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264629
524	80261805 (1047, 1048)	Novel Protein sim. GBank gi 4033608 (dbj BAA35136) - (AB012308) B2HC [Anthracidaris crassispina]		ATPase_associated	264092, 264596, 265011
525	76610046 (1049, 1050)				284907
526	38827630 (1051, 1052)	Novel Protein sim. GBank gi 4106610 (emb CAA21365) - (AL031866) ORF42, len=386 aa, similarity to an aminotransferase, in P85957 Sulfolobus solfataricus (401 aa), 33.1% identity in 393 aa overlap. FastA scores: opt:488, E(-): 8.5e-24, In Q64602 R. norvegicus, (425 aa), 28.6% ident...		UNCLASSIFIED	264758
527	80504729 (1053, 1054)			UNCLASSIFIED	264769
528	65484134 (1055, 1056)			UNCLASSIFIED	56182575, 265017, 265018
529	17936810 (1057, 1058)	Novel Protein sim. GBank gi 731088 (sp P24215) UJUA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)	hydrolase		265019
530	10887336 (1059, 1060)	Novel Protein sim. GBank gi 42144 (emb CAA25200) - (X00513) NusA protein (nusA) [Escherichia coli]		UNCLASSIFIED	264687
531	80226576 (1061, 1062)			UNCLASSIFIED	264555, 264556, 264557, 264558, 18108385
532	90933444 (1063, 1064)	Novel Protein sim. GBank gi 5262640 (emb CAB45758.1) - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264488, 264490, 264259, 264592, 264760, 265021, 264690, 2639976, 264558

533	87761531 (1065, 1066)	Novel Protein sim. GBank gi1488363 gb AAD31593.1 AF11229 Integral inner nuclear membrane protein MAN1 [Homo sapiens]			264907, 264909, 264768, 35695917, 264630, 264555
534	82368264 (1067, 1068)	Novel Protein sim. GBank gi12985352 emb CAA04906.1 - (AJ001206) pep1 [Streptomyces coelicolor]	UNCLASSIFIED		264805, 265011, 264601, 264602, 264605, 264762, 264768, 265020, 264693, 264636 264806
535	79641850 (1069, 1070)	Novel Protein sim. GBank gi1387863 emb CAA8953 - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	ATPase-associated	
536	79907207 (1071, 1072)	Novel Protein sim. GBank gi2495828 sp P55757 YOH1_SERMA - HYPOTHETICAL 10.1 KD PROTEIN IN BIOA 5/REGION		reductase	18108376, 264905, 264908, 264907, 264909
537	94147448 (1073, 1074)	Novel Protein sim. GBank gi134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	collagen	265008, 264605, 65274781 29331822, 29331824, 29331825, 29331826, 29331827, 264908, 52644045, 33657402, 265017, 264762, 264683, 264288, 264685, 21906765, 35695783, 264558, 60170394, 264559, 22279002 264602, 265019
539	26396269 (1077, 1078)	Novel Protein sim. GBank gi2498433 sp Q12341 HAT1_YEAST - HISTONE ACETYLTRANSFERASE		histone	
540	79637077 (1079, 1080)	Novel Protein sim. GBank gi13882241 db BAA34480.1 - (AB018303) KIAA0760 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	264893 18108394, 22278997, 22278998, 264259, 264112, 265009, 33657402, 55812038, 52646317, 265017, 21906765, 264693, 55811576, 264635, 56526486, 264568 264910, 265018, 264689, 264638, 264486
542	95295838 (1083, 1084)	Novel Protein sim. GBank gi15042272 emb CAB44526.1 - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	
543	79786280 (1085, 1086)	Novel Protein sim. GBank gi2791398 emb CAA15994 - (AL021184) hypothetical protein Rv1464 [Mycobacterium tuberculosis]	UNCLASSIFIED	UNCLASSIFIED	264602, 264908 264605
544	20437191 (1087, 1088)	Novel Protein sim. GBank gi1350855 sp P19176 RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT)			264768, 264634, 264907, 264592, 264809 264600, 264602, 21908765
545	80434504 (1089, 1090)	Novel Protein sim. GBank gi14887211 gb AAD32237.1 AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]			
546	80249016 (1091, 1092)	Novel Protein sim. GBank gi1350855 sp P19176 RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT)		mapolymerase	264604
547	11077563 (1093, 1094)	Novel Protein sim. GBank gi2330021 (AF019250) - kinesin- related protein; KRP; Costal2 [Drosophila melanogaster]	UNCLASSIFIED		264488, 264905, 264910, 264760, 264693, 264639, 264563, 264564

548	95421904 (1097, 1098)	Novel Protein sim. GBank gi 4337460 gb AAD18133 - (AF056195) neuroblastoma-amplified protein [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 18108398, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 28331826, 35696052, 265007, 265008, 264910, 264592, 33657402, 33109954, 265017, 265018, 265019, 18108351, 264448, 264764, 264369, 264288, 264766, 264686, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 33657023, 264692, 264693, 65274620, 52845129, 33657109, 27486261, 27486262, 27486264, 33657349, 55811576, 18108387, 80432113, 22279002
550	10886816 (1099, 1100)				264688
551	80439990 (1101, 1102)	Novel Protein sim. GBank gi 3122893 sp P94985 SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	264908, 264909, 264768
552	84672870 (1103, 1104)				
553	80106002 (1105, 1106)	Novel Protein sim. GBank gi 552087 (M33753) - crumbs protein [Drosophila melanogaster]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264689, 264639, 264563
554	79818379 (1107, 1108)	Novel Protein sim. GBank gi 5019771 gb AAD37857.1 AF13326 - (AF133263) histidine protein kinase-response regulator hybrid protein CvgSY [Pseudomonas syringae pv. syringae]	kinase		264906
555	78896347 (1109, 1110)	Novel Protein sim. GBank gi 131515 sp P02908 PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIIA-GLC)	Contains protein domain (PF00358) - phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1	transport	264762
556	20457127 (1111, 1112)	Novel Protein sim. GBank gi 3914014 sp P96380 IMFD_MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)		transcriptfactor	264508, 264605, 264559
557	19523405 (1113, 1114)	Novel Protein sim. GBank gi 5042273 emb CAB44527.1 - (AL078618) nuoE, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	264488
558	20724429 (1115, 1116)	Novel Protein sim. GBank gi 170933 sp P45331 METE_HAEIN - 5-METHYL TETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)		UNCLASSIFIED	264602
559	80084353 (1117, 1118)	Novel Protein sim. GBank gi 4980567 gb AAD35173.1 AE001694 iron(III) ABC transporter, permease protein [Thermotoga maritima]		UNCLASSIFIED	264634

560	80066533 (1119, 1120)	Novel Protein sim. GBank gi 2492595 sp Q53193 Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF00005) - ABC transporter	transport	18108396, 264906, 264602, 264604, 18108374
561	20293187 (1121, 1122)			UNCLASSIFIED	264600
562	11698161 (1123, 1124)			UNCLASSIFIED	264689
563	79761420 (1125, 1126)	Novel Protein sim. GBank gi 4104925 (AF042276) - poly(hydroxycarbonate) granule associated protein GA2 [Pseudomonas putida]		UNCLASSIFIED	264910, 264691
564	56716390 (1127, 1128)	Novel Protein sim. GBank gi 2792310 (AF040570) - unknown [Amycolatopsis mediterranei]	dehydrogenase		264592
565	56465618 (1129, 1130)	Novel Protein sim. GBank gi 3449284 (dbj BAA32462) - (AB011532) MEGF8 [Rattus norvegicus]	Contains protein domain (PF00009) - EGF-like domain	synthase	265010
566	94323888 (1131, 1132)	Novel Protein sim. GBank gi 4539568 (emb CAB38487.1) - (AL035636) putative helicase [Streptomyces coelicolor]		helicase	264909, 264510, 265008, 284910, 264758, 264600, 264602, 264604, 264605, 264768, 264687, 264689, 35695917, 264693, 65274820, 264488
567	79560955 (1133, 1134)	Novel Protein sim. GBank gi 100506 pir J17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flavaria trimeria (fragment)	Contains protein domain (PF00390) - Malic enzyme	UNCLASSIFIED	264681, 264691, 264593
568	94681793 (1135, 1136)	Novel Protein sim. GBank gi 3915843 sp O31212 RS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF00318) - Ribosomal protein S2	dehydrogenase	264689
569	38506897 (1137, 1138)	Novel Protein sim. GBank gi 15122 sp P21627 BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		ribosomal prot	264565
570	78375927 (1139, 1140)	Novel Protein sim. GBank		UNCLASSIFIED	18108376, 18108387, 264565
571	79793961 (1141, 1142)	Novel Protein sim. GBank gi 15122 sp P21627 BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		transport	264907, 264909
572	36996838 (1143, 1144)	Novel Protein sim. GBank gi 4539223 (emb CAB39881.1) - (AL049497) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	264782
573	20715521 (1145, 1146)	Novel Protein sim. GBank gi 4539223 (emb CAB39881.1) - (AL049497) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	265007, 264601
574	13521592 (1147, 1148)	Novel Protein sim. GBank gi 118794 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264636 264687
575	13076416 (1149, 1150)	Novel Protein sim. GBank gi 118794 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN			264605
576	20482246 (1151, 1152)	Novel Protein sim. GBank gi 5457625 (emb CAB49116.1) - (AJ248283) PAB2227 [Pyrococcus abyssi]			
577	66727102 (1153, 1154)	Novel Protein sim. GBank gi 5042274 (emb CAB44528.1) - (AL078618) nuoD, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF00346) - Respiratory-chain NADH dehydrogenase, 49 Kd subunit	dehydrogenase	35696052, 264636
578	11804477 (1155, 1156)	Novel Protein sim. GBank			264638
579	11794723 (1157, 1158)	Novel Protein sim. GBank gi 1723081 sp Q11046 Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09		transport	264682, 264556

580	80059417 (1159, 1160)					22278999, 35696052, 284555, 284556, 284558	UNCLASSIFIED	
581	79230833 (1161, 1162)	Novel Protein sim. GBank gij3243131 (AF045777) - Iitin			Contains protein domain (PF00047)	285008, 264564	struct	
582	80049817 (1163, 1164)	[Drosophila melanogaster]			Immunoglobulin domain	265021, 264555, 264557		
583	79321392 (1165, 1166)	Novel Protein sim. GBank gij2501162[sp]P7726[YAJR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION]				264594	transport	
584	78845024 (1167, 1168)	Novel Protein sim. GBank gij3882221[dbj]BAA34470.1] - (AB018293) KIAA0750 protein [Homo sapiens]				264488, 264908, 264766, 284687, 35696423	UNCLASSIFIED	
585	79581454 (1169, 1170)	Novel Protein sim. GBank gij4467250[emb]CAB37575] - (AL035569) probable Glu-IRNA Gln amidotransferase subunit [Streptomyces coelicolor]				265018, 284684, 21908769	UNCLASSIFIED	
586	38277488 (1171, 1172)	Novel Protein sim. GBank gij5689519[dbj]BAA83043.1] - (AB028014) KIAA1091 protein [Homo sapiens]				264908, 265007	UNCLASSIFIED	
587	80497359 (1173, 1174)	Novel Protein sim. GBank gij5689519[dbj]BAA83043.1] - (AB028014) KIAA1091 protein [Homo sapiens]				264600, 264602, 264605, 264769, 284690, 264557	hydrolase	
588	79557239 (1175, 1176)	Novel Protein sim. GBank gij5689519[dbj]BAA83043.1] - (AB028014) KIAA1091 protein [Homo sapiens]				265020, 264692	UNCLASSIFIED	
589	79805828 (1177, 1178)	Novel Protein sim. GBank gij2143293[emb]CAB09390] - (Z95972) rpoB [Mycobacterium tuberculosis]				22278996, 264907, 264909, 264510, 285009, 265010, 284687, 264769, 35695917, 18108376, 264634, 264636, 264638	UNCLASSIFIED	
590	79815629 (1179, 1180)	Novel Protein sim. GBank gij2143293[emb]CAB09390] - (Z95972) rpoB [Mycobacterium tuberculosis]				264906, 264909	UNCLASSIFIED	
591	10313540 (1181, 1182)	Novel Protein sim. GBank gij4511983[gb]AAD21543.1] - (AF088896) electroltransfer ubiquinone oxidoreductase [Zymomonas mobilis]				264691	mapolymerase	
592	13889767 (1183, 1184)	Novel Protein sim. GBank gij1272368 (U51896) - LIgE [Vibrio parahaemolyticus]				263972	MHC	
593	82348699 (1185, 1186)	Novel Protein sim. GBank gij1272368 (U51896) - LIgE [Vibrio parahaemolyticus]				284511, 264762, 264769, 284486	dehydrogenase	
594	20212392 (1187, 1188)	Novel Protein sim. GBank gij1272368 (U51896) - LIgE [Vibrio parahaemolyticus]				264605	UNCLASSIFIED	
595	10064064 (1189, 1190)	Novel Protein sim. GBank gij125328[sp]P20966[PTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EIIF-FRU)]				264769		
596	13085170 (1191, 1192)					264636	UNCLASSIFIED	
597	80259003 (1193, 1194)					264592	UNCLASSIFIED	
598	94140216 (1195, 1196)					264758, 55810764, 264555, 284656, 264837, 83373044	UNCLASSIFIED	
599	20385137 (1197, 1198)	Novel Protein sim. GBank gij125328[sp]P20966[PTFB_ECOLI - 3-DEOXY-MANNO-OCTULONATE CYTIDYLTRANSFERASE (CMP-KOO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULONIC ACID SYNTHETASE) (CKS)]				264603	UNCLASSIFIED	
600	10357663 (1199, 1200)							
601	79610404 (1201, 1202)	Novel Protein sim. GBank gij2127414[pir]J560064 - hypothetical protein 2 - Corynebacterium glutamicum				264906, 264510	UNCLASSIFIED	

602	79250502 (1203, 1204)	Novel Protein sim. GBank gij3522961[gblAAC34243.1]- (AC004411) putative pio kinase [Arabidopsis thaliana]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	265007
603	11466067 (1205, 1206)			UNCLASSIFIED	264595
604	81675420 (1207, 1208)			UNCLASSIFIED	264758
605	20436657 (1209, 1210)	Novel Protein sim. GBank gij1175322[sp]P44917Y883_HAEIN - HYPOTHETICAL PROTEIN H10883		UNCLASSIFIED	264605
608	80334582 (1211, 1212)	Novel Protein sim. GBank gij5020284[gblAAD38043.1]AF15136 - (AF151383) Cdc42 GTPase-activating protein [Mus musculus]		UNCLASSIFIED	264764
607	95361506 (1213, 1214)	Novel Protein sim. GBank gij1188864 (M74027) - mucin [Homo sapiens]		UNCLASSIFIED	264508, 264908, 85658542, 264682, 264687, 264689, 264534, 18108376, 35896423, 264638, 264555, 264638
608	11810888 (1215, 1216)			UNCLASSIFIED	264682
609	80084775 (1217, 1218)	Novel Protein sim. GBank gij2498701[sp]P55552[Y4LL_RHISN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	Contains protein domain (PF00989) - PAS domain	UNCLASSIFIED	264605
610	79629413 (1219, 1220)				264692
611	87586205 (1221, 1222)				264508, 264905, 264907, 264908, 264909, 264511, 264910, 264758, 264604, 264684, 264766, 264689, 264692, 264628, 264635, 264638, 264637, 264558
612	95287851 (1223, 1224)	Novel Protein sim. GBank gij197366[gbl]CAB07118] - (Z92772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	nuclease	264600, 264601, 264604, 264769, 264558, 264565
613	7523475 (1225, 1226)			UNCLASSIFIED	264369
614	79969348 (1227, 1228)	Novel Protein sim. GBank gij5114231[gblAAD40238.1]AF13670 - (AF136709) histidine kinase YycG [Staphylococcus aureus]		Kinase	18108372, 264563
615	38586998 (1229, 1230)	Novel Protein sim. GBank gij1339950[gbl]BAA12741] - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]		synthase	264600, 264602, 264629
616	20465331 (1231, 1232)	Novel Protein sim. GBank gij544387[sp]P35673[GALE_ERWAM - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE)		isomerase	264605
617	91227222 (1233, 1234)	Novel Protein sim. GBank gij2498097[sp]Q60769[TNP3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	Int	52645156, 21906765, 35696423, 21906768, 21908769, 22278994, 35696286, 22278998, 265020, 265021, 265007, 265008, 264638, 52844150, 33657023, 264692, 264693, 29331822, 29331824, 55812038, 83373044, 56182181, 60424269, 66714117, 29331825, 33657109, 29331826, 33657182, 29331827, 35696052, 29331828, 27486262, 33657349, 56526486, 265018, 265019, 22279002, 264482, 264448, 29331830, 66712502, 264909

618	20632843 (1235, 1236)	Novel Protein sim. GBank gij5459388[embjCAB50746.1] - (AL098839) putative aminotransferase [Streptomyces coelicolor]		isomerase	264603	
619	91227224 (1237, 1238)				56994075, 29331826, 33656970, 265008, 33857402, 33109954, 87168559, 264448, 18108374, 83373044	
620	81183143 (1239, 1240)	Novel Protein sim. GBank gij464335[spjQ05922]DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1)		phosphatase	28146498, 264758, 284369, 29148627	
621	30239251 (1241, 1242)			UNCLASSIFIED	284556, 264558, 264639	
622	20456427 (1243, 1244)	Novel Protein sim. GBank gij2633557[embjCAB13060] - (Z99110) ylf [Bacillus subtilis]		UNCLASSIFIED	264605	
623	10131788 (1245, 1246)	Novel Protein sim. GBank gij1857710[gbjAAB48482] - (U87224) contadin associated protein [Rattus norvegicus]	Contains protein domain (PF00054) - laminin Laminin G domain	laminin	264906	
624	18534127 (1247, 1248)	Novel Protein sim. GBank gij1705703[spjP52225]CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK		cytochrome	264596	
625	13084618 (1249, 1250)	Novel Protein sim. GBank gij2894252[embjCAA17114.1] - (AL021841) hypothetical protein RV3342 [Mycobacterium tuberculosis]		UNCLASSIFIED	264688	
626	88062603 (1251, 1252)	Novel Protein sim. GBank gij416592[spjP32323]AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	29331822, 264905, 264908, 33657023, 33657109, 264558	
627	80255457 (1253, 1254)	Novel Protein sim. GBank gij3098418 (AF040944) - P140 [Mus musculus]		UNCLASSIFIED	18108394, 264112, 264593, 265022, 264635	
628	80077096 (1255, 1256)	Novel Protein sim. GBank gij1711543[spjP50526]SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1	Contains protein domain (PF00069) - Kinase Eukaryotic protein kinase domain	kinase	264600	
629	79851602 (1257, 1258)	Novel Protein sim. GBank gij1143204 (U34305) - ORF2; Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	284906, 264907	
630	39565156 (1259, 1260)	Novel Protein sim. GBank gij3236368 (AF064748) - S3-12 [Mus musculus]		UNCLASSIFIED	264490	
631	20598718 (1261, 1262)	Novel Protein sim. GBank gij140887[spjP11666]YGGG_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286)			263978	
632	27843890 (1263, 1264)			UNCLASSIFIED	264906, 264600, 264605, 264769, 264689, 264486	
633	80477772 (1265, 1266)			UNCLASSIFIED	264769	
634	17938808 (1267, 1268)				265019	
635	79574508 (1269, 1270)			UNCLASSIFIED	264689	
636	79910381 (1271, 1272)			UNCLASSIFIED	264596, 264762, 264693	

637	82455796 (1273, 1274)	Novel Protein sim. GBank gij2326739[embjCAB10953] - (Z98268) recN [Mycobacterium tuberculosis]		nuclease	264906, 264907, 264510, 264511, 264601, 264602, 264603, 264604, 264605, 18108351, 264762, 264766, 264687, 264769, 264689, 35695917, 264693, 264634, 264638, 264639, 264558, 18108385
638	14997457 (1275, 1276)	Novel Protein sim. GBank gij4676632[embjCAB41074.1] - (AL049645) putative large ATP-binding protein [Streptomyces coelicolor]			264636
639	80204210 (1277, 1278)	Novel Protein sim. GBank gij4588628[jb BAA76838.1] - (AB023209) KIAA0992 protein [Homo sapiens]		strut	264112, 263974
640	17929579 (1279, 1280)	Novel Protein sim. GBank gij1432083 (U00981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]	Contains protein domain (PF01466) - Skp1 family	mapolymerase	265009, 265010
641	79636398 (1281, 1282)			UNCLASSIFIED	264693
642	19898737 (1283, 1284)			UNCLASSIFIED	264565
643	81516220 (1285, 1286)			UNCLASSIFIED	264635, 264639, 264564
644	11751387 (1287, 1288)			UNCLASSIFIED	264694
645	95010907 (1289, 1290)			UNCLASSIFIED	264906, 264762, 264693, 264639, 264559
646	80069083 (1281, 1292)				264595, 264566
647	80257085 (1293, 1294)				264909, 264591
648	80077428 (1295, 1296)	Novel Protein sim. GBank gij4507613[re NP_003738.1 pTNKS - TANKYRASE	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	264600
649	80247447 (1297, 1298)	Novel Protein sim. GBank gij1044963[jbbs 169648 - protamine [Monodonta turbinata, gonads, Peptide, 106 aa]		UNCLASSIFIED	263978
650	11798316 (1299, 1300)			UNCLASSIFIED	264686
651	11776932 (1301, 1302)	Novel Protein sim. GBank gij1346916[sp P12283 PURA_ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE LIGASE)]			264602, 264638
652	85516704 (1303, 1304)			UNCLASSIFIED	264905, 264907, 264909, 263978, 264637
653	82124947 (1305, 1306)	Novel Protein sim. GBank gij1722977[sp Q10638 Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	22278996, 264510, 264511, 264512, 264593, 21906754, 264603, 264760, 18108376, 264556
654	95010589 (1307, 1308)			UNCLASSIFIED	264905, 264595, 264632
655	79320692 (1309, 1310)	Novel Protein sim. GBank gij130327[sp P26647 PLSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)]	Contains protein domain (PF01553) - Acyltransferase	transferase	264592
656	80416739 (1311, 1312)			UNCLASSIFIED	264602, 264605, 264766, 264691
657	20811010 (1313, 1314)			UNCLASSIFIED	264557, 264558

658	87761815 (1315, 1316)	Novel Protein sim. GBank gij5689493dbj BAA83030.1 - (AB029001) KIAA1078 protein (Homo sapiens)		UNCLASSIFIED	22278996, 60432049, 29331822, 29331824, 29331828, 265007, 265009, 33657402, 33657084, 265017, 264448, 21906765, 21906766, 263967, 20281149, 18108370, 18108374, 264482
659	87718663 (1317, 1318)	Novel Protein sim. GBank gij2137872 pir 48724 - zinc finger protein PFZ - mouse	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcriptfactor	22278999, 60432049, 66714117, 29331827, 265007, 264766, 58181562, 18108359, 18108365, 18108370, 18108381
660	81897822 (1319, 1320)			UNCLASSIFIED	264757
661	80028023 (1321, 1322)	Novel Protein sim. GBank gij134180 sp P15401 SACY_BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTITERMINATOR	Contains protein domain (PF00874) - Transcriptional antiterminator bglG family	UNCLASSIFIED	264510, 265009, 264600, 264602, 264603, 264604, 264605, 32833986, 18108376, 264636, 18108387, 22279000
662	20463731 (1323, 1324)	Novel Protein sim. GBank gij454528 gb AAD22450.1 AF11618 - (AF11618) SecA homolog [Acidobacillus acidinomycescomitans]		UNCLASSIFIED	264605
663	20628080 (1325, 1326)	Novel Protein sim. GBank gij5689250 dbj BAA82881.1 - (AB024335) similar to orf5 [Comamonas testosteroni]		dehydrogenase	264605
664	80508512 (1327, 1328)	Novel Protein sim. GBank gij1652848 dbj BAA17766 - (D90909) DNA photolyase [Synecchocystis sp.]		UNCLASSIFIED	264769
665	80078053 (1329, 1330)	Novel Protein sim. GBank gij116841 sp P21640 COBJ_PSEDE - PRECORRIN-3B C17 METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE)		isomerase	264600
666	78603142 (1331, 1332)	Novel Protein sim. GBank gij3261829 emb CAB10927 - (Z98260) hypothetical protein Rv1230c [Mycobacterium tuberculosis]		glycoprotein	264907, 265007
667	94631802 (1333, 1334)	Novel Protein sim. GBank gij568885 dbj BAA82702.1 - (AB017438) Orf5 [Streptomyces coelicolor]		UNCLASSIFIED	264689, 264602, 264593
668	82051891 (1335, 1336)	Novel Protein sim. GBank gij3581853 emb CAA20809 - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	Contains protein domain (PF00453) - Ribosomal protein L20	ribosomalprot	264905, 264908, 264908, 264600, 264601, 264603, 264605, 264760, 264689, 264636, 264638, 264639
669	12867154 (1337, 1338)			UNCLASSIFIED	264637
670	80238549 (1339, 1340)	Novel Protein sim. GBank gij2582531 (AF026444) - 2-Isopropylmalate synthase [Streptomyces coelicolor]		synthase	264905, 264906, 264908, 264601, 264762, 264766, 264689, 264638, 18108385, 264486
671	78601368 (1341, 1342)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264690, 264692, 264693, 264636, 18108387
672	79834371 (1343, 1344)	Novel Protein sim. GBank gij2114430 (U92703) - Olf-1/EBF-like-3 transcription factor [Mus musculus]		transcriptfactor	264910, 265017
673	82285788 (1345, 1346)	Novel Protein sim. GBank gij4589285 gb AAD26430.1 AF13515 - (AF135154) ferric alkaline siderophore receptor [Bordetella pertussis]			264759
674	78189259 (1347, 1348)			UNCLASSIFIED	264629

675	87895870 (1349, 1350)	Novel Protein sim. GBank gi 4980755 gb AAD35347.1 AE001708 - (AE001708) D- alanine-D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-ala D-ala ligase	UNCLASSIFIED	264488, 22278999, 66714117, 264508, 264511, 265008, 60433438, 264600, 264601, 264602, 264603, 264604, 264605, 264762, 264687, 264769, 60431602, 18108374, 264636, 264638 265010
676	78899807 (1351, 1352)	Novel Protein sim. GBank gi 1723568 sp Q10479 YDF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07			
677	21644312 (1353, 1354)	Novel Protein sim. GBank gi 687208 (U03976) - dynein heavy chain isoform 5C [Tripteneustes grallia]		ATPase-associated	264591, 264632
678	84225200 (1355, 1356)	Novel Protein sim. GBank gi 1586274 pr j2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264758, 264682, 264557
679	78868855 (1357, 1358)	Novel Protein sim. GBank gi 3928723 emb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278996, 264693
680	20726424 (1359, 1360)	Novel Protein sim. GBank gi 5174493 ref NP_005080.1 pLAMC - laminin, gamma 3	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264600, 264602 264102, 264907, 264908, 265006, 264693, 263972, 83373044, 264568
681	84322017 (1361, 1362)	Novel Protein sim. GBank gi 5174493 ref NP_005080.1 pLAMC - laminin, gamma 3		UNCLASSIFIED	264595 264634
682	11392478 (1363, 1364)	Novel Protein sim. GBank gi 4758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	
683	80083660 (1365, 1366)	Novel Protein sim. GBank gi 4758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)			264605
684	20465367 (1367, 1368)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]			
685	80246735 (1369, 1370)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]			264909, 263967, 263981
686	79208808 (1371, 1372)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]			264631 264693, 264635
687	80085629 (1373, 1374)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		peptidase	264907, 264638
688	79853412 (1375, 1376)	Novel Protein sim. GBank gi 2688962 (AF027768) - LspA [Serratia marcescens]			
689	88064256 (1377, 1378)	Novel Protein sim. GBank gi 3046931 (AF049330) - PPAR gamma coactivator [Mus musculus]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264906, 264907, 265007, 265009, 60433438, 21908754, 264760, 18108358, 21908768, 21906769, 265021, 18108361, 263974, 18108379, 264557, 18108385, 22279002 264510, 264511, 264764, 264769
690	80389750 (1379, 1380)	Novel Protein sim. GBank gi 2498941 sp Q15426 SP62_HUMAN - SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)		UNCLASSIFIED	
691	81854392 (1381, 1382)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264757 55812038, 55811957, 265018, 55811150, 18108351, 264908, 60431528, 264594
692	83608938 (1383, 1384)	Novel Protein sim. GBank gi 2687327 sp Q10103 VC48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN		UNCLASSIFIED	264635
693	79586116 (1385, 1386)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 8]			
694	82455983 (1387, 1388)	Novel Protein sim. GBank gi 2687327 sp Q10103 VC48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278996, 264510, 264602, 264603, 264762, 264687, 264769, 264693

695	94147849 (1389, 1390)	Novel Protein sim. GBank gij4468339[emb]CAB38059.1] - (AJ010901) MUC4 [Homo sapiens]	Contains protein domain (PF000094) - von Willebrand factor type D domain	UNCLASSIFIED	56182575, 264509, 264905, 264907, 29331830, 264908, 264909, 264511, 265007, 264910, 264758, 264764, 264288, 65274791, 264905, 264595
696	78830882 (1391, 1392)	Novel Protein sim. GBank gij2649950 (AE001058) - glutamine ABC transporter, ATP-binding protein (gho) [Archaeoglobus fulgidus]	Contains protein domain (PF000005) - ABC transporter	transport	
697	11767889 (1393, 1394)	Novel Protein sim. GBank gij1731343[sp]Q10694[Y25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY49.25]	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	264682
698	68895862 (1395, 1398)			UNCLASSIFIED	264688, 35695917
699	79582558 (1397, 1398)			UNCLASSIFIED	264682
700	78830898 (1399, 1400)				264693
701	80230242 (1401, 1402)	Novel Protein sim. GBank gij1001236[db]BAA10477] - (DB4003) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	264488, 264510, 264511, 264602, 264605, 264689
702	78814789 (1403, 1404)	Novel Protein sim. GBank gij2488935[sp]Q46338[SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT]		UNCLASSIFIED	264909
703	20446820 (1405, 1406)			oxidase	264604
704	94312224 (1407, 1408)	Novel Protein sim. GBank gij3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264288, 56181562, 33657109, 264629, 55811576
705	17832141 (1408, 1410)	Novel Protein sim. GBank gij421091[pir]S30730 - hypothetical protein o208 - Escherichia coli		UNCLASSIFIED	265006
706	20288062 (1411, 1412)	Novel Protein sim. GBank gij3024872[sp]Q55790[Y074_SYNY3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074]			264600
707	20638065 (1413, 1414)	Novel Protein sim. GBank gij3420608[sp]AAC31907.1] - (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]	transport		264603
708	20708292 (1415, 1416)	Novel Protein sim. GBank gij3649741[emb]CAA03985] - (AJ000281) mucin [Homo sapiens]	struct		264601, 264692
709	88001439 (1417, 1418)	Novel Protein sim. GBank gij3080425[emb]CAA18744.1] - (AL022604) putative protein [Arabidopsis thaliana]			18108398, 264637, 264908, 264909
710	11356683 (1419, 1420)				264369
711	17931418 (1421, 1422)	Novel Protein sim. GBank gij4758686[ref]NP_002323.1[lpLRP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)]	Contains protein domain (PF00056) - apolipoprotein repeat class B		265019
712	80258164 (1423, 1424)				264591
713	79263126 (1425, 1426)	Novel Protein sim. GBank gij1703268[sp]Q11056[AM12_MYCTU - PUTATIVE AMIDASE CY50.19C]	hydrolase		264906, 264907
714	27847651 (1427, 1428)	Novel Protein sim. GBank gij4502351[ref]NP_001692.1[lpBAAT - bile acid Coenzyme A: amino acid N-acyltransferase; glycine N-choyloltransferase]			264508, 264555

715	78639423 (1428, 1430)	Novel Protein sim. GBank gjl1780035 (AE000352) - ori, hypothetical protein [Escherichia coli]		UNCLASSIFIED	264907	
716	78559072 (1431, 1432)				264692	
717	79491842 (1433, 1434)	Novel Protein sim. GBank gjl2494074 (spjP55653) GABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+)(SSDH)		dehydrogenase	264636	
718	94319658 (1435, 1436)	Novel Protein sim. GBank gjl3873679 (embjCAA94886) (Z71178) similar to pro-collagen domains: cDNA EST. EMBL:D27978 comes from this gene: cDNA EST. EMBL:D27977 comes from this gene: cDNA EST. EMBL:D34199 comes from this gene: cDNA EST. EMBL:D64392 comes from this gene: cDNA EST. EMBL... Novel Protein sim. GBank gjl2104302 (embjCAB08631) (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]	Contains protein domain (PF000093) - von Willebrand factor type C domain	kinase	18108392, 22278994, 22278998, 265008, 265018, 264681, 18108354, 264684, 264685, 264686, 264687, 264689, 21906769, 18108361, 264691, 264692, 55810764, 264635, 18108381, 18108382, 83373044, 18108388	
719	17679564 (1437, 1438)			UNCLASSIFIED	265011	
720	79841684 (1439, 1440)				264908	
721	15020180 (1441, 1442)	Novel Protein sim. GBank gjl123530 (spjP04929) HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	264629	
722	9882603 (1443, 1444)	Novel Protein sim. GBank gjl498253 (U02372) - Integrase [Vibrio cholerae]			264910	
723	19755599 (1445, 1446)	Novel Protein sim. GBank gjl2253054 (embjCAB10705) (Z97559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	264691	
724	10126494 (1447, 1448)	Novel Protein sim. GBank gjl4083015 (AF083061) - protease P1A [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	protease	264909	
725	79878679 (1449, 1450)			UNCLASSIFIED	264905, 264907	
726	13086282 (1451, 1452)			UNCLASSIFIED	264636	
727	13522872 (1453, 1454)				264634	
728	20268471 (1455, 1456)	Novel Protein sim. GBank gjl2633910 (embjCAB13411) (Z99112) similar to hypothetical proteins [Bacillus subtilis]			264587	
729	11293753 (1457, 1458)			UNCLASSIFIED	264490	
730	18900373 (1459, 1460)	Novel Protein sim. GBank gjl2494860 (spjQ45291) GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	264564	
731	80058750 (1461, 1462)	Novel Protein sim. GBank gjl1146192 (L47838) - putative [Bacillus subtilis]		UNCLASSIFIED	264605	
732	80258175 (1463, 1464)	Novel Protein sim. GBank gjl1168396 (spjP46681) AIP2_YEAST - ACTIN INTERACTING PROTEIN 2		struct	264591, 264594, 264595	
733	20446839 (1465, 1466)			UNCLASSIFIED	264604	
734	20435987 (1467, 1468)	Novel Protein sim. GBank gjl3184080 (embjCAA19336) (AL023781) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	264604	

735	11607959 (1469, 1470)	Novel Protein sim. GBank gi401382[sp]P27432[YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELC INTERGENIC REGION				264594
736	10879734 (1471, 1472)	Novel Protein sim. GBank gi400831[sp]P31135[POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport		264636
737	78945340 (1473, 1474)		Contains protein domain (PF00815) - Regulator of G protein signaling domain	UNCLASSIFIED		265020
738	17895353 (1475, 1476)					265008
739	78833670 (1477, 1478)	Novel Protein sim. GBank gi250666[sp]P33225[TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)		oxidase		264910
740	19881557 (1479, 1480)	Novel Protein sim. GBank gi250666[sp]P33225[TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)				264907, 264764, 264634, 264637
741	78827273 (1481, 1482)	Novel Protein sim. GBank gi250666[sp]P33225[TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED		264689, 35696286, 264510, 264908, 18108362
742	82393795 (1483, 1484)	Novel Protein sim. GBank gi250666[sp]P33225[TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)	Domain of unknown function	UNCLASSIFIED		29331822, 264910, 264762
743	82300051 (1485, 1486)	Novel Protein sim. GBank gi127420[sp]P19888[MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)]	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase	UNCLASSIFIED		264488, 264259, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264596, 264759, 265010, 265011, 18108351, 264763, 264288, 264766, 264768, 264693, 18108370, 264629, 18108372, 264630, 264631, 264634, 264558, 18108385, 264482, 264564, 264567
744	80230421 (1487, 1488)					18108397, 264511, 264690, 264628, 264638, 264692, 264639, 264768
745	9841963 (1489, 1490)	Novel Protein sim. GBank gi178921[pr]J[S04846 - UDP-N- acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate--D- alanine-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli		glycoprotein		264906
746	11073229 (1491, 1492)	Novel Protein sim. GBank gi3386354 (AF074705) - pyocelin synthetase [Pseudomonas aeruginosa]		synthase		264600
747	94322044 (1493, 1494)	Novel Protein sim. GBank gi288741[dbj]BA24848 - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	oxidase		66714117, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264681, 264288, 264766, 264687, 264768, 264769, 21906768, 35695917, 264691, 264693, 264628, 264634, 264635, 264639, 56182323, 83373044
748	11617923 (1495, 1496)					264690

749	20469119 (1497, 1498)	Novel Protein sim. GBank gi 1169727 sp P44948 PF000069 - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY- DNA GLYCOSYLASE)		UNCLASSIFIED	264604 264600
750	20296427 (1499, 1500)				
751	21636169 (1501, 1502)	Novel Protein sim. GBank gi 5360068 gb AAD42851.1 AF15968 - (AF15968) serine/threonine kinase PKM3 [Myxococcus xanthus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264605, 264559
752	82450366 (1503, 1504)	Novel Protein sim. GBank gi 1168662 sp P44426 BIOA_HAEIN - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	UNCLASSIFIED	264508, 264907, 264510, 265011, 264762, 264689, 35695855, 264638, 18108387
753	80508718 (1505, 1506)	Novel Protein sim. GBank gi 2851530 sp P32399 YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORFB)		UNCLASSIFIED	264909, 264600, 264602, 264604, 264760, 264769, 264634
754	95083741 (1507, 1508)				
755	80185448 (1509, 1510)	Novel Protein sim. GBank gi 3449276 emb CAA20420 - (AL031317) putative dehydrogenase [Streptomyces coelicolor]		UNCLASSIFIED	264448, 264690 264769, 264689, 264638, 264639
756	94631686 (1511, 1512)				
757	79488533 (1513, 1514)	Novel Protein sim. GBank gi 4580331 emb CAB40107.1 - (AJ001206) putative glycogen debranching enzyme [Streptomyces coelicolor]		UNCLASSIFIED	264682, 264685 265007, 18108387, 265007, 18108387
758	78963176 (1515, 1516)			amylase	
759	79475667 (1517, 1518)	Novel Protein sim. GBank gi 2911858 (AF047659) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264684, 264686
760	87628888 (1519, 1520)	Novel Protein sim. GBank gi 3451312 emb CAA20449 - (AL031324) membrane atpase [Schizosaccharomyces pombe]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	29331822, 264908, 5264045, 56182435, 60170831, 21906754, 265017, 265019, 264681, 264687, 264688, 21906768, 21906768, 265020, 265021, 265022, 264635, 22279000
761	79877966 (1521, 1522)	Novel Protein sim. GBank gi 3327158 db BAA31647 - (AB014572) KIAA0672 protein [Homo sapiens]		UNCLASSIFIED	264766
762	80023563 (1523, 1524)	Novel Protein sim. GBank gi 4981266 gb AAC35822.1 AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdB [Thermotoga maritima]		UNCLASSIFIED	264907, 264593, 265020
763	20294813 (1525, 1526)				264600
764	39515024 (1527, 1528)				264603

765	80025347 (1529, 1530)	Novel Protein sim. GBank gij3845093 (AE001371) - erythrocyte membrane protein PIEMP3 (Plasmodium falciparum)		struct	264805, 264906, 264594, 264686, 33657023
766	82417404 (1531, 1532)	Novel Protein sim. GBank gij541121 (pirjS40827 - hypothetical protein o300 - Escherichia coli)		UNCLASSIFIED	264605, 264762, 18108374
767	10296742 (1533, 1534)	Novel Protein sim. GBank gij541121 (pirjS40827 - hypothetical protein o300 - Escherichia coli)		UNCLASSIFIED	264907
768	79416080 (1535, 1536)	Novel Protein sim. GBank gij2982501 (embjCAA06164) - (AJ004832) neuropathy target esterase (Homo sapiens)		UNCLASSIFIED	264592, 264595
769	80086554 (1537, 1538)	Novel Protein sim. GBank gij283437 (pirjS27850 - hypothetical protein - Trypanosoma cruzi (fragment))		esterase	55810764, 264559
770	80417847 (1539, 1540)	Novel Protein sim. GBank gij4769004 (gbjAAD29715.1) (AF140598) ring-box protein 1 (Homo sapiens)		UNCLASSIFIED	264905, 264907, 264828, 264909, 265010, 264766, 264628, 264629, 264834, 264836, 264555
771	95329509 (1541, 1542)	Novel Protein sim. GBank gij4769004 (gbjAAD29715.1) (AF140598) ring-box protein 1 (Homo sapiens)	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	56182575, 35696286, 264259, 66714117, 264107, 66712502, 56182435, 264112, 55812038, 87168559, 264288, 21906766, 33657023, 65274620, 65274791, 18108381
772	76971362 (1543, 1544)	Novel Protein sim. GBank gij5531324 (embjCAB51045.1) - (AJ009579) putative alkane 1-monoxygenase (Pseudomonas fluorescens)		UNCLASSIFIED	264910
773	76945363 (1545, 1546)	Novel Protein sim. GBank gij5531324 (embjCAB51045.1) - (AJ009579) putative alkane 1-monoxygenase (Pseudomonas fluorescens)		UNCLASSIFIED	265020
774	79856129 (1547, 1548)	Novel Protein sim. GBank gij5531324 (embjCAB51045.1) - (AJ009579) putative alkane 1-monoxygenase (Pseudomonas fluorescens)		UNCLASSIFIED	264909
775	20620141 (1549, 1550)	Novel Protein sim. GBank gij4505461 (refNP_003624.1) (nRNPB - nuclear restricted protein, BTB domain-like (brain))	Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	UNCLASSIFIED	264555
776	76942693 (1551, 1552)	Novel Protein sim. GBank gij4505461 (refNP_003624.1) (nRNPB - nuclear restricted protein, BTB domain-like (brain))	Contains protein domain (PF01344) - Kelch motif		265019
777	79960378 (1553, 1554)	Novel Protein sim. GBank gij4505461 (refNP_003624.1) (nRNPB - nuclear restricted protein, BTB domain-like (brain))		protease	21906754, 265020, 60170615, 264691
778	20691310 (1555, 1556)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase (Mycobacterium tuberculosis)		UNCLASSIFIED	264511
779	80054024 (1557, 1558)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase (Mycobacterium tuberculosis)			264603
780	95288987 (1559, 1560)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase (Mycobacterium tuberculosis)		synthase	264907, 264600, 264601, 264602, 264603, 264604, 264605, 264486
781	80250049 (1561, 1562)	Novel Protein sim. GBank gij4155447 (AE001517) - proline/betaine transporter (Helicobacter pylori J99)		UNCLASSIFIED	264905, 264907, 265010, 264600, 264601, 18108362, 18108374, 264556
782	8758529 (1563, 1564)	Novel Protein sim. GBank gij4155447 (AE001517) - proline/betaine transporter (Helicobacter pylori J99)		UNCLASSIFIED	264605
783	16410791 (1565, 1566)	Novel Protein sim. GBank gij4155447 (AE001517) - proline/betaine transporter (Helicobacter pylori J99)			265020
784	80051197 (1567, 1568)	Novel Protein sim. GBank gij4155447 (AE001517) - proline/betaine transporter (Helicobacter pylori J99)		UNCLASSIFIED	264635, 33657023, 29331828, 265017, 264565, 264566
785	56073541 (1569, 1570)	Novel Protein sim. GBank gij3451335 (AC005525) - F22162_1 (Homo sapiens)	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696052, 264604
786	20438842 (1571, 1572)	Novel Protein sim. GBank gij136748 (spP10905) (UGPA_ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA)		transport	264603
787	80258364 (1573, 1574)	Novel Protein sim. GBank gij136748 (spP10905) (UGPA_ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA)		UNCLASSIFIED	264593

788	80507844 (1575, 1576)	Novel Protein sim. GBank gij2746079 (AF015310) - BTH1 [Brassica napus]		synthase	264908, 264602, 264603, 264769, 264638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gij2351849 (U933357) - 40 kDa heat shock chaperone protein [Halobacterium salinarum]		UNCLASSIFIED	265007
790	86284406 (1579, 1580)	Novel Protein sim. GBank gij5706378 [dbj]BAA83099.1 - (AB026118) MALT1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	22279899, 28331824, 264828, 87188559, 265018, 21906765, 21906767, 21906768, 21906769, 265020, 264692, 22279000, 264563
791	94851627 (1581, 1582)	Novel Protein sim. GBank gij5689948 [emb]CA851985.1 - (AL109863) putative isocitryl-IRNA synthetase [Streptomyces coelicolor A3(2)]			264601, 264605, 264636
792	80058786 (1583, 1584)	Novel Protein sim. GBank gij393194 (L023375) - S-anilgen [Plasmodium falciparum]		struct	265021, 264631, 264635, 264556
793	79838730 (1585, 1586)	Novel Protein sim. GBank gij1345408 [dbj]BAA05046 - (D26046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264693
794	81839294 (1587, 1588)	Novel Protein sim. GBank gij105884 [pir]S24023 - dopamine receptor D4 - human (fragment)		UNCLASSIFIED	264603, 264604, 264910, 264762, 264906, 264639, 264909, 264757
795	80074988 (1589, 1590)	Novel Protein sim. GBank gij1877334 [emb]CA807082 - (Z92771) birA [Mycobacterium tuberculosis]		carboxylase	264488, 35696052, 264905, 264907, 265010, 35696423, 264636
796	86569451 (1591, 1592)				60432229, 55811150, 264630, 264637, 264565
797	87771781 (1593, 1594)	Novel Protein sim. GBank gij2995447 [emb]CAA71519 - (Y10495) CDV-1R protein [Mus musculus]		struct	22278998, 264093, 264094, 66714117, 21906767, 21906769, 265020, 265022
798	79855209 (1595, 1596)			transcriptfactor	264687, 264768, 264693
799	79857816 (1597, 1598)	Novel Protein sim. GBank gij4467250 [emb]CA837575 - (AL035569) probable Glu-IRNA Gln amidotransferase subunit [Streptomyces coelicolor]		hydrolase	264909, 264910, 264638, 264638
800	79970189 (1599, 1600)				
801	80499399 (1601, 1602)	Novel Protein sim. GBank gij2791517 [emb]CAA16054 - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		UNCLASSIFIED	264488
802	79834598 (1603, 1604)	Novel Protein sim. GBank gij4887211 [gb]AAD32237.1 [AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]		transport	264508, 264511, 265006, 265009, 264769, 264567, 264486
803	20467520 (1605, 1606)			struct	264605
804	10174239 (1607, 1608)	Novel Protein sim. GBank gij1176152 [sp]P44507 [YHAD_HAEIN - HYPOTHETICAL PROTEIN H0091]		kinase	264510
805	79599993 (1609, 1610)				
806	80484113 (1611, 1612)	Novel Protein sim. GBank gij2764612 [emb]CAA04683 - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	- transferase	264508, 264769
807	80381812 (1613, 1614)	Novel Protein sim. GBank gij2833311 [sp]Q21828 [YNF0 CAEEI - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III]			264764

808	35106817 (1615, 1616)	Novel Protein sim. GBank gi 3913092 sp Q46170 ARCD_CLOPE - ARGININE/ORNITHINE ANTIporter		transport	264909, 264602, 21906764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gi 3913016 sp P74309 ALF1_SNNY3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	264508, 264906, 264909, 265007, 264910, 264758, 264600, 264602, 264603, 264605, 264687, 264769, 264889, 264636, 264486
810	80192761 (1618, 1620)	Novel Protein sim. GBank gi 401472 sp P30863 YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MLTD INTERGENIC REGION	Contains protein domain (PF00248) - Aldoketo reductase family	reductase	284369
811	80079280 (1621, 1622)			UNCLASSIFIED	264558
812	10297654 (1623, 1624)			UNCLASSIFIED	264692
813	79612280 (1625, 1626)			UNCLASSIFIED	264906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gi 146168 (J01617) - glutaminyl- RNA synthetase [Escherichia coli]		synthase	264905, 264602, 264605, 264682, 264687, 264769, 264636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gi 4589652 dbj BAA76848.1 - (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	264488, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29146489, 264905, 264908, 265007, 33657402, 60433356, 60433438, 264758, 265011, 265017, 265018, 265019, 264369, 264288, 264685, 21906765, 21906767, 265020, 265021, 264892, 65274620, 33657109, 264629, 18108376, 264635, 264638, 60170394, 58182323, 264564 264600
816	18881910 (1631, 1632)			UNCLASSIFIED	264595
817	95293316 (1633, 1634)	Novel Protein sim. GBank gi 1781144 emb CAB06254 - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]			
818	80938190 (1635, 1636)	Novel Protein sim. GBank gi 1477468 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]			65274572, 22278999, 60424269, 35696052, 55812038, 21906768, 55811957, 35695917, 33657023, 18108370, 18108374, 55810764, 35696423, 55811576, 264638
819	80254977 (1637, 1638)	Novel Protein sim. GBank gi 1001352 dbj BAA10839 - (DB4006) ABC transporter [Synecocystis sp.]		transport	264585
820	80059568 (1639, 1640)	Novel Protein sim. GBank gi 586814 sp P37484 YYBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION		UNCLASSIFIED	264600, 264602, 264604
821	79762590 (1641, 1642)			UNCLASSIFIED	264910
822	80215310 (1643, 1644)			UNCLASSIFIED	264510, 264594, 264637
823	94992299 (1645, 1646)	Novel Protein sim. GBank gi 3878400 emb CAA95828 - (Z71264) predicted using GeneFinder; Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL:D32742 comes from this gene; cDNA EST EMBL:D33617 comes from this gene; cDNA EST....		struct	264509, 264687, 264691
824	80411171 (1647, 1648)	Novel Protein sim. GBank gi 1370076 emb CAA66887 - (X98235) type I [Drosophila melanogaster]	Contains protein domain (PF01429) - Methyl-CpG binding domain		264910, 264763, 264769, 264693

825	20638600 (1649, 1650)	Novel Protein sim. GBank gij3025132[sp]P77391[YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION (AL021646) hypothetical protein Rv3202c [Mycobacterium tuberculosis]		UNCLASSIFIED	264592	
826	11075047 (1651, 1652)	Novel Protein sim. GBank gij324228[1emb]CAA16669] - (AL021646) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605	
827	80054207 (1653, 1654)	Novel Protein sim. GBank gij3417424[emb]CAA20312] - (AL031261) putative transport protein [Schizosaccharomyces pombe]			264603	
828	95106322 (1655, 1656)	Novel Protein sim. GBank gij4336692[gb]AAD17897] - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 264508, 264905, 264509, 264906, 264807, 264908, 264909, 264512, 264910, 264591, 264758, 264600, 264768, 264768, 21908768, 35695917, 284691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 264639, 83373044, 18108385, 264563, 264566, 264466	
829	81742215 (1657, 1658)	Novel Protein sim. GBank gij3820539 (AF080002) - UDP-N- acetyluramyl triphosphate synthetase MurC [Helicobacter mobilis]		UNCLASSIFIED	264758, 264634	
830	20396091 (1659, 1660)	Novel Protein sim. GBank gij1870004[emb]CAB06855] - (Z82539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	66714117, 264910, 264639	
831	87112435 (1661, 1662)	Novel Protein sim. GBank gij2500056[sp]Q46267[PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264906	
832	19536322 (1663, 1664)	Novel Protein sim. GBank gij2497531[sp]Q46078[KPYK_CORGL - PYRUVATE KINASE (PK)		UNCLASSIFIED	264602	
833	20726654 (1665, 1666)	Novel Protein sim. GBank gij2497531[sp]Q46078[KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	UNCLASSIFIED	264600, 264602, 264769, 264689, 264636	
834	21428762 (1667, 1668)	Novel Protein sim. GBank gij2497531[sp]Q46078[KPYK_CORGL - PYRUVATE KINASE (PK)			264768, 263994, 21908767, 264910, 264632, 264635, 264259, 264639, 264693, 83373044, 264758, 35695052, 22278002, 264508, 264905, 264906, 264448, 263972, 264908, 264909	
835	94140482 (1669, 1670)	Novel Protein sim. GBank gij699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		transport	35695917, 264557	
836	56126552 (1671, 1672)	Novel Protein sim. GBank gij728867[sp]P40602[APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	264595	
837	79450450 (1673, 1674)	Novel Protein sim. GBank gij2496533[sp]Q50598[Y0D8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	264687	
838	79184203 (1675, 1676)	Novel Protein sim. GBank gij4557753[re]NP_000372.1[pMD1 - midline 1 protein		UNCLASSIFIED	264806	
839	78641125 (1677, 1678)	Novel Protein sim. GBank gij4557753[re]NP_000372.1[pMD1 - midline 1 protein	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264762, 264556	
840	80059851 (1679, 1680)	Novel Protein sim. GBank gij4557753[re]NP_000372.1[pMD1 - midline 1 protein				

841	80376318 (1681, 1682)	Novel Protein sim. GBank glt139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript/flactor	264764
842	80078724 (1683, 1684)	Novel Protein sim. GBank glt2114321[dbj]BAA200371 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	264905, 264908, 265008, 265009, 18108374, 56182323, 264558
843	87002847 (1685, 1686)	Novel Protein sim. GBank glt3882325[dbj]BAA34522.1] - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	264091, 29331825, 264906, 264768, 264563
844	17941439 (1687, 1688)	Novel Protein sim. GBank glt224721[dbj]BAA20844] - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript/flactor	265011
845	18346844 (1688, 1690)				264629
846	79863441 (1691, 1692)	Novel Protein sim. GBank glt625679[pir]A36929 - virulence regulatory protein VsrB - Pseudomonas solanacearum		Kinase	264907
847	78695348 (1693, 1694)				264909
848	78489365 (1695, 1696)			UNCLASSIFIED	265020
849	78756367 (1697, 1698)			UNCLASSIFIED	264568
850	78817849 (1699, 1700)	Novel Protein sim. GBank glt3183245[sp]P78061[JC_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)]	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264909
851	95320333 (1701, 1702)	Novel Protein sim. GBank glt5454130[re]NP_008280.1p[TLN] - talin	Contains protein domain (PF01608) - ILWEQ domain		264488, 52644507, 264489, 18108398, 65274572, 56182575, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 20281171, 264490, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264107, 264905, 264908, 264907, 264908, 52644045, 56182435, 265006, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433356, 33657402, 60433438, 264595, 264758, 264759, 21906754, 33109954, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 264762, 264681, 18108351, 264763, 264448, 264682, 264784, 264683, 18108354, 264288, 264369, 264685, 264766, 264687, 264768, 264769, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 29148629, 55811857, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 264692, 33657023, 264693, 263966, 33657109, 27486261, 27486262, 27486264, 27486265, 35695763, 60431602, 18108370, 20281089, 264629, 18108374, 18108376, 55811576, 35696423, 35695855, 264634, 264635, 264636, 264555, 60431850, 264556, 264691
852	10147366 (1703, 1704)				

853	13032587 (1705, 1706)					264636
854	80052438 (1707, 1708)	Novel Protein sim. GBank gij3402836[emb]CAA76082] - (Y16136) 2-enoate reductase [Moorella thermoacetica]		reductase		264566
855	79641130 (1709, 1710)					264692
856	11594238 (1711, 1712)			UNCLASSIFIED		264591
857	79210165 (1713, 1714)			UNCLASSIFIED		264630, 264634
858	80248910 (1715, 1716)					265008, 265009, 264601, 264602, 264603, 18108351
859	20296634 (1717, 1718)					264559
860	80041749 (1718, 1720)			UNCLASSIFIED		264489
861	55857045 (1721, 1722)			UNCLASSIFIED		33857023, 264630
862	80079467 (1723, 1724)					264600
863	80578931 (1725, 1726)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED		264488, 18108398, 35696286, 264259, 18108351, 264288, 265021
864	94839904 (1727, 1728)			UNCLASSIFIED		264259, 264112, 263974
865	80045310 (1729, 1730)	Novel Protein sim. GBank gij5689884[emb]CAB52047.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01479) - S4 domain			264635, 264600, 264636, 264591, 264602, 264693
866	80162031 (1731, 1732)	Novel Protein sim. GBank gij455787[ref]NP_000341.1pABCR - ATP binding cassette transporter		transport		264288, 264557, 264558
867	80062402 (1733, 1734)					264605
868	10075364 (1735, 1736)			UNCLASSIFIED		264909
869	80062406 (1737, 1738)					264605, 264687, 18108374
870	80248651 (1739, 1740)	Novel Protein sim. GBank gij628660[pir]S37755 - Adenyl-transferase - Escherichia coli		transferase		264601, 264636
871	20378285 (1741, 1742)	Novel Protein sim. GBank gij1708180[sp]Q10602[HEMK_MYCTU - HEMK PROTEIN HOMOLOG		UNCLASSIFIED		264603
872	95197114 (1743, 1744)	Novel Protein sim. GBank gij1545959[emb]CAA67763] - (X99384) paladin [Mus musculus]		UNCLASSIFIED		35696286, 22278998, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 264910, 264591, 60433356, 264596, 52646317, 87168474, 265010, 264602, 264603, 265017, 265018, 264605, 18108351, 264764, 264766, 264768, 52644229, 264769, 21906765, 265021, 264534, 264691, 52645129, 264628, 264629, 35698423, 65274781, 264631, 264632, 264635, 264636, 264556, 264637, 264638, 264639, 60432113, 22279000, 22279002, 264594
873	20189728 (1745, 1746)	Novel Protein sim. GBank gij4156104 (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED		264595

874	8007662 (1747, 1748)	Novel Protein sim. GBank gii134319sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264600
875	86608446 (1748, 1750)	Novel Protein sim. GBank gii481000 pfrj S37594 - mucin - human (fragment)			264259, 264448, 264288, 264557, 87168518
876	86465157 (1751, 1752)	Novel Protein sim. GBank gii3128283 (AF010496) - Iron(III) dicitrate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF000005) - transport ABC transporter		264907, 264601, 264602, 264605, 265020, 60431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gii731074 sp P40349 URB1_USTMA - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1	Contains protein domain (PF00320) - transcriptfactor GATA zinc finger		22278998, 264909, 264369
878	80187289 (1755, 1756)	Novel Protein sim. GBank gii1351614 sp Q09853 YAED_SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I	ATPase-associated		264369, 264555
879	94328962 (1757, 1758)	Novel Protein sim. GBank gii3875304 emb CAA98434 - (Z74030) predicted using GeneFinder; cDNA EST EMBL: C07609 comes from this gene; cDNA EST EMBL: C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com...			56182575, 29331824, 264508, 264906, 265018, 18108351, 264448, 264683, 21908768, 21908768, 60170815, 33657023, 65274620, 33657109, 18108374, 35695855, 264563
880	8491135 (1759, 1760)	Novel Protein sim. GBank gii137120 sp P11214 UROT_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)	Contains protein domain (PF00051) - cathepsin Kringle domain		264508
881	11290122 (1761, 1762)			UNCLASSIFIED	264508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gii2632098 emb CAA75667 - (Y15513) Prodos protein [Drosophila melanogaster]		UNCLASSIFIED	264558
883	79582968 (1765, 1766)	Novel Protein sim. GBank gii1155068 emb CAA64425 - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264688
884	13517921 (1767, 1768)	Novel Protein sim. GBank gii2078027 emb CAB08467 - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED	264636
885	80052457 (1769, 1770)			UNCLASSIFIED	264605, 18108362
886	11685136 (1771, 1772)	Novel Protein sim. GBank gii2695834 emb CAA15904 - (AL021006) sucA [Mycobacterium tuberculosis]			264690
887	94315307 (1773, 1774)	Novel Protein sim. GBank gii5689395 dbj BAA82981.1 - (AB028952) KIAA1029 protein [Homo sapiens]	dehydrogenase		35696052, 264906, 264600, 264603, 35695917, 35695855, 264636
888	10083399 (1775, 1776)	Novel Protein sim. GBank gii1881338 dbj BAA19365 - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE [Bacillus subtilis]	UNCLASSIFIED		264908
889	20385917 (1777, 1778)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			264603
890	19904337 (1779, 1780)				264629

891	13516879 (1781, 1782)	Novel Protein sim. GBank gi 4959396 gb AAD34331.1 AF11248 - (AF11248.1) RAD54B protein [Homo sapiens]		UNCLASSIFIED	264636
892	87634157 (1783, 1784)	Novel Protein sim. GBank gi 545526 bbs 143833 - LBP- 1b=transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namahwa cells, Peptide, 541 aa]		transcriptfactor	22278986, 22278999, 29331828, 35696052, 264908, 264909, 265009, 265011, 264602, 265018, 264766, 21908765, 21908768, 21906769, 265020, 265021, 56526486
893	79168037 (1785, 1786)	Novel Protein sim. GBank gi 2829688 sp P80508 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) [CSASE]		synthase	264689, 263967
894	11102240 (1787, 1788)				263978
895	80239868 (1789, 1790)			UNCLASSIFIED	264508, 264600, 264555, 264559
896	79747803 (1791, 1792)			264632	
897	94991923 (1793, 1794)			UNCLASSIFIED	264686, 29331828, 264511
898	87895109 (1795, 1796)		Contains protein domain (PF000047) - Immunoglobulin domain		56182575, 60432289, 56182435, 60432229, 55011957, 22279000, 264486
899	11100463 (1797, 1798)	Novel Protein sim. GBank gi 1750127 (U66480) - YncC [Bacillus subtilis]		transport	264601
900	80499768 (1799, 1800)	Novel Protein sim. GBank gi 3122879 sp O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - tRNA synthetases class II (A)	synthase	264907, 264602, 264605, 264769, 35695917, 18108376, 264563
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi 335570 emb CAA20001 - (AL031124) 3-Isopropylmalate dehydratase large subunit [Streptomyces coelicolor]	Contains protein domain (PF00330) - Aconitase family (aconitase hydratase)	isomerase	264909, 265008, 264602, 264604, 264769, 264689, 264693
903	82060208 (1805, 1806)	Novel Protein sim. GBank gi 2960120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	kinase	35996052, 264905, 264510, 264511, 264512, 264605, 264760, 18108351, 264762, 264687, 264768, 264769, 264688, 21908764, 35695917, 27486262, 35695855, 264634, 264638, 264486
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi 728887 sp P40506 ARGI_COCIM - ARGINASE	Contains protein domain (PF00491) - Arginase family	hydrolase	264604
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi 4567200 gb AAD23616.1 AC00718 - (AC007166) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264909
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi 3738200 emb CAA21292 - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			264595, 264605
907	87913201 (1813, 1814)			UNCLASSIFIED	60432289, 264601, 264690
908	11754482 (1815, 1816)	Novel Protein sim. GBank gi 3668940 dbj BAA34296 - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	264638
909	20727907 (1817, 1818)	Novel Protein sim. GBank gi 4569726 dbj BAA76883.1 - (AB003137) DnaJ homolog protein [Salix glauca]		UNCLASSIFIED	264602
910	16776206 (1819, 1820)		Contains protein domain (PF00584) - DnaJ central domain (4 repeats)	eph	265009

911	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P35685 RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomalprot	265010, 264604, 60432113
912	20448863 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AAD07921.1 - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 266895]		hydrolase	284559
913	20469357 (1825, 1826)				
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi 417657 sp Q03604 RIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	UNCLASSIFIED - reductase	264604 264636
915	87606703 (1829, 1830)	Novel Protein sim. GBank gi 5689571 dbj BAA83069.1 - (AB029040) KIAA1117 protein [Homo sapiens]			18108398, 22278996, 66714117, 264906, 284591, 21908768, 265020, 55811576, 264638
916	79444091 (1831, 1832)	Novel Protein sim. GBank gi 4186110 emb CAA71790 - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264595
917	20195985 (1833, 1834)				
918	91228795 (1835, 1836)	Novel Protein sim. GBank gi 1655699 emb CAA69032 - (Y07752) pterophorin-S [Volvox carter]		UNCLASSIFIED synthase	264605 264259, 28331826, 264908, 265019, 264448, 265020, 284835, 83373044
919	80436785 (1837, 1838)	Novel Protein sim. GBank gi 5689968 emb CAB52005.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265006, 264512, 264600, 264602, 264604, 264768, 18108370, 264563
920	79608095 (1839, 1840)	Novel Protein sim. GBank gi 1168448 sp Q05813 JAMP1_STRLI - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYL PROLINE AMINOPEPTIDASE I)		peptidase	264508
921	19858634 (1841, 1842)	Novel Protein sim. GBank gi 3850084 emb CAA21811.1 - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
922	78982605 (1843, 1844)				
923	86695830 (1845, 1846)	Novel Protein sim. GBank gi 267079 sp P29514 TB86_ARATH - TUBULIN BETA-6 CHAIN		tubulin	265018, 22279002 264907, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
924	21431341 (1847, 1848)				
925	20630332 (1849, 1850)	Novel Protein sim. GBank gi 2497688 sp Q60963 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	264510 264603
926	79397657 (1851, 1852)	Novel Protein sim. GBank gi 3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]			55811957, 263972, 264639
927	37036201 (1853, 1854)			UNCLASSIFIED	264769

928	80070610 (1855, 1856)	Novel Protein sim. GBank gij156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]			dehydrogenase	264605
929	20530336 (1857, 1858)				UNCLASSIFIED	264603
930	5496348 (1859, 1860)	Novel Protein sim. GBank gij115936[gblAAD03446.1] - (AF118223) No definition line found [Arabidopsis thaliana]				264259
931	10245731 (1861, 1862)	Novel Protein sim. GBank gij4490809[embjCAB38642.1] - (AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]		Contains protein domain (PF00317) - Ribonucleotide reductase	reductase	264486
932	80420813 (1863, 1864)	Novel Protein sim. GBank gij5459396[embjCAB50754.1] - (AL096839) putative integral membrane transport protein [Streptomyces coelicolor]			transport	264508, 264905, 264906, 264909, 264800, 264602, 264603, 264605, 264766, 264558, 18108387, 264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gij5689523[dbjBAA83045.1] - (AB029016) KIAA1093 protein [Homo sapiens]		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264508, 264686, 264693, 27486261, 18108370, 65274791, 264636, 264559, 22279002
934	80039105 (1867, 1868)	Novel Protein sim. GBank gij119111[spP12978][EBN2_EBV - EBNA-2 NUCLEAR PROTEIN]				264369, 22279002
935	80063162 (1869, 1870)				UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
936	80026632 (1871, 1872)	Novel Protein sim. GBank gij845686 (M32103) - ORF-27 [Staphylococcus aureus]			UNCLASSIFIED	22278995, 22278996, 264602, 264687, 32833986, 18108387
937	80250273 (1873, 1874)	Novel Protein sim. GBank gij1360669[pri][CGHU1V - collagen alpha 1(V) chain precursor - human]			synthase	263978
938	80026633 (1875, 1876)	Novel Protein sim. GBank gij2226243[embjCAA74531.1] - (Y14083) hypothetical protein [Bacillus subtilis]			UNCLASSIFIED	264602
939	11071694 (1877, 1878)					264600
940	94144252 (1878, 1880)	Novel Protein sim. GBank gij3560166[embjCAA20678] - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]		Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264905, 264906, 264907, 264908, 264909, 264511, 264910, 264592, 33657402, 264596, 264758, 264760, 264683, 264768, 264768, 264769, 33657023, 33657109, 264628, 264629, 264630, 264635, 264636, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264565, 18108391
941	11398414 (1881, 1882)					264593
942	19484122 (1883, 1884)				UNCLASSIFIED	264760
943	80080258 (1885, 1886)	Novel Protein sim. GBank gij4033729 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]			UNCLASSIFIED	264600, 264687, 264689, 264563
944	80216096 (1887, 1888)	Novel Protein sim. GBank gij2494764[spQ50729][GJAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)]			synthase	264511, 264603
945	80052477 (1889, 1890)	Novel Protein sim. GBank gij732353[spP39606][VWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION]		Contains protein domain (PF00818) - Ice nucleation protein repeat	UNCLASSIFIED	264906, 264604, 264605, 265020, 18108387
946	78248402 (1891, 1892)					265017

947	81802698 (1893, 1894)	Novel Protein sim. GBank gij2898770[emb]CAA172471 - (AL021899) hypothetical protein Rv2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18108394, 22278896, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264602, 265018, 264805, 264769, 264889, 264693
948	88185538 (1895, 1896)	Novel Protein sim. GBank gij2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		lgf	18108398, 56182575, 22278897, 22278999, 60432049, 28331822, 29331826, 284907, 56182435, 55811388, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486265, 263972, 55811576, 264638, 60170394, 264566
949	88081786 (1897, 1898)	Novel Protein sim. GBank gij4507985[ref]NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	29331825, 21906764, 27486261, 21906766, 52644298, 33657349, 87188518, 56994075, 265020, 265021, 87188559, 52644150, 264637
950	79485872 (1899, 1900)	Novel Protein sim. GBank gij1079461[pil]S43865 - cytochrome b, type II - potaroo (fragment)	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264683, 18108361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264604
952	79566954 (1903, 1904)	Novel Protein sim. GBank gij5305702[gb]AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	264910, 264691
953	10196003 (1905, 1906)	Novel Protein sim. GBank gij2495842[sp]Q47142 YFHS_ECOLI - HYPOTHETICAL 41.8 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION		transport	264510
954	9893326 (1907, 1908)	Novel Protein sim. GBank gij2360985 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	264508
955	95313410 (1909, 1910)	Novel Protein sim. GBank gij5454064[ref]NP_006319.1 pSIP1 - SYT interacting protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56994075, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264601, 264760, 18108351, 264762, 264763, 264764, 264766, 264686, 264767, 264687, 264768, 264769, 264689, 264828, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182323, 264639, 18108388, 264563, 284564
956	80064224 (1911, 1912)	Novel Protein sim. GBank gij2052129[emb]CAB08155 - (Z94752) rimJ [Mycobacterium tuberculosis]			264605
957	80056208 (1913, 1914)	Novel Protein sim. GBank gij1709787[sp]Q00451 PRF1_LYCES - 36.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	264603, 18108362
958	80036448 (1915, 1916)	Novel Protein sim. GBank gij2131050[emb]CAB09260 - (Z95844) opca [Mycobacterium tuberculosis]		UNCLASSIFIED	264908, 264910, 264762, 263978, 264637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gij2128478[pri]S51839 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264602, 264692
960	37815406 (1919, 1920)			UNCLASSIFIED	264259
961	20567383 (1921, 1922)				263978
962	11398318 (1923, 1924)				264593

963	80590374 (1925, 1926)				UNCLASSIFIED	264510, 264288, 264555, 264556, 264559, 264486
964	79832019 (1927, 1928)	Novel Protein sim. GBank glij458622[dbj]BAA76833.1] - (AB023206) KIAA0889 protein [Homo sapiens]			UNCLASSIFIED	264112, 264910, 264689
965	91229485 (1929, 1930)	Novel Protein sim. GBank glij542038[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	264488, 265017, 264448, 264634, 264558, 83373044
966	95292815 (1931, 1932)				UNCLASSIFIED	264908, 264592, 264596, 264604, 264768, 21906764, 264692, 264693, 264629, 264636, 264638
967	79255708 (1933, 1934)	Novel Protein sim. GBank glij1731207[sp]Q11156[RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3	Contains protein domain (PF00072) - Response regulator receiver domain		phosphatase	264780
968	78560269 (1935, 1936)	Novel Protein sim. GBank glij2661836[emb]CAA75187] - (Y14864) putative transport protein [Methylophilus methylotrophus]			transport	264693
969	79918470 (1937, 1938)	Novel Protein sim. GBank glij5419878[emb]CAB46422.1] - (AL098747) hypothetical protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type		dna_rna_bind	35696286, 264685, 264686, 35695917, 264692, 18108374, 264635
970	95085947 (1939, 1940)				UNCLASSIFIED	18108392, 18108394, 18108398, 22278995, 22278996, 22278998, 22278999, 29147620, 264828, 265006, 265007, 265008, 265009, 18108348, 33109954, 265010, 265011, 18108351, 264288, 21906767, 21906768, 18108370, 18108374, 18108377, 264630, 264635, 18108380, 83373044, 18108387, 18108388
971	78919770 (1941, 1942)				UNCLASSIFIED	265007, 265020, 22279002
972	20710704 (1943, 1944)					264557
973	20370183 (1945, 1946)	Novel Protein sim. GBank glij1723119[sp]P53990[Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174				264604
974	80037103 (1947, 1948)				UNCLASSIFIED	264565
975	10196018 (1949, 1950)				UNCLASSIFIED	264510
976	80205742 (1951, 1952)	Novel Protein sim. GBank glij3881459[emb]CAA92988.1] - (Z68753) predicted using GeneFinder; Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27680 comes from this gene; cDNA EST EMBL:D27679 comes from this gene; cDNA EST EMBL:D64477 comes from this ge...			UNCLASSIFIED	264508, 264906, 264756, 264632, 264639, 264563
977	10355349 (1953, 1954)	Novel Protein sim. GBank glij549456[sp]Q05335]XYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3			UNCLASSIFIED	264906
978	80025927 (1955, 1956)				UNCLASSIFIED	264600, 264602, 264603, 264604
979	80447820 (1957, 1958)	Novel Protein sim. GBank glij3171904[emb]CAA75869] - (Y15908) DIA-12C protein [Homo sapiens]			UNCLASSIFIED	264767, 264768, 265006, 265007, 264906
980	80025928 (1959, 1960)				UNCLASSIFIED	264600, 264602, 264605
981	80098550 (1961, 1962)	Novel Protein sim. GBank glij3599940 (AF017368) - (adogenital dysplasia protein 2 [Mus musculus])			UNCLASSIFIED	264692, 264555, 264556, 264557, 264559

982	80195670 (1983, 1984)	Novel Protein sim. GBank gij2950220[emb]CAA71575] - (Y10545) fused-cdb [Escherichia coli]		UNCLASSIFIED	264404
983	90995041 (1965, 1966)	Novel Protein sim. GBank gij476389[pil]B43402 - myosin heavy chain-B, neuronal - chicken		struct	65274572, 56182575, 264908, 264909, 265007, 265008, 264758, 265010, 55811150, 33657023, 264634, 264557, 264558
984	20468878 (1987, 1988)			UNCLASSIFIED	264605
985	65461368 (1969, 1970)	Novel Protein sim. GBank gij3451504[emb]CAA07660.1] - (A007747) hypothetical protein BbLPS1.21 [Bordetella bronchiseptica]	Contains protein domain (PF00534) - Glycosyl transferases group 1	transferase	56182435, 264600
986	87102868 (1971, 1972)			UNCLASSIFIED	264106, 264110, 265020, 60170615
987	79867231 (1973, 1974)			UNCLASSIFIED	264909
988	19858661 (1975, 1976)			UNCLASSIFIED	264600
989	88095329 (1977, 1978)			UNCLASSIFIED	264508, 265017, 264534, 264564
990	88057746 (1979, 1980)	Novel Protein sim. GBank gij5725506[gb]AAD48080.1]AF08015 - (AF060152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Reprolysin (M12B) family zinc metalloprotease	oxidase	264259, 264908, 265009, 264910, 264596, 264369, 264288, 264768, 264628, 264635, 264588
991	10108140 (1981, 1982)			UNCLASSIFIED	264909
992	78845694 (1983, 1984)	Novel Protein sim. GBank gij2105049[emb]CAB08635] - (Z95436) hypothetical protein Rv3845 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylyate and Guanylate cyclase catalytic domain	UNCLASSIFIED	264508, 264593
993	10814053 (1985, 1986)				264807
994	11090590 (1987, 1988)	Novel Protein sim. GBank gij3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	264602
995	94321911 (1988, 1990)	Novel Protein sim. GBank gij5106572[gb]AAD39760.1]AF14394 - (AF143946) transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	18108398, 65274572, 22278996, 264490, 60432049, 29331827, 29146498, 264508, 264905, 264907, 264908, 56182435, 265008, 264591, 264592, 60432229, 60431735, 33657402, 264595, 264758, 21906754, 265010, 265017, 265018, 264605, 264760, 264448, 264763, 264768, 21906785, 21906788, 21906789, 55811957, 264692, 264693, 264629, 35695423, 55811576, 35695855, 264636, 264555, 264556, 264558, 83373044, 22279002, 264563
996	91013745 (1991, 1992)	Novel Protein sim. GBank gij2911719 (AC004227) - KIA0011LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 29331824, 263978, 55811957, 56528486, 87168518, 264910, 264908, 264565, 264566, 264693, 264766
997	80503347 (1993, 1994)	Novel Protein sim. GBank gij2649101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	35696286, 22278997, 22278999, 264508, 264905, 264908, 265010, 264600, 264602, 264605, 264688, 264768, 265021, 264585, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gij1235303[sp]PD4929]HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR			264595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gi 2506697 sp P46480 YFCA_HAEN - HYPOTHETICAL PROTEIN HI0198		UNCLASSIFIED	264682	
1000	20727944 (1999, 2000)			UNCLASSIFIED	264602	
1001	86673131 (2001, 2002)	Novel Protein sim. GBank gi 2224699 db BAA20833 - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	60432049, 264807, 264909, 264511, 264603, 264693, 264684, 264687, 264689, 29148627, 21906769, 264692, 18108385, 22279000 265009, 264369, 265020	
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gi 58612 sp P37709 TRHY_RABIT - TRICHOHYALIN		strud		
1003	17633491 (2005, 2006)				265019	
1004	18314887 (2007, 2008)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X93413) U88 [Human herpesvirus 6]			264635	
1005	79617144 (2009, 2010)	Novel Protein sim. GBank gi 114073 sp P07672 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	264508	
1006	37815429 (2011, 2012)			UNCLASSIFIED	264259	
1007	79620871 (2013, 2014)	Novel Protein sim. GBank gi 4062979 db BAA36210.1 - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		synthase	264905	
1008	88094444 (2015, 2016)	Novel Protein sim. GBank gi 2808807 emb CAA04607.1 - (AJ001206) putative trehalose synthase [Streptomyces coelicolor]		synthase	265007, 264802, 264605, 264760, 264636	
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gi 3639077 AF090113 - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264102, 264288	
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gi 3746332 AF016307 - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		dehydrogenase	264592	
1011	85546918 (2021, 2022)	Novel Protein sim. GBank gi 2342847 gb AA86591.1 - (U90653) DHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	35696052, 264905, 264764, 264768, 35695917, 264629	
1012	95294456 (2023, 2024)	Novel Protein sim. GBank gi 341341 emb CAA20272 - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	phosphorylase	35696052, 264905, 264600, 264601, 264602, 264605, 264762, 264766, 264768, 264689	
1013	86095772 (2025, 2026)			UNCLASSIFIED	264591, 21906768	
1014	86088828 (2027, 2028)				29331824, 265019, 265020	

1015	95418879 (2029, 2030)	Novel Protein sim. GBank gi 4159995 (AF063095) - SELIL [Mus musculus]	Contains protein domain (PF00040) - Fibronectin type II domain	struct	22278994, 22278995, 56994075, 22278996, 22278999, 284259, 29331825, 29331828, 284907, 56182435, 284510, 284591, 284593, 60433356, 284594, 55812038, 284758, 21908754, 33857084, 265010, 284600, 265017, 265018, 265019, 18108351, 21906765, 21906766, 21906767, 21906768, 55811957, 265022, 33657023, 65274620, 33657182, 32833986, 18108370, 18108377, 55811576, 35696423, 284630, 22279000, 284565
1016	78559694 (2031, 2032)	Novel Protein sim. GBank gi 2506989 (sp P41407 ACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)		esterase	284686, 284693
1017	11069213 (2033, 2034)	Novel Protein sim. GBank gi 5103943 (dbj BAA79259.1) - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	284600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gi 4493973 (emb CAB39032.1) - (AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w). Hypothetical protein, len: 489 aa [Plasmodium falciparum]			22278996, 29148627, 284563
1019	11703607 (2037, 2038)			UNCLASSIFIED	284686
1020	80234432 (2039, 2040)				284508, 284509, 284512, 284600, 284762, 284769, 284688, 18108370, 284636, 284638, 284486
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gi 4633807 (gb AAD26859.1) AFI12779 - (AF127795) trehalase biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]		synthase	284769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gi 1781230 (emb CAB06271) - (Z83867) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	35696052, 284508, 285008, 265009, 284769, 18108387, 284563
1023	11399341 (2045, 2046)	Novel Protein sim. GBank gi 3777495 (U92083) - calcium transporting ATPase [Pichia angusta]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated	284593
1024	80057129 (2047, 2048)			UNCLASSIFIED	52646842, 33657402, 33657023, 18108379, 55811576, 284631, 284556, 284557, 284559, 18108388, 284566
1025	78644200 (2049, 2050)	Novel Protein sim. GBank gi 3483045 (emb CAA20556) - (AL031371) putative transport system permease protein [Streptomyces coelicolor]		transport	284693
1026	80025948 (2051, 2052)	Novel Protein sim. GBank gi 1174922 (sp Q02322 UVRD_HAEIN - DNA HELICASE II		helicase	284602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gi 4757728 (ref NP_004886.1) pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	265017

1028	20297928 (2055, 2056)	Novel Protein sim. GBank gi 2791409 emb CAA16003 - (AL021184) aco [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	264800
1029	94665090 (2037, 2058)			UNCLASSIFIED	264595
1030	88095343 (2059, 2060)			UNCLASSIFIED	264907, 264908, 264510, 264512, 265009, 265010, 265011, 264600, 264602, 264603, 264605, 264769, 18108372, 18108374
1031	95289117 (2081, 2082)			UNCLASSIFIED	264905, 264906, 264909, 264595, 264692, 264630, 264634, 264638
1032	94673275 (2063, 2084)	Novel Protein sim. GBank gi 4503895 ref NP_000145.1 pGALK - galactokinase 1		UNCLASSIFIED	264689
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gi 2982990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35896052, 264908, 264510, 18108354, 264687, 264769, 264689, 80431602, 18108385, 264486
1034	79245937 (2087, 2088)	Novel Protein sim. GBank gi 405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	264906
1035	79956355 (2089, 2070)			UNCLASSIFIED	264692
1036	85804998 (2071, 2072)			UNCLASSIFIED	264905, 66712502, 264908, 264766
1037	87860588 (2073, 2074)			UNCLASSIFIED	29331824, 264809, 80433438, 265019
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gi 790819 (L39891) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLAT/LH2 domain		264604, 264634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gi 2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	264092, 264093, 264094, 264683, 264689, 263967
1040	80026840 (2079, 2080)	Novel Protein sim. GBank gi 2352095 (U97022) - DNA topoisomerase I [Fervidobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase	isomerase	264595
1041	10156682 (2081, 2082)	Novel Protein sim. GBank gi 3256535 dbj BAA29218.1 - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]		kinase	264907
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gi 2058299 emb CAA66953 - (X98309) ARI protein [Drosophila melanogaster]			264605
1043	80057136 (2085, 2086)	Novel Protein sim. GBank gi 1870167 emb CAA70125 - (Y08921) msK [Streptomyces reliculi]	Contains protein domain (PF00005) - ABC transporter	transport	264565, 264567
1044	80025952 (2087, 2088)	Novel Protein sim. GBank gi 5689890 emb CAB52053.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	265006, 264602, 265017
1045	52415482 (2089, 2090)				29331825, 264637
1046	11754882 (2091, 2092)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		helicase	264686
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gi 4210471 dbj BAA74535.1 - (AB019033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	264769
1048	79188400 (2095, 2096)	Novel Protein sim. GBank gi 3413419 emb CAA20279 - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophysial hormones, N-terminal Domain	UNCLASSIFIED	264687
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gi 5051636 gb AAD38326.1 AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	264905, 264634
1050	79471521 (2099, 2100)			UNCLASSIFIED	264686

1051	80475471 (2101, 2102)				UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442862 (2103, 2104)	Novel Protein sim. GBank gi 3123275 sp P35138 SERA_BACSU - D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	dehydrogenase		264508, 264762, 264687, 264486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank gi 5441319 emb CAB46717.1 - (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]				264686, 18108374, 29331824, 83373044, 21906754, 52645158, 56182435, 264689, 29331827, 27486281, 35696052, 21908765, 35696423, 21906768, 56182575, 21906769, 55811957, 87168518, 35696286, 22278997, 265020, 265011, 265021, 265022, 265007, 265018, 22279000, 22279002, 264482, 264906, 52644150, 264909, 264288, 29331822, 52645080, 264768
1054	79580225 (2107, 2108)			UNCLASSIFIED		264686
1055	80594138 (2109, 2110)	Novel Protein sim. GBank gi 5052508 gb AAD38594.1 AF145609) BCDNA_GH02833 [Drosophila melanogaster] Novel Protein sim. GBank gi 3021676 dbj BAA25358 - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens] Novel Protein sim. GBank gi 1226281 (U50308) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase		264907, 264602, 264681, 264288, 21906768, 33657109, 55810764, 35695855, 264631
1056	17882319 (2111, 2112)			mapolymerase		264906
1057	85667216 (2113, 2114)			UNCLASSIFIED		264682
1058	80376576 (2115, 2116)					264764
1059	84662754 (2117, 2118)	Novel Protein sim. GBank gi 1170016 sp P46808 GREY_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREY (TRANSCRIPT CLEAVAGE FACTOR GREY) Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) Novel Protein sim. GBank gi 90254 pir J28334 - protein- tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse		transcriptfactor		35696052, 35695855, 265009, 264636
1060	79481169 (2119, 2120)			glycoprotein		29146498, 264681, 264683, 264687
1061	11034025 (2121, 2122)			phosphatase		264634
1062	39567837 (2123, 2124)	Novel Protein sim. GBank gi 3334200 sp O49954 GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) Novel Protein sim. GBank gi 2499986 sp Q41228 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A) Novel Protein sim. GBank gi 82654 pir JUA0086 - 10K zein precursor - maize		dehydrogenase		264593
1063	8480481 (2125, 2126)					264508
1064	78891783 (2127, 2128)					265007, 265008, 18108351, 18108385

1065	80021208 (2129, 2130)	Novel Protein sim. GBank gij2120998[pir][S70682 - glycosyltransferase homolog - Bordetella pertussis]		transferase	264600, 264602, 264689
1066	17696879 (2131, 2132)	Novel Protein sim. GBank gij2508382[sp]P15042[DNLJ_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))]		synthase	265009
1067	10132178 (2133, 2134)				264909
1068	82062057 (2135, 2136)	Novel Protein sim. GBank gij4007668[emb]CAA22355] - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) - Aldol/keto reductase family	reductase	264688, 18108362, 264558, 264600, 264760
1069	83002954 (2137, 2138)	Novel Protein sim. GBank gij4589484[dbj]BAA76770.1] - (AB023143) KIAA0928 protein [Homo sapiens]		UNCLASSIFIED	264604
1070	82101992 (2139, 2140)	Novel Protein sim. GBank gij120304[sp]P15932[FLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)]		UNCLASSIFIED	264604, 264760
1071	20710589 (2141, 2142)	Novel Protein sim. GBank gij1750397 (U81261) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	264602
1072	82356540 (2143, 2144)			UNCLASSIFIED	264687, 264688, 21908784, 35696052, 35695917, 35695855, 264600, 264601, 264602, 265009, 264605, 264508, 264905, 264690, 264906, 264762, 264628, 264768
1073	79814400 (2145, 2146)	Novel Protein sim. GBank gij477532[pir]J49175 - Motch B protein - mouse (fragment)	Contains protein domain (PF00008) - EGF-like domain	synthase	264909
1074	80105992 (2147, 2148)	Novel Protein sim. GBank gij3893109[emb]CAA76940] - (Y17920) CALO protein [Drosophila melanogaster]		UNCLASSIFIED	264908
1075	81850293 (2148, 2150)			UNCLASSIFIED	56994075, 22278998, 264594, 264757, 264596, 265018, 265019, 264681, 264368, 264688, 265020, 18108364, 18108374
1076	80477264 (2151, 2152)	Novel Protein sim. GBank gij1176203[sp]P46442[YHGM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)]		ATPase-associated	264769
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gij4033487[sp]Q44472[TUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		kinase	264905
1078	20288874 (2155, 2156)			UNCLASSIFIED	264600
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gij3413828[emb]CAA20296] - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	18108394, 264769, 264634, 264636
1080	11767188 (2159, 2160)			UNCLASSIFIED	264684
1081	94747080 (2161, 2162)				83373044, 265019, 22278002, 264482, 18108351, 264682, 264908, 264693, 264487
1082	81490656 (2163, 2164)			UNCLASSIFIED	264758, 264768, 264769, 21906767, 264511, 264910, 264634, 264635, 264905, 264636, 264906, 264637, 264907, 264908, 264764, 264638, 20281089, 264768, 264595

1083	87446717 (2165, 2166)	Novel Protein sim. GBank gij1722845[sp]Q10523[Y01N_MYCTU - HYPOTHETICAL 44.6 KO PROTEIN CY427.23		UNCLASSIFIED	60424179, 264905, 264908, 264510, 60432229, 264759, 87168474, 264605, 264769, 264689, 18108364, 18108376, 35695855, 264636 264769
1084	37789308 (2167, 2168)	Novel Protein sim. GBank gij18384[sp]P32057[WCAI_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	
1085	86475368 (2169, 2170)	Novel Protein sim. GBank gij1899190 (U90204) - heat shock protein 60 [Tsukamurella tyrosinosolvens]	Contains protein domain (PF00118) - eph TCP-1/cpn60 chaperonin family		60432229, 264687
1086	79608269 (2171, 2172)	Novel Protein sim. GBank gij1172858[sp]P46176[RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - ribosomalprot Ribosomal protein L14		264486
1087	78603978 (2173, 2174)	Novel Protein sim. GBank gij160198[emb]CAA15431 - (AL008583) dJ327J16.3 (novel CHROMobox family protein) [Homo sapiens]	Contains protein domain (PF00385) - helicase 'chromo' (CHR)romatin Organization Modifier domain		29331827, 264693
1088	78654963 (2175, 2176)	Novel Protein sim. GBank gij2883155 (AE000593) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aeolicus]		UNCLASSIFIED	264905, 264601, 18108387
1089	80216800 (2177, 2178)	Novel Protein sim. GBank gij14981768[gb]AAD36290.1(AE00177) - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	264488, 264511, 265011, 264682, 264768, 264689, 21906764, 35695917, 265020, 32633986, 18108370, 35695855
1090	11083825 (2179, 2180)	Novel Protein sim. GBank gij4007680[emb]CAA22366 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			264604
1091	12817471 (2181, 2182)	Novel Protein sim. GBank gij2485562[sp]P77239[YLCD_ECOLI - HYPOTHETICAL 44.3 KO PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264637
1092	80252286 (2183, 2184)	Novel Protein sim. GBank gij2860098[emb]CAA17996.1 - (AL022121) ntl [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - Endonuclease III		264566
1093	80496304 (2185, 2186)	Novel Protein sim. GBank gij1001642[db]BAA10373 - (D64002) dGTP triphosphohydrolase [Synecococcus sp.]		UNCLASSIFIED	264769, 35695917, 35695855, 264600, 264602, 264603, 264605, 18108351 264686
1094	10880972 (2187, 2188)	Novel Protein sim. GBank gij4585587[emb]CAB40855.1 - (AL049828) putative adenine glycosylase [Streptomyces coelicolor]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family		264906, 265007, 264595, 264600, 264602, 264603, 264604, 264605, 264762, 264768, 264769, 264636, 264558, 18108387, 80432113, 284482, 264486
1095	87457250 (2189, 2190)	Novel Protein sim. GBank gij115001[sp]P19206[BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)]			264600, 264602, 264603, 264604, 264605, 35695917, 264692, 264631
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gij114135[sp]P08205[JARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)]		UNCLASSIFIED	285019 264687
1097	79239560 (2193, 2194)	Novel Protein sim. GBank			
1098	79186424 (2195, 2196)	Novel Protein sim. GBank			

1099	39523838 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE- N1)-METHYLTRANSFERASE (MIG- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)			UNCLASSIFIED	264603
1100	85736571 (2189, 2200)	Novel Protein sim. GBank gi 3023255 sp Q64420 ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)			desaturase	264259, 264636
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi 1174735 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger		isomerase	264769
1102	79777614 (2203, 2204)	Novel Protein sim. GBank gi 1906596 (U81788) - kinesin-73			UNCLASSIFIED	264910, 264909
1103	81897259 (2205, 2206)	[Drosophila melanogaster]			struct	264757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 2935448 (AF048976) - synaptic ras GTPase-activating protein p135 SynGAP (Rattus norvegicus)			UNCLASSIFIED	29331822, 21906754, 264555, 264556, 264558, 22279002
1105	80255121 (2209, 2210)					264566
1106	79314110 (2211, 2212)				UNCLASSIFIED	264555, 264369
1107	80470019 (2213, 2214)					264906, 264769
1108	80440616 (2215, 2216)	Novel Protein sim. GBank gi 173421 sp P43416 SECY_STRSC - PREPROTEIN TRANSLOCASE SECY SUBUNIT			transport	264907, 264510, 264511, 264600, 264602, 264605, 264768, 264769
1109	80084615 (2217, 2218)	Novel Protein sim. GBank gi 2895310 emb CAA18338 - (AL022268) putative ATP-dependent helicase (Streptomyces coelicolor)			helicase	264602, 264605, 264636
1110	80503554 (2219, 2220)					264908, 264593, 265010, 264601, 264603, 264604, 264605, 264682, 264769, 264693, 264636
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 2622039 (AE000868) - type I restriction modification system, subunit S (Methanobacterium thermoautotrophicum)				18108370, 264557
1112	95010088 (2223, 2224)	Novel Protein sim. GBank gi 3218376 emb CAA18628 - (AL023862) putative oxidoreductase [Streptomyces coelicolor]			UNCLASSIFIED	264908
1113	82456352 (2225, 2226)					264600, 264602, 264604, 264605, 264762, 264769, 264565
1114	14998014 (2227, 2228)	Novel Protein sim. GBank gi 1083428 pir S54876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse			dehydrogenase	264636
1115	11765583 (2229, 2230)					264686
1116	79841152 (2231, 2232)				UNCLASSIFIED	264908

1117	95305485 (2233, 2234)	Novel Protein sim. GBank gi 3255965 emb CAA94089 - (Z70200) U5 snRNP-specific 200kD protein [Homo sapiens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108392, 264488, 263994, 264489, 18108398, 56182575, 22278995, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 68714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 28146488, 284508, 264905, 264509, 264906, 264907, 264908, 66712502, 264909, 52644045, 56182435, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264596, 264758, 264759, 21906754, 33109954, 33657084, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 264604, 265018, 264605, 265019, 264760, 55811150, 264681, 264762, 18108351, 264448, 264682, 264764, 264683, 264288, 264389, 264684, 264685, 264766, 264767, 264686, 264687, 264768, 264769, 264688, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148784, 35695917, 265020, 265021, 265022, 60170615, 264690, 264691, 33657023, 264692, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 27486284, 33657349, 27486285, 35695763, 264691
1118	79563326 (2235, 2236)			UNCLASSIFIED	264691
1119	79642463 (2237, 2238)			UNCLASSIFIED	264807
1120	79480463 (2239, 2240)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		collagen	29331827, 265018, 265019, 264681, 265021, 60170615, 18108387
1121	79471716 (2241, 2242)	Novel Protein sim. GBank gi 1644450 U67864 - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264683, 264632, 18108388
1122	79456246 (2243, 2244)			UNCLASSIFIED	264639, 264583
1123	79637119 (2245, 2246)	Novel Protein sim. GBank gi 98800 pir J17768 - 3-dehydroquinolate synthase (EC 4.6.1.3) - Mycobacterium tuberculosis		synthase	264683, 27486265
1124	79811596 (2247, 2248)			UNCLASSIFIED	264909
1125	79757861 (2249, 2250)			UNCLASSIFIED	264910
1126	79758914 (2251, 2252)	Novel Protein sim. GBank gi 138154 sp P03643 VGG_BPPHX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)		eph	264905, 264909, 264910
1127	11800930 (2253, 2254)			UNCLASSIFIED	264682
1128	8384885 (2255, 2256)	Novel Protein sim. GBank gi 5002704 emb CAB44358.1 - (AJ242630) DNA polymerase I [Methylobacterium sp. DMA]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	264511

1129	80422480 (2257, 2258)	Novel Protein sim. GBank gij5689485[dbj]BAA03026.1] - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264766
1130	79420151 (2259, 2260)	Novel Protein sim. GBank gij4981328[gbj]AAD35881.1 AE00174 - (AE001747) bioY protein [Thermotoga maritima]		UNCLASSIFIED	264595
1131	80055391 (2261, 2262)	Novel Protein sim. GBank gij1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	35696286, 22278998, 29331828, 264603, 264605, 264559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank gij1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	22278996, 264906, 265009, 264600, 264602, 264604, 264605, 264760, 32833986, 18108374
1133	17280437 (2265, 2266)			UNCLASSIFIED	265018
1134	80235376 (2267, 2268)			UNCLASSIFIED	264512, 264534
1135	80029393 (2269, 2270)	Novel Protein sim. GBank gij4539171[emb]CAB39700.1] - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264600, 264602, 264603, 18108376
1136	79842052 (2271, 2272)	Novel Protein sim. GBank gij4982454[gbj]AAD36931.1 AE00182 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264906, 264908
1137	90931557 (2273, 2274)	Novel Protein sim. GBank gij4972746[gbj]AAD34768.1] - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - TPR Domain	collagen	22278998, 22278999, 35696052, 264907, 265009, 60433396, 264598, 265010, 264448, 264882, 264767, 264689, 265020, 264692, 55811576, 35695855, 264631, 264632, 22278002
1138	79841163 (2275, 2276)	Novel Protein sim. GBank gij731607[spj]P38739[HYC8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR		strud	264908
1139	79633561 (2277, 2278)	Novel Protein sim. GBank gij3650031 (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264893
1140	39480358 (2279, 2280)			UNCLASSIFIED	264593
1141	79638019 (2281, 2282)			UNCLASSIFIED	265019, 264693
1142	19635848 (2283, 2284)			UNCLASSIFIED	264631
1143	87762158 (2285, 2286)	Novel Protein sim. GBank gij3928000[emb]CAA05880] - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	oxidase	56182575, 264908, 264600, 264632, 87168518
1144	80068998 (2287, 2288)			UNCLASSIFIED	264635, 264636, 264907, 264593, 264908, 264566, 264909
1145	14610262 (2289, 2290)			UNCLASSIFIED	264112
1146	82062092 (2291, 2292)			UNCLASSIFIED	264769, 264689, 35696286, 264760, 264905, 264486, 264559
1147	80071761 (2293, 2294)				264557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank gij2499003[spj]P76422[THID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)	kinase		264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank gij2896734[emb]CAA17213.1] - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]			264591

1150	81325074 (2289, 2300)	Novel Protein sim. GBank gij2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]			ATPase associated	264488, 35696286, 264907, 264908, 264909, 264910, 264593, 264598, 264758, 264764, 264766, 264768, 264693, 264628, 60431850, 264564, 264566, 264567
1151	80070874 (2301, 2302)	Novel Protein sim. GBank gij4324655jgbjA016978] - (AF108191) DNA polymerase III alpha subunit [Streptomyces coelicolor]			polymerase	264555
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gij3874275jembjCA087311.1] - (Z92825) predicted using GeneFinder: Similarity to Yeast low affinity glucose transporter HXT4 (PS:32467); cDNA EST EMBL: C12555 comes from this gene; cDNA EST yk404c10.3 comes from this gene; cDNA EST yk404c10.5 comes from thi...			glycoprotein	264488, 22278998, 264905, 264629, 264486
1153	80027783 (2305, 2306)	Novel Protein sim. GBank gij4240315jdbjBAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]			UNCLASSIFIED	264910, 264555, 264557
1154	83002995 (2307, 2308)	Novel Protein sim. GBank gij586655jpp37617jATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZNIH)-TRANSLATING P. TYPE ATPASE)		Contains protein domain (PF00122) - E1-E2 ATPase	UNCLASSIFIED	264690, 264636
1155	78411098 (2308, 2310)	Novel Protein sim. GBank gij418480jpp32139jYIHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION			UNCLASSIFIED	264906, 264907, 264758, 284768, 264769, 264689, 264638, 264566
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gij2498481jpp050724jY09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY7B.27C				264906, 264762, 264687, 264769, 264689, 18108374, 35695855
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gij1138408jdbjBAA11490] - (D79996) similar to pig tubulin-tyrosine ligase. [Homo sapiens]				264687
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gij4503375jreijNP_001376.1]pDPYS - dihydropyrimidinase			UNCLASSIFIED	264693
1159	79186451 (2317, 2318)	Novel Protein sim. GBank gij2443342jdbjBAA22380] - (D88764) alpha 2 type I collagen [Rana catesbeiana]			UNCLASSIFIED	29331827, 264906
1160	91229893 (2318, 2320)	Novel Protein sim. GBank gij5052554jgbjAAD38607.1]AF145632 - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]			transport	18108398, 29331827, 29331828, 29146488, 29146489, 18108354, 21908788, 29148627, 21908789, 264693, 18108382, 18108385
1161	7417143 (2321, 2322)	Novel Protein sim. GBank gij4509476jdbjBAA76766.1] - (AB023138) KIAA0922 protein [Homo sapiens]			UNCLASSIFIED	264602, 264605, 264769, 18108370, 18108374, 264565
1162	79635357 (2323, 2324)	Novel Protein sim. GBank gij4509476jdbjBAA76766.1] - (AB023138) KIAA0922 protein [Homo sapiens]				264488, 35696286, 22278999, 264259, 66714117, 60432289, 35696052, 264905, 56182435, 265006, 60433438, 264759, 21908754, 33109954, 265017, 265019, 264448, 264288, 264766, 264685, 35696423, 35695855, 264558, 18108385, 60432113
1163	79563186 (2325, 2326)	Novel Protein sim. GBank gij4509476jdbjBAA76766.1] - (AB023138) KIAA0922 protein [Homo sapiens]				
1164	79650829 (2327, 2328)	Novel Protein sim. GBank gij4509476jdbjBAA76766.1] - (AB023138) KIAA0922 protein [Homo sapiens]				
1165	80481888 (2329, 2330)	Novel Protein sim. GBank gij4509476jdbjBAA76766.1] - (AB023138) KIAA0922 protein [Homo sapiens]				
1166	80096456 (2331, 2332)	Novel Protein sim. GBank gij4509476jdbjBAA76766.1] - (AB023138) KIAA0922 protein [Homo sapiens]				

1167	78963862 (2333, 2334)	Novel Protein sim. GBank gij2580433[jb]BAA23138] - (D76414) ppGpp hydrolase [Staphylococcus aureus]			kinase	264488
1168	88094678 (2335, 2336)				UNCLASSIFIED	264259, 29331827, 56182435, 60433438, 265019, 33657023, 35695855, 264568
1169	11805403 (2337, 2338)				UNCLASSIFIED	264681
1170	21632244 (2339, 2340)				UNCLASSIFIED	264602
1171	20434582 (2341, 2342)	Novel Protein sim. GBank gij2772914 (AF028249) - procollagen D [Mytilus edulis]			UNCLASSIFIED	264556
1172	78610113 (2343, 2344)	Novel Protein sim. GBank gij4757848[ref]NP_004317.1pBCL9 - B-cell CLL/lymphoma 9			UNCLASSIFIED	55810764, 35696052, 264634, 264488
1173	80235713 (2345, 2346)	Novel Protein sim. GBank gij2564053[jb]BAA22946] - (AB007832) Bm trachealless [Bombyx mori]				264508, 264906, 264907, 264909, 264591, 264632, 264638, 264639
1174	20283077 (2347, 2348)	Novel Protein sim. GBank gij2911027[emb]CAA17520] - (AL021958) mmsA [Mycobacterium tuberculosis]			dehydrogenase	264600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank gij1183333[sp]P23234[DCIP_ENTCL - INDOLE-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)]			carboxylase	264601
1176	80252645 (2351, 2352)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]			synthase	264509, 264805, 264593, 264602, 264605
1177	80064647 (2353, 2354)	Novel Protein sim. GBank gij118791[sp]P28643[FABG_CUPLA - 3-OXOACYL-ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)			reductase	264605
1178	94128641 (2355, 2356)	Novel Protein sim. GBank gij5031697[ref]NP_005594.1pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)			ATPase-associated E1-E2 ATPase	65274572, 18108398, 22278998, 22278999, 29331826, 264508, 264908, 264828, 33657402, 33109854, 264769, 21906765, 21908768, 21908768, 55811957, 33657023, 264629, 55811576, 35696423, 264636, 264556, 56182323, 60432113, 22279000, 22279002
1179	80055575 (2357, 2358)	Novel Protein sim. GBank gij2960090[emb]CAA17988.1] - (AL022121) dppA [Mycobacterium tuberculosis]			transport	264603
1180	11794446 (2359, 2360)	Novel Protein sim. GBank gij2558614[emb]CAA0478] - (AJ001493) dehydroquinase dehydratase [Streptomyces coelicolor]			synthase	264638
1181	17946362 (2361, 2362)				UNCLASSIFIED	265017
1182	81494264 (2363, 2364)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]				265007, 265009, 264564, 264909, 264693
1183	78574044 (2365, 2366)					264689, 35696423, 264638, 18108385
1184	52559833 (2367, 2368)	Novel Protein sim. GBank gij4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]			UNCLASSIFIED	264602
1185	79491185 (2369, 2370)	Novel Protein sim. GBank gij2129478[pir]S51839 - chitinase (EC 3.2.1.14) precursor - beet			glycoprotein	263967

1186	20224012 (2371, 2372)				UNCLASSIFIED	264559	
1187	70248834 (2373, 2374)				UNCLASSIFIED	29331825, 265017, 18108351	
1188	79831387 (2375, 2376)	Novel Protein sim. GBank gi 2996039 (AF054525) - hypothetical protein [Synechococcus PCC7002]			UNCLASSIFIED	264905, 264908	
1189	79609367 (2377, 2378)					264692	
1190	79930589 (2379, 2380)				UNCLASSIFIED	265018	
1191	80310105 (2381, 2382)				UNCLASSIFIED	264600, 264605, 264764, 35695955, 264638, 264486	
1192	13521641 (2383, 2384)			Contains protein domain (PF01581) - FMRFamide related peptide family		264636	
1193	11103584 (2385, 2386)				UNCLASSIFIED	263978	
1194	79893947 (2387, 2388)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [human herpesvirus 6]			UNCLASSIFIED	265007, 265008	
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gi 1790277 (AE000459) - putative oxidoreductase [Escherichia coli]			UNCLASSIFIED	264605	
1196	13000888 (2391, 2392)					264689	
1197	11392317 (2393, 2394)	Novel Protein sim. GBank gi 2497360 sp Q50715 IMDH_MYCTU - INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)		Contains protein domain (PF00571) - CBS domain	dehydrogenase	264594	
1198	95290101 (2395, 2396)					264603	
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gi 1709525 sp P54673 P3K1_DICD1 - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)				264259, 264757, 33109954, 21906768	
1200	9848880 (2399, 2400)						
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gi 2499877 sp P70645 BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)			UNCLASSIFIED	264910	
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gi 606342 (U18997) - ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]			cathepsin	264766, 264769	
1203	82125373 (2405, 2406)				ribosomalprot	264600, 264558	
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gi 2500728 sp Q59912 SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT			UNCLASSIFIED	264768, 264769, 35695917, 264910, 264760, 264908, 264907, 264629, 264908, 264909, 264766	
1205	80053961 (2409, 2410)					264905, 264769, 264636	
1206	80241965 (2411, 2412)				UNCLASSIFIED	264566	
1207	79841192 (2413, 2414)				UNCLASSIFIED	264556, 264557, 264558	
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gi 2645560 (AF027954) - Bcl-2-related ovarian killer protein [Rattus norvegicus]		Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family		29331824, 264909, 265021, 18108370, 29331824, 29331825, 29331827, 265007, 264764, 264683, 264769, 264688, 264689	

1209	79185742 (2417, 2418)	Novel Protein sim. GBank gi1175033 sp P44398 XYLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	264687, 264688
1210	56426884 (2419, 2420)	Novel Protein sim. GBank gi121095 prf S30688 - hypothetical protein o246 - Escherichia coli		UNCLASSIFIED	264907, 264693
1211	94665655 (2421, 2422)	Novel Protein sim. GBank gi3980625 emb CAB07858 - (Z93785) predicted using GeneFinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transferase	264591, 264592, 264595
1212	79187829 (2423, 2424)	Novel Protein sim. GBank gi121095 prf S30688 - hypothetical protein o246 - Escherichia coli			264689, 263967
1213	79859633 (2425, 2426)	Novel Protein sim. GBank gi1226292 prf 1505375A - vir gene [Bordetella pertussis]		kinase	264909
1214	10144306 (2427, 2428)	Novel Protein sim. GBank gi15726285 gb AA048396.1 AF12616 - (AF126162) HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	264908
1215	80050108 (2429, 2430)	Novel Protein sim. GBank gi12326739 emb CAB10953 - (Z98268) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	265009, 264601, 264602, 264603, 33657109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gi1417328 sp P33038 MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYLPIRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOLPYRUVYL TRANSFERASE) (EPT)		transferase	264604
1217	95011344 (2433, 2434)			UNCLASSIFIED	264905, 264907, 264908, 264591, 264766, 264691, 264693, 264629, 264630, 264636, 264564
1218	11093680 (2435, 2436)	Novel Protein sim. GBank gi1805460 dbj BAA08022 - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		dehydrogenase	264601
1219	91216252 (2437, 2438)				56181688, 29331822, 60432289, 264601,
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gi12420315 dbj BAA74936.1 - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	264692, 264629
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gi12143886 prf 152523 - nucleoporin p82 homolog - rat (fragment)		UNCLASSIFIED	52644507, 264905, 264909, 265008, 265019, 265020, 52644150, 33657023, 264693, 33657182, 35695763, 264634, 22279000, 22279002, 264482
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gi1730805 sp P39663 SPHR_SYN7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	phosphatase	264768, 265020, 264906
1223	11615647 (2445, 2446)				264593
1224	80432645 (2447, 2448)	Novel Protein sim. GBank gi1172627 sp P46548 PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - PUA domain	kinase	264593, 264599, 264600, 264601, 264603, 264605, 264768, 18108378, 264635, 18108387

1225	80434427 (2449, 2450)	Novel Protein sim. GBank gij2105050[emb][CAB08836] - (Z95436) hypothetical protein RV3844c [Mycobacterium tuberculosis]			polymerase	264788 264905, 264512, 264689
1226	80237518 (2451, 2452)	Novel Protein sim. GBank gij1706768[sp]P98133[FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)]			UNCLASSIFIED	264908, 264637, 264839
1227	79422138 (2453, 2454)	Novel Protein sim. GBank gij16533901[db][BAA18811] - (D90917) acriflavine resistance protein [Synecocystis sp.]			UNCLASSIFIED	264605, 264634
1228	79208027 (2455, 2456)	Novel Protein sim. GBank gij116230[sp]P28598[CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL-PROTEIN)]			UNCLASSIFIED	87168474, 265011, 87168559, 264681, 264689, 264693, 65274820, 18108374, 264909, 264605, 18108388
1229	94329135 (2457, 2458)	Novel Protein sim. GBank gij118298[sp]P20730[CHHC_BOOMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)]			eph	
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			UNCLASSIFIED	264908 264909
1231	79843141 (2461, 2462)	Novel Protein sim. GBank gij118298[sp]P20730[CHHC_BOOMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)]			UNCLASSIFIED	265017, 264564
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			transport	
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			UNCLASSIFIED	
1234	79242158 (2467, 2468)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			UNCLASSIFIED	
1235	78914423 (2469, 2470)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			histone	265008, 265010, 18108381
1236	81927147 (2471, 2472)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			UNCLASSIFIED	264634, 264762
1237	83371782 (2473, 2474)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			UNCLASSIFIED	265018, 5581150, 264565, 264757
1238	87411577 (2475, 2476)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			UNCLASSIFIED	264758, 264601, 264766, 264687, 18108372, 264555, 264559
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			glycoprotein	264259, 29331822, 29331824, 35696052, 264508, 264908, 52644045, 52646317, 264288, 264769, 264693, 264632, 264634, 264558, 87168518, 264563
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			oncogene	264509, 264511, 264759, 264760, 264764, 264557
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			UNCLASSIFIED	264769
1242	79755890 (2483, 2484)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			UNCLASSIFIED	264601, 264604, 264638

1243	79779458 (2485, 2486)	Novel Protein sim. GBank gij3355671[emb CAA19971] - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695917, 35695855, 265009, 264508, 264909
1244	10284821 (2487, 2488)	Novel Protein sim. GBank gij2970846 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank gij4586338[dbj BAA76357.1] - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - Cytochrome C and Quinol oxidase polypeptide I	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank gij3581849[emb CAA20805] - (AL031541) putative phenylalanyl-IRNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264636, 264557, 284584
1247	80084831 (2493, 2494)	Novel Protein sim. GBank gij2621684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank gij1352403[sp P09467]F16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264258, 29331826, 264106, 264508, 264907, 264828, 265009, 60433356, 264757, 264758, 21908754, 265010, 265011, 265018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank gij2791407[emb CAA16001] - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]		transport	264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2499, 2500)	Novel Protein sim. GBank gij112785[sp P05100]3MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	79850448 (2501, 2502)				264909
1252	79458087 (2503, 2504)			UNCLASSIFIED	264683, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. GBank gij5670176[gb AAD46616.1]AF16131 - (AF161317) NRAMP manganese transport protein MnaA [Salmonella typhimurium]		glycoprotein	264800, 264603, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. GBank gij103160[ipr S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)]		UNCLASSIFIED	35695286, 264910, 264764, 264688, 21906767, 55811957, 264692, 264556, 264639
1255	79189728 (2509, 2510)				264836
1256	87889508 (2511, 2512)	Novel Protein sim. GBank gij2985353[emb CAA04608.1] - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	60432289, 264600, 264605, 264764, 264687, 264769, 264689, 27486265, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. GBank gij3193306 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20708150 (2515, 2516)			UNCLASSIFIED	264602, 263978
1259	80186012 (2517, 2518)			UNCLASSIFIED	264906, 264448, 264908
1260	80084806 (2519, 2520)			UNCLASSIFIED	264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank gij5889511[dbj]BAA03039.1] - (AB029010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	cadherin	29331824, 264906, 264909, 264768, 264769, 264689, 264693, 264639, 18108384, 264563, 264634
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gij95100[pir]S21334 - hypothetical protein 4 - Agrobacterium tumefaciens		UNCLASSIFIED	
1263	20710997 (2525, 2526)	Novel Protein sim. GBank gij3550958 (AF004840) - CDO [Rattus norvegicus]		struct	264602, 264634
1264	80083396 (2527, 2528)			UNCLASSIFIED	264563
1265	80233578 (2529, 2530)			UNCLASSIFIED	264766, 264636, 264639, 264567
1266	78914604 (2531, 2532)	Novel Protein sim. GBank gij1085002[pir]S55056 - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264259, 21906754, 264389
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gij4886445[emb]CAB43370.1] - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18108398, 22278995, 56994075, 60424269, 29331827, 264109, 264512, 265007, 265008, 265009, 264595, 33109954, 33657084, 87168559, 264600, 265018, 265019, 264369, 264688, 21906767, 265020, 52644150, 264691, 33657023, 33657349, 18108374, 264556, 18108385, 60432113, 22279002, 264486
1268	88178473 (2535, 2536)			UNCLASSIFIED	264508, 264905, 264908, 264687, 264693
1269	79821946 (2537, 2538)	Novel Protein sim. GBank gij3334791[emb]CAA19939] - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]			
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gij2851634[sp]Q50591Y0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	dehydrogenase	265010, 264601
1271	79840499 (2541, 2542)			ATPase associated	35696052, 264908
1272	79462878 (2543, 2544)				264686, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gij1655665[emb]CAB03731] - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)			UNCLASSIFIED	
1275	20730763 (2548, 2550)	Novel Protein sim. GBank gij123726[sp]P10413[HTPG_ECOLI] - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.5)	Contains protein domain (PF00183) - Hsp90 protein	eph	264905, 264908, 264809, 264769, 264602
1276	21148844 (2551, 2552)	Novel Protein sim. GBank gij2129478[pir]S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264369
1277	20438195 (2553, 2554)			UNCLASSIFIED	264556
1278	11088385 (2555, 2556)	Novel Protein sim. GBank gij1175473[sp]P44555[YAAJ_HAEIN] - HYPOTHETICAL PROTEIN H10183		UNCLASSIFIED	264803
1279	21658756 (2557, 2558)	Novel Protein sim. GBank gij1929513 [U64318] - ATP synthase subunit beta [Mycobacterium thermorescens]		synthase	264605
1280	79310959 (2559, 2560)	Novel Protein sim. GBank gij4938504[emb]CAB43862.1] - (AL078465) putative protein [Arabidopsis thaliana]		struct	263976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gi 1136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	28331825, 29331828, 264766, 83373044
1282	87537695 (2563, 2564)	Novel Protein sim. GBank gi 3328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	265008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank gi 3261721 (emb CAB07057) - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20636325 (2567, 2568)	Novel Protein sim. GBank gi 3929022 (AF057696) - LspB [Haemophilus ducreyi]			264604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gi 417154 (sp P33126 HS82_ORYSA - HEAT SHOCK PROTEIN 82 (Z95207) gorA [Mycobacterium tuberculosis])	Contains protein domain (PF00183) - eph Hsp90 protein		264766, 264689, 263967
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gi 2078004 (emb CAB08451) - (Z95207) gorA [Mycobacterium tuberculosis]		reductase	264605, 264639
1287	80417530 (2573, 2574)			UNCLASSIFIED	265011, 264602, 264766, 264687, 264769, 264689, 18108370, 264636, 18108385, 264563
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gi 5353510 (gb AAD42161.1 AF088916) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - collagen C1q domain		35856052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 33657402, 264595, 264758, 265011, 265019, 264760, 18108351, 264681, 264764, 264288, 264585, 264766, 264687, 264768, 264769, 265020, 265021, 284534, 264682, 18108370, 264628, 18108374, 35896423, 264555, 264556, 264557, 264558, 18108385, 264564, 264566, 264567, 264686, 18108391
1289	11813847 (2577, 2578)	Novel Protein sim. GBank gi 1169995 (sp P46023 GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR (Z95120) rhIE [Mycobacterium tuberculosis])	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	UNCLASSIFIED	264637
1290	19526027 (2579, 2580)			Im7	264563
1291	80470266 (2581, 2582)	Novel Protein sim. GBank gi 2072674 (emb CAB08305) - (Z95120) rhIE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	265007, 265008, 264769
1292	94723316 (2583, 2584)	Novel Protein sim. GBank gi 1835755 (U86336) - zinc finger protein Prg-1 [Mus musculus]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcript factor	264092, 264259, 29331822, 29331824, 264508, 264908, 264909, 264512, 265008, 265009, 264591, 265019, 264369, 264288, 264686, 264768, 264693, 18108374, 264632, 56182323, 264639, 83373044, 22279002, 264482, 264563
1293	80067536 (2585, 2586)	Novel Protein sim. GBank gi 2129173 (pr F64453 - oxaloacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii		UNCLASSIFIED	265006, 55812038, 264369, 264556
1294	82125908 (2587, 2588)	Novel Protein sim. GBank gi 5441778 (emb CAB46803.1) - (AL098811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]		biolindp	264602, 264605, 264760, 18108351, 264689, 33657023, 264559
1295	11686851 (2589, 2590)			dehydrogenase	264689

1296	11687904 (2591, 2592)	Novel Protein sim. GBank gi 4982191 gb AAD36686.1 AE00180 - (AE001805) DNA- directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01367) - 5'-3' exonuclease	UNCLASSIFIED	264591, 264639 264693
1297	78639300 (2593, 2594)	Novel Protein sim. GBank gi 1943770 gb U97191 - F53F10.1 gene product [Caenorhabditis elegans]		struct	18108348, 265017
1298	94239508 (2595, 2596)	Novel Protein sim. GBank gi 4082973 dbj BAA36204.1 - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264488, 264906, 264908, 22279002, 264566 264605
1299	80255378 (2597, 2598)	Novel Protein sim. GBank gi 3445181 AC005498 - R31665.2 [Homo sapiens]		UNCLASSIFIED	264906
1300	80064867 (2599, 2600)	Novel Protein sim. GBank gi 3242273 emb CAB07017 - (Z92669) hypothetical protein Rv0236c [Mycobacterium tuberculosis]		UNCLASSIFIED	85658542, 265020 264908
1301	17939814 (2601, 2602)	Novel Protein sim. GBank gi 3242273 emb CAB07017 - (Z92669) hypothetical protein Rv0236c [Mycobacterium tuberculosis]		UNCLASSIFIED	264508 264566 264636
1302	95416198 (2603, 2604)	Novel Protein sim. GBank gi 1502421 U59433 - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - Envelope glycoprotein GP120	UNCLASSIFIED	264907, 264592, 264764 264555
1303	9684121 (2605, 2606)	Novel Protein sim. GBank gi 95819 jpl S16298 - ferric enterobactin transport protein fepC - Escherichia coli		transport	264906, 18108354
1304	78377196 (2607, 2608)	Novel Protein sim. GBank gi 5458220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264605
1305	19905898 (2609, 2610)	Novel Protein sim. GBank gi 4455118 gb AAD21084 - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	35696286, 29331827, 264908, 265008, 264764, 264766, 264686, 21908767, 21906769, 35695917, 264891, 264693, 22278995, 22278998, 22278999, 264905, 264908, 265011, 265017, 265019, 264687, 21908768, 265020, 265021, 33657023, 22279002, 264564
1306	13069230 (2611, 2612)	Novel Protein sim. GBank gi 4928733 gb AAD34127.1 AF15189 - (AF151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00886) - Ribosomal protein S16	ribosomalprot	22278996, 22278999, 264259, 20281099, 29146498, 264508, 264908, 66712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906765, 21908767, 29148827, 21908768, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22279000, 264563, 18108390
1307	82201028 (2613, 2614)	Novel Protein sim. GBank gi 2589223 AF026565 - (ing finger protein [Mus musculus])	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264693 264691
1308	21426814 (2615, 2616)				
1309	79263011 (2617, 2618)				
1310	20466319 (2619, 2620)				
1311	87613142 (2621, 2622)				
1312	88061720 (2623, 2624)				
1313	91225458 (2625, 2626)				
1314	56926053 (2627, 2628)				
1315	84357192 (2629, 2630)				

1316	95361609 (2631, 2632)	Novel Protein sim. GBank gij5689407[dbj][BAA82987.1] - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181686, 20281171, 28331822, 29331824, 60424269, 29331825, 35696052, 52644045, 264591, 60432229, 265018, 265019, 55811150, 56181562, 21906765, 21906767, 21906768, 35695917, 60170615, 33657023, 65274620, 33657109, 35695763, 35695855, 18108387, 87168518, 60432113, 22279002, 264584
1317	88055167 (2633, 2634)	Novel Protein sim. GBank gij4836757[gb][AAD30541.1][AF13491] - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264093, 264806, 264909, 264369, 264684
1318	95322893 (2635, 2636)	Novel Protein sim. GBank gij4680204[gb][AAD27567.1][AF11417] - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108362, 56182323, 18108385, 22279000
1319	94238546 (2637, 2638)				264908, 264909, 265006, 265008, 264592, 265019, 264766, 56181562, 18108368, 264628, 264629, 18108377, 264638
1320	86603567 (2639, 2640)	Novel Protein sim. GBank gij4240163[dbj][BAA74870.1] - (AB020654) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35698286, 55812038, 265018, 21906768, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank gij4886503[emb][CAB43377.1] - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcriptfactor	60432049, 29331828, 264907, 264908, 264909, 264910, 55812038, 264601, 264762, 264784, 264766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank gij5262591[emb][CAB45736.1] - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331828, 264908, 265020, 33657023, 264693, 264404
1323	94845931 (2645, 2646)	Novel Protein sim. GBank gij5459516[dbj][BAA82407.1] - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994075, 264259, 29331822, 29331827, 264104, 56182435, 87168474, 18108351, 264288, 21906768, 21906767, 35695917, 265020, 264693, 65274781, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank gij5031717[ref][NP_005704.1]pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278998, 22278998, 29331828, 264905, 264907, 29331830, 264908, 264510, 265008, 264595, 264759, 21906754, 265018, 264288, 264768, 264769, 21906768, 265022, 18108376, 264631, 264632, 264634, 264636, 264638, 264563, 264564, 264565, 264566
1325	94847471 (2649, 2650)	Novel Protein sim. GBank gij3294501 (UB4857) - similar to the DPTUKunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35698286, 264905, 264908, 264907, 264908, 264909, 264910, 264593, 33657402, 264758, 85658542, 264760, 264768, 264769, 264691, 35698423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank gij1397275 (U61947) - C06G3.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635

1327	85322897 (2653, 2654)	Novel Protein sim. GBank gi 7283216 p P39189 ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278996, 22278997, 22278999, 284091, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284105, 284905, 56182435, 264112, 265008, 265009, 21906754, 265010, 265011, 265017, 265019, 264681, 264448, 264764, 264684, 284288, 264685, 264768, 264688, 21906767, 21906769, 29148629, 265020, 264690, 284691, 284692, 284693, 283667, 33657109, 33657182, 27486262, 33657349, 18108370, 18108374, 55810764, 35895855, 264634, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002, 264553, 264567, 264488, 22278997, 29331826, 264595, 18108351, 264766, 22279002, 264482, 264567
1328	87753493 (2655, 2656)			UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1329	87755276 (2657, 2658)	Novel Protein sim. GBank gi 4678224 gb AA026969.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264259, 29331825, 284512, 265019, 265021, 264555, 264558, 56526486
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gi 437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 60170831, 284448, 264686, 21906765, 55811957, 265020, 33657023, 33657109, 263973, 55811576, 35696423, 35695855, 56182323
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gi 4589586 dbj BAA76815.1 - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	65274572, 22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 21906754, 87168559, 265018, 265019, 264448, 264288, 264369, 284686, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1332	84845937 (2663, 2664)	Novel Protein sim. GBank gi 5459516 dbj BAA82407.1 - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]	synthase		60432289, 66712502, 264591, 60433356, 60433438, 55812038, 265010, 264639, 56526486
1333	88098476 (2665, 2666)	Novel Protein sim. GBank gi 5689527 dbj BAA83047.1 - (AB029018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	264905
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi 2662536 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]	phosphatase		22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21906754, 87168559, 265017, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 33657109, 27486264, 18108374, 264556, 264638, 264557, 60170394, 264559, 18108385, 264563
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gi 4240285 dbj BAA74921.1 - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00843) - B-box zinc finger.	UNCLASSIFIED	

1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi 465445 sp P33485 VNUA_PRVKA - PROBABLE NUCLEAR ANTIGEN			UNCLASSIFIED	264509, 264905, 264512, 264764, 264693, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gi 5689471 dbj BAA83019.1 - (AB028990) KIAA1067 protein [Homo sapiens]			UNCLASSIFIED	56182575, 56994075, 22278998, 22278999, 264092, 264259, 60432289, 29331826, 264906, 264908, 264909, 264112, 265008, 265009, 60433356, 55812038, 33657084, 265011, 265017, 265018, 265019, 264682, 264448, 264883, 264369, 264688, 264689, 21806766, 21906769, 265020, 264691, 27489261, 20281089, 18108379, 55811576, 35695855, 56182323, 60432113, 22279002, 264567
1338	80366114 (2675, 2676)				UNCLASSIFIED	29331822, 265010, 264288, 264689, 18108370, 35695855
1339	80249231 (2677, 2678)	Novel Protein sim. GBank gi 1176422 (U43194) - rhophilin [Mus musculus]			UNCLASSIFIED	35696052, 264909, 264688, 264556, 264558
1340	88316311 (2678, 2680)					264905, 264907, 87168559, 264764
1341	86101485 (2681, 2682)					264681, 264685, 264686, 264692
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi 5019564 emb CAB44507.1 - (AL035542) dJ994E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like protein)) [Homo sapiens])	Contains protein domain (PF00001) - im7 7 transmembrane receptor (rhodopsin family)			264629
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi 4557543 ref NP_001384.1 pECM2 - extracellular matrix protein 2	Contains protein domain (PF00560) Leucine Rich Repeat	struct		264910, 264686, 264534
1344	20562559 (2687, 2688)	Novel Protein sim. GBank gi 2144101 pir I55210 - Iricarboxylate carrier - rat (fragment)			glycoprotein	263978 264909, 60170394
1345	91225546 (2689, 2690)	Novel Protein sim. GBank gi 3881052 emb CAA19523 - (AL023943) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST yk246a12.3 comes from this gene; cDNA EST yk356c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk246a12.5 comes...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		22278998, 264907, 264681, 264685, 264689, 265020, 264693, 22279000, 22279002, 264566
1346	80255717 (2691, 2692)					
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi 4504379 ref NP_003658.1 pHG38 - orphan G protein- coupled receptor HG38	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein		264906, 264908, 264909, 265006, 264910, 265011, 265017, 264764, 264766, 264767, 264769, 264631, 264634, 264638, 264567, 264486
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi 3399720 dbj BAA32100 - (AB010999) peptidylarginine deiminase type IV [Rattus norvegicus]			UNCLASSIFIED	264488, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 264592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 264557, 264558, 22279002, 264486

1349	91225548 (2697, 2698)	Novel Protein sim. GBank gij2144101 prj I55210 - Irtcarboxylate carrier - rat (fragment)		UNCLASSIFIED	52646842, 35686286, 22278996, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265008, 264512, 264910, 60170831, 264591, 60433438, 264757, 21906754, 265017, 265018, 264605, 264760, 264762, 264288, 264766, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265020, 264534, 264691, 264692, 33657023, 264693, 33657349, 18108374, 18108376, 35696423, 60170394, 22279000, 22279002, 264563, 264564
1350	87093136 (2689, 2700)			UNCLASSIFIED	52646842, 264259, 29331825, 264908, 264511, 264804, 264288, 21906769, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264558, 18108385, 22279002, 264486
1351	87361327 (2701, 2702)	Novel Protein sim. GBank gij4887239 gb AAD32246.1 - (AF084584) BAW protein [Fugu rubripes]		UNCLASSIFIED	264906, 264907, 264638
1352	80076386 (2703, 2704)			UNCLASSIFIED	284693, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gij2144101 prj I55210 - Irtcarboxylate carrier - rat (fragment)			35696286, 60424269, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264758, 264598, 55811386, 265011, 264605, 55811150, 264762, 264764, 264766, 52644229, 56181562, 35695917, 265022, 33657023, 264693, 35695763, 60431528, 264629, 263978, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gij4689108 gb AAD27763.1 AF07703 - (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331826, 264906, 265008, 33657402, 21906754, 265011, 87168559, 264684, 264369, 264769, 264689, 21906765, 21906766, 52644150, 33657023, 264692, 264693, 18108374, 83373044, 87168518, 22279000
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gij469199 dbj BAA09487 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278996, 22278997, 264259, 66714117, 264511, 21906754, 265010, 264769, 264689, 21906765, 21906766, 21906769, 284532, 27486262, 264629, 264638, 264556, 264638, 264639, 264482, 264484

1356	95313991 (2711, 2712)	Novel Protein sim. GBank gii113865 (U40342) - ninein [Mus musculus]		struct	18108397, 22278995, 22278998, 22278998, 264094, 29331828, 264905, 265006, 265007, 265008, 265010, 265017, 265018, 265019, 264764, 18108354, 264689, 21906785, 265022, 18108364, 35686423, 83373044, 18108387
1357	88260268 (2713, 2714)	Novel Protein sim. GBank gii837693[emb]CAA90330] - (Z50028) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain		264259, 29331822, 29331825, 264510, 87168559, 265018, 264448, 264288, 21906785, 21806766, 21808768, 285021, 264693, 18108376
1358	38718455 (2715, 2716)	Novel Protein sim. GBank gii556219 (L36831) - transcription regulator [Mus musculus]			284757
1359	87771643 (2717, 2718)			UNCLASSIFIED	264907, 264909, 264510, 264511, 264512, 18108351, 264764, 264534, 33657023, 18108374, 264634, 264635, 264638, 264639, 18108385, 264486, 284587
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gii2588282[emb]CAA75612] - (Y15417) acetate-CoA ligase [Coprinus cinereus]		synthase	60432289, 264605
1361	87593527 (2721, 2722)	Novel Protein sim. GBank gii5689443[db]BAA83005.1] - (AB028976) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00536) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	35696286, 22278997, 22278999, 264259, 29331826, 264508, 264509, 264905, 264907, 264908, 265007, 265009, 33109954, 21908754, 87168474, 265011, 264761, 264683, 264288, 264768, 264769, 264689, 21906768, 265020, 265021, 33657023, 55811576, 35696423, 264634, 60432113, 22279002, 264482, 264486
1362	95287961 (2723, 2724)	Novel Protein sim. GBank gii5689411[db]BAA82989.1] - (AB028960) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	eph	56182575, 56181686, 60432049, 264259, 29331822, 56182181, 29331827, 35696052, 29331828, 264905, 264906, 264908, 264595, 55812038, 85658542, 55811150, 264681, 264288, 264369, 56181582, 60431528, 55810764, 35696423, 60431850, 264558
1363	85758476 (2725, 2726)	Novel Protein sim. GBank gii1130494 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	264488, 29331826, 264907, 264687, 264689, 264693
1364	88179488 (2727, 2728)				60432289, 60433356, 60433438, 87168559, 264603, 18108351, 21808766, 35696423, 60432113
1365	83003108 (2729, 2730)	Novel Protein sim. GBank gii4589562[db]BAA76803.1] - (AB023176) KIAA0959 protein [Homo sapiens]		oncogene	264766
1366	87003262 (2731, 2732)	Novel Protein sim. GBank gii1084944[pir]J554495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	265007

1367	87721210 (2733, 2734)	Novel Protein sim. GBank gij488408[emb](CAB43240.1) - (AL050018) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - SAND domain	UNCLASSIFIED	264488, 52646842, 52646365, 22278995, 56994075, 35696286, 22278996, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 264805, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 265009, 60170831, 33657402, 55812038, 21906754, 265011, 87168559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264368, 264686, 264767, 264688, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 265022, 264534, 60170615, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264635, 264555, 264637, 264556, 52644332, 60170394, 264558, 18108381, 18108385, 56526486, 22279000, 264583, 264587
1368	94320078 (2735, 2736)	Novel Protein sim. GBank gij464561[sp]P35289[Rb15_RAT RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - Ras family	oncogene	264259, 29331822, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264908, 264909, 264510, 265007, 264910, 60433438, 264758, 85658542, 87168559, 264600, 264601, 264760, 264764, 264765, 264768, 52644229, 264689, 35695917, 265020, 265021, 264631, 264632, 264634, 264637, 52644332, 264558, 264639, 83373044, 264563, 264588, 264486, 264587, 265008, 60432229, 60433356, 33657084, 21906784, 21906768, 264555, 264638, 264559, 264567
1369	86634033 (2737, 2738)	Novel Protein sim. GBank gij2062702 (U90550) - butyrophilin [Homo sapiens]		UNCLASSIFIED	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264766, 264768, 21906767, 35695917, 18108362, 35696423, 264632, 264635, 264636, 264555, 264638, 264558, 264639, 18108385, 65274727, 264404, 264563, 264566, 264488
1370	95316910 (2739, 2740)	Novel Protein sim. GBank gij5031823[ref]NP_005823.1pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264766, 264768, 21906767, 35695917, 18108362, 35696423, 264632, 264635, 264636, 264555, 264638, 264558, 264639, 18108385, 65274727, 264404, 264563, 264566, 264488
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gij5032203[ref]NP_005714.1pTSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	glycoprotein	22278996, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264905, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657182, 33657349, 35695855, 264558, 22279002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gij840708[dj]BAA093341 - (D50685) trans-aldolase [Trypanosoma cruzi]		collagen	263978	264769, 21906765, 21906767, 22278999, 264691, 264910, 55812038, 265010, 264681, 264684
1373	80469421 (2745, 2746)			UNCLASSIFIED		264907, 264510, 265007, 264512, 265008, 60432229, 264689, 65274791, 264555, 264556, 264557, 83373044, 60432113
1374	95087036 (2747, 2748)	Novel Protein sim. GBank gij111876[pjrl]JC1241 - beta-interferon-induced protein - rat		interferon		52044507, 52845156, 52846842, 52846365, 56182575, 56181686, 22278998, 56994075, 35698286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 284905, 264509, 264906, 264907, 264908, 29331830, 264909, 265006, 264511, 265007, 265008, 265009, 33657402, 60433358, 52846317, 33109954, 33657084, 52844298, 87168474, 87168559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 264764, 264286, 264369, 264766, 52844229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 27486261, 33657349, 27486265, 35695763, 18108376, 55810764, 35698423, 35695855, 264630, 264631, 264634, 264636, 264555, 264638, 18108385, 87168518, 60432113, 22279000, 22279002, 264583, 264564, 264568, 264587
1375	94236942 (2748, 2750)	Novel Protein sim. GBank gij5649176[gj]AAD03500.21 - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase		264768, 264769, 35695917, 22278997, 35696052, 264508, 284509, 264905, 264906, 264928, 264908, 264629, 18108372, 264909, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 284592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56528488, 265010, 265011, 264600, 264563, 264762, 264564, 264565, 264764, 264488, 264766
1376	87399050 (2751, 2752)	Novel Protein sim. GBank gij138350[sp]P28968[VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED		29331824, 264591, 265019, 264686, 264768, 55811957, 264693, 22279002
1377	86864242 (2753, 2754)	Novel Protein sim. GBank gij1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated		

1378	87595071 (2755, 2756)	Novel Protein sim. GBank gij4107015[dbj BAA36293] - (AB001772) PEM-5 [Clona savignyi]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264369, 264288, 29148627, 55811957, 264691, 18108368, 33657109, 18108368, 264635, 263981, 18108385
1379	85879344 (2757, 2758)	Novel Protein sim. GBank gij3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627862 (2759, 2760)	Novel Protein sim. GBank gij483737[gbj AAD30662.1] - (AF088834) germ cell specific Y-box binding protein [Homo sapiens]		nuc_rept	264510, 264512, 265008, 264288, 264564
1381	88178858 (2761, 2762)	Novel Protein sim. GBank gij4731580[gbj AAD28508.1 AF12538 - (AF125384) L82A [Drosophila melanogaster]		UNCLASSIFIED	87168559, 265017, 264628, 22279002
1382	84847576 (2763, 2764)		Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432229, 60433356, 85558542, 265017, 265018, 264685, 264768, 21906766, 35695917, 33657023, 27486261, 27486262, 35695763, 35695855, 87168518, 22279002
1383	87860598 (2765, 2766)			UNCLASSIFIED	18108396, 264692
1384	86915895 (2767, 2768)			UNCLASSIFIED	264488, 264508, 264509, 264905, 264908, 264908, 264909, 264511, 264512, 264910, 264760, 18108351, 264766, 264769, 35695855, 264630, 264636, 264555, 264638, 264483, 264584, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gij2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]		UNCLASSIFIED	35696052, 55811386, 264688, 21906765, 265020, 33657023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gij2384910 (AF022982) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]		Inf	60432289, 29331828, 264906, 264907, 56182435, 265011, 264681, 60170615, 33657023, 83373044, 264566
1387	87797958 (2773, 2774)	Novel Protein sim. GBank gij4160304[embj CAA10600] - (AJ132192) HS1 binding protein 3 [Mus musculus]		UNCLASSIFIED	264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gij4895184[gbj AAD32753.1 AC007231] putative disease resistance protein [Arabidopsis thaliana]		glycoprotein	65274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264909, 265006, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87168559, 264600, 265017, 264683, 18108354, 52844229, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 264692, 33657023, 33657109, 35695855, 264558, 60170394, 83373044, 22278000

1388	91256016 (2777, 2778)	Novel Protein sim. GBank gij5689387[dbj BAA82977.1] - (AB028948) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29148499, 264908, 66712502, 55812038, 265017, 265018, 265019, 18108351, 264369, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 264692, 33657023, 33657349, 18108370, 18108374, 55811576, 264555, 264556, 264557, 60170394, 83373044, 22279000, 264563, 264564, 52645156, 52646365, 264259, 52645080, 29331825, 29331826, 264908, 52644045, 265009, 33657084, 52644298, 87168474, 87168559, 265017, 265018, 264760, 264682, 264288, 264686, 264687, 56181562, 52644229, 21906765, 21906769, 35695917, 265020, 265021, 80170615, 52644150, 33657023, 27486281, 27486284, 65274791, 264631, 264555, 52644332, 87168518, 22279000, 264567
1389	94111916 (2779, 2780)	Novel Protein sim. GBank gij3702295 (AC005783) - R33083_1 [Homo sapiens]	peptidase		
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gij1346910[sp P28650 PUA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE (ISOZYME (IMP--ASPARTATE LIGASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase		29331826, 29331828, 29331830, 264448, 264288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gij726286 (U22394) - mSin3A [Mus musculus]			52646842, 65274572, 22278994, 22278895, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656970, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644286, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264369, 264766, 21906764, 21906787, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486282, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264566, 18108391
1393	80409472 (2785, 2786)		Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264763, 264631
1394	15028819 (2787, 2788)			UNCLASSIFIED	264629
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gij2274845[dbj BAA21534] - (D88461) N-WASP [Rattus rattus]		UNCLASSIFIED	265009, 18108381

1396	95363253 (2781, 2782)	Novel Protein sim. GBank gi 2135904 pir 54810 - pHLE1F1 - human			22278997, 22278999, 264259, 29331825, 60432289, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 265006, 265007, 265008, 265009, 60433356, 265010, 264802, 265017, 265018, 265019, 18108354, 52644229, 18108358, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 18108368, 18108374, 56182323, 18108385, 264563, 264567, 35696286, 264907, 66712502, 264510, 35695917, 264692, 264693, 35696423, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 87168474, 265018, 265019, 264682, 264768, 21906767, 265020, 33657023, 27486261, 55811576, 264632, 264639, 83373044, 87168518, 22279002
1397	87631317 (2783, 2784)		UNCLASSIFIED		
1398	91233667 (2785, 2786)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]			
1399	87631076 (2787, 2788)	Novel Protein sim. GBank gi 2486887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III	UNCLASSIFIED		
1400	95419064 (2789, 2800)	Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken	UNCLASSIFIED	Contains protein domain (PF00017) - Src homology domain 2	56182575, 22278994, 22278997, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264908, 56182435, 264112, 265009, 265011, 265017, 265018, 265019, 264760, 264762, 264765, 264288, 264685, 264687, 56181562, 264769, 21906768, 21906767, 55811957, 264691, 264692, 264628, 264629, 55811576, 264634, 264555, 264637, 264557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226379 (2801, 2802)	Novel Protein sim. GBank gi 3256185 emb CAA15485 - (AL008635) dJ510H18.1 [Homo sapiens]	UNCLASSIFIED	Contains protein domain (PF00790) - VHS domain	65274572, 60432289, 264809, 264758, 264788, 21906769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gi 1515427 (U57523) - nel homolog [Homo sapiens]	lgf	Contains protein domain (PF00008) - EGF-like domain	264905, 264907, 264908, 264809, 264112, 264693, 33657109, 264634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]			65274572, 66712502, 265017, 264448, 264288, 21906765, 21906769, 264693, 55811576, 65274791, 60432113
1404	90935393 (2807, 2808)		UNCLASSIFIED		65274572, 22278998, 29331822, 29331828, 66712502, 265008, 60433438, 265017, 264693, 18108385

1405	95095068 (2808, 2810)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]			264488, 56994075, 35696286, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264908, 264907, 264908, 264510, 264511, 264910, 33657402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33657023, 33657109, 264628, 264634, 83373044, 22279002, 264563, 264482, 284486, 264567, 284907, 264605
1408	87812369 (2811, 2812)	Novel Protein sim. GBank gij624076[g]AAC96425.1] - (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramecium bursaria Chlorella virus 1]	collagen		
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gij2827886 (AF015037) - endonucleotidase A related protein; EOPA related protein [Oryctolagus cuniculus]	UNCLASSIFIED		35696286, 22278999, 264094, 264259, 68714117, 29331826, 29331827, 29331828, 29146498, 264107, 264908, 265006, 265008, 264910, 60433438, 285011, 285017, 18108351, 264448, 264288, 264686, 21906765, 21908769, 264692, 33657109, 18108370, 264628, 263972, 18108374, 35696423, 55811576, 264631, 264557, 264558, 83373044, 18108385, 87168518, 60432113, 22279002
1408	95361477 (2815, 2816)	Novel Protein sim. GBank gij2564953 (AF030001) - unknown [Mus musculus]	oncogene	Contains protein domain (PF000008) - EGF-like domain	264488, 264489, 35696286, 264109, 264508, 264905, 264508, 264906, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 285011, 264601, 265017, 264760, 264762, 264683, 264685, 264766, 264687, 264689, 21908767, 285021, 264690, 264691, 33657023, 264692, 264693, 33657109, 264628, 264629, 35696423, 35695855, 264631, 284632, 284634, 264635, 264555, 264636, 264637, 264638, 56182323, 284639, 264563, 264564, 264565, 264566, 264567, 264693
1409	66644385 (2817, 2818)	Novel Protein sim. GBank gij2662165[dbj]BAA23714] - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gij2493780[sp]Q60994[ACR3] MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)	complement C1q domain	Contains protein domain (PF003386) - C1q domain	29331826, 264112, 264512, 265009, 265010, 264601, 264686, 264769, 21906767, 263974, 264631, 264566

1411	87818841 (2821, 2822)	Novel Protein sim. GBank gij3123155lsp91343YJM3M_CAEEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	22278995, 22278997, 22278999, 29331822, 60432289, 29331828, 284907, 265017, 265018, 264682, 21906767, 21906768, 21906769, 265020, 264690, 264691, 33657023, 33657109, 27486284, 264628, 263972, 264634, 264558, 18108385 264757
1412	84390918 (2823, 2824)	Novel Protein sim. GBank gij3879121emb CAA94370 - (Z70310) Predicted using GeneFinder. Similarity to Mouse ankyrin (PIR Acc. No. S3771); cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED homeobox	55994075, 29331822, 35695052, 29331828, 29331830, 264909, 52644045, 264510, 52644296, 85658542, 87168474, 265017, 265018, 264681, 264687, 21906768, 35695917, 265020, 52644150, 264692, 263967, 27486284, 35695763, 264639, 18108387, 264566
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gij3252981 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264682, 264683, 265022, 264636
1415	94326948 (2829, 2830)	Novel Protein sim. GBank gij1871187 (U90439) - unknown protein [Arabidopsis thaliana]			52646365, 56182575, 22278994, 22278995, 55994075, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 66712502, 29331830, 52644045, 264113, 264511, 33657402, 264757, 21906754, 55811388, 265017, 265018, 265019, 264761, 264683, 264369, 264288, 264686, 264689, 21906768, 21906767, 29148627, 21906769, 55811957, 265020, 265021, 264690, 33657023, 65274620, 52645129, 27486282, 27486284, 60431528, 264629, 35695855, 56182323, 264559, 60432113, 264404, 22279002, 264482

1416	84325977 (2831, 2832)	Novel Protein sim. GBank gi 5106557 gb AAD39749.1 AF123052 MLL sepiin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - Cell division protein	struct	18108392, 18108394, 18108397, 18108398, 22278995, 22278996, 35698286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29146498, 264905, 264907, 264908, 264828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21906754, 87188474, 265010, 265011, 87188559, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264682, 264683, 264766, 52644229, 264688, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 55811957, 29148629, 265020, 52644150, 18108361, 33657023, 18108362, 18108368, 264628, 18108370, 264629, 18108374, 18108379, 55811576, 65274791, 264634, 264636, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22279000
1417	87826563 (2833, 2834)	Novel Protein sim. GBank gi 4958935 dbj BAA78095.1 - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]		ATPase_associated	264107, 264448
1418	87594276 (2835, 2836)			UNCLASSIFIED	264259, 264808, 265010, 52644229, 21906764, 21906768, 264690, 264639, 18108388
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gi 2072294 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]		struct	264259, 60432289, 265006, 87168474, 264288
1420	87298628 (2839, 2840)	Novel Protein sim. GBank		ATPase_associated	29331824, 265007, 264563
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gi 3876090 emb CAA83459.1 - (Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST yk209h1.5 comes from this gen...		kinase	18108358, 18108396, 18108397, 21906766, 18108398, 21906767, 56182575, 21906768, 21906769, 56181686, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170615, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331826, 27486261, 29331828, 35696052, 33657349, 264905, 264509, 20281149, 18108370, 264907, 60431528, 68712502, 263972, 55811576, 35696423, 35695855, 264512, 285007, 60431850, 60432229, 60431735, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21906754, 55811386, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264563, 264682, 264763, 264448, 264566, 264488, 18108391

1422	88178777 (2843, 2844)	Novel Protein sim. GBank gil4505939[ref]NP_000928.1lpPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)		mapolymerase	56984075, 35696286, 87168559, 55811957, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)			UNCLASSIFIED	264686, 264489, 264692, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gil437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]	Contains protein domain (PF00620) - struct RhoGAP domain		29331822, 29331825, 29331827, 29146498, 264905, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 29148627, 55811957, 29148629, 265021, 264691, 264692, 56526486, 22279002, 264563
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gil100798[pr]S14959 - proline- rich protein - wheat		UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gil2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP:P25386) [Caenorhabditis elegans]		UNCLASSIFIED	264488, 60424179, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331827, 56182435, 264910, 60433356, 60433438, 21906754, 265018, 264288, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 33657109, 18108370, 18108376, 264558, 83373044, 18108385, 56526486, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gil5816074[gb]AAD45616.1AF08194 - (AF061943) prolute- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 56994075, 22278997, 29331828, 29331830, 264828, 265006, 265007, 265008, 265009, 264683, 264288, 18108354, 21906765, 21906768, 29148629, 33657023, 18108374, 35695855, 83373044, 22279002, 264564
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gil138350[sp]P28968[VLX]_HSVEB - GLYCOPROTEIN X PRECURSOR		glycoprotein	56181686, 264259, 264907, 265007, 265009, 264595, 265010, 264686, 65274620, 264629, 65274791, 22279002, 264566
1429	87888689 (2857, 2858)			UNCLASSIFIED	264112, 264595, 265017, 265019, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gil1181619[dbj]BAA11565] - (D82364) a variant of TSC-22 [Gallus gallus]			264094, 29331824, 264591, 264593, 265018, 264681, 21906765, 21906767, 65274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gil5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gil414797 (L18966) - pyruvate dehydrogenase phosphatase [Bos taurus]		phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29148629, 263969
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gil2460316 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]	Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	264259, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)			UNCLASSIFIED	264682, 264691

1435	94708213 (2868, 2870)	Novel Protein sim. GBank gij3970850[dbj BAA34789.1] - (AB015330) HRIHFB2007 [Homo sapiens]		transcript factor	22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 33656970, 264508, 264905, 66712502, 29331830, 264909, 265007, 265008, 264910, 265009, 60433356, 60433438, 264598, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264789, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264690, 264691, 33657109, 264628, 18108374, 18108376, 55811576, 264636, 60170394, 56182323, 264559, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264482, 264565, 263978, 264557, 264559
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gij3183977[emb CAA39515] - (X56044) protein HIFC [Mus musculus]		UNCLASSIFIED	
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gij2496887[sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	22278997, 66714117, 29331826, 264907, 56182435, 265009, 18108351, 264692, 264693
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gij1905906 (AD000092) - hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264488, 264508, 264908, 264909, 264757, 264600, 264601, 264605, 264768, 264769, 264690, 35696423, 264558, 264563, 264566
1439	91231884 (2877, 2878)	Novel Protein sim. GBank gij3876299[emb CAA94892] - (Z71180) similar to BPTIKUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabditis...]	Contains protein domain (PF00450) - Serine carboxypeptidase	cathepsin	264489, 18108394, 65274572, 56182575, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33856970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 264511, 265006, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811386, 265011, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 18108355, 264767, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 264638, 56182323, 83373044, 18108387, 87168518, 60432113, 22279000, 264486
1440	87423643 (2878, 2880)	Novel Protein sim. GBank gij2662165[dbj BAA23714] - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	264887, 264259, 264906, 264907, 264908, 264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

1441	95317662 (2881, 2882)	Novel Protein sim. GBank gj1493956[embjCAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PF00845c). Hypothetical proteins, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR)...	Contains protein domain (PF00646) - helicase F-box domain.	18108392, 264488, 263994, 264488, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 56182181, 66714117, 29331826, 29331827, 29331828, 35696052, 29146498, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264910, 264592, 264593, 33657402, 60433438, 264595, 264758, 21906754, 85658542, 87168474, 265010, 87168559, 264600, 264602, 265017, 264604, 265018, 264605, 265019, 264760, 264761, 264762, 264881, 264448, 264764, 264683, 264288, 264766, 264768, 264769, 52644229, 264689, 21908765, 21906766, 21906787, 21906788, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 52644150, 264691, 264692, 33657023, 65274620, 33657109, 35695763, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 65274791, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 56182323, 264558, 60170394, 264639, 264559, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563, 264483, 264564, 264566, 264567, 264486
1442	63367491 (2883, 2884)	Novel Protein sim. GBank gj15103027[dbjBAA78765.1] - (AB023419) mSox7 [Mus musculus]		transcriptfactor
1443	87108935 (2885, 2886)	Novel Protein sim. GBank gj14887229[gb AAD32244.1 AF15075] - (AF150755) microtubule-actin crosslinking factor. [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	52645080, 264691, 264628, 264555
1444	87620478 (2887, 2888)	Novel Protein sim. GBank gj13874447[embjCAB02772] - (Z81039) predicted using Genefinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...	UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 29331828, 264288, 35695917, 33657023, 264635, 60170394
1445	94990470 (2889, 2890)	Novel Protein sim. GBank gj12959886[embjCAA11022] - (A1222988) L-perflaxin [Mus musculus]	UNCLASSIFIED	264369
1446	85079268 (2891, 2892)	Novel Protein sim. GBank gj15081610[gb AAD39464.1 AF13544] - (AF135440) huntington yeast partner C [Mus musculus]	Contains protein domain (PF01846) - FF domain	264369
1447	86945392 (2893, 2894)	Novel Protein sim. GBank gj15081610[gb AAD39464.1 AF13544] - (AF135440) huntington yeast partner C [Mus musculus]	Contains protein domain (PF01846) - FF domain	18108396, 35696286, 22278997, 66714117, 29331828, 265009, 264758, 265018, 264288, 21908766, 21906767, 264692, 264634, 264566
1448	94990477 (2895, 2896)	Novel Protein sim. GBank gj13980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain	29331827, 264509, 264908, 265008, 264595, 18108357, 18108385, 264566, 264486

1449	87860859 (2897, 2898)				UNCLASSIFIED	66714117, 264908, 264908, 264591, 264601, 264764, 264832
1450	87458686 (2899, 2900)	Novel Protein sim. GBank gij1707074 (U80450) - M01E11.2 [Caenorhabditis elegans]			UNCLASSIFIED	35698286, 35698052, 265008, 265009, 60170831, 33109954, 264683, 264689, 35698423, 35698555, 56526488
1451	87797970 (2801, 2802)	Novel Protein sim. GBank gij4160304[emb]CAA106001 - (AJ132192) HS1 binding protein 3 [Mus musculus]			UNCLASSIFIED	29331826, 264683, 264693, 263978, 264630
1452	85682899 (2903, 2904)	Novel Protein sim. GBank gij282906[id]BAA24608.11 - (D89340) dipeptidyl peptidase III [Rattus norvegicus]			peptidase	264681, 33657023, 264629
1453	86130434 (2905, 2906)	Novel Protein sim. GBank gij728831[sp]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]			kinase	264510, 264768
1454	11204698 (2907, 2908)					264556
1455	87797896 (2809, 2910)				UNCLASSIFIED	29331822, 66714117, 29331825, 264905, 29331830, 265006, 265008, 265009, 265011, 265019, 18108351, 21906768, 33657109, 18108376, 264632, 56182323, 87168518
1456	86320218 (2911, 2912)	Novel Protein sim. GBank gij728230[sp]P41004[CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3]			transport	22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 264107, 265017, 21906765, 21906766, 21906767, 21906769, 29148629, 18108370, 22278000
1457	80076900 (2913, 2914)				UNCLASSIFIED	264107, 264566
1458	87800460 (2915, 2916)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			transport	56182575, 22278999, 60432049, 264259, 29331826, 29331827, 29331828, 264102, 264107, 264110, 265009, 60432229, 265019, 265020, 263972, 263976, 264635, 22279002, 264566
1459	85360920 (2917, 2918)	Novel Protein sim. GBank gij5524667[gb]AAD44333.1[AF159356] Munc13-4 protein [Rattus norvegicus]	Contains protein domain (PF00168) - C2 domain		kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 265017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 264692, 33657023, 33657109, 35698555, 264566
1460	95354602 (2919, 2920)				UNCLASSIFIED	29331822, 264591, 55811957, 264691, 264693, 65274620
1461	94741513 (2921, 2922)	Novel Protein sim. GBank gij1707274 (U80931) - strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate		gaba	22278997, 29331822, 35698052, 265009, 264758, 265017, 265018, 265019, 264760, 264369, 264687, 21906765, 21906768, 265022, 33657109, 27488281, 264555, 83373044
1462	87732018 (2923, 2924)				UNCLASSIFIED	264555, 264556
1463	88090605 (2925, 2926)	Novel Protein sim. GBank gij1770466[emb]CAA669121 - (X98259) M-phase phosphoprotein 8 [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR)romatin Organization (Modifier) domain		struct	60432049, 264259, 29146499, 264906, 264907, 264512, 265017, 264763, 264766, 18108370, 18108374, 264636, 18108385, 18108388

1464	87620482 (2827, 2828)	Novel Protein sim. GBank gij3874447[emb]CAB02772] - (Z81039) predicted using Genelinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264569, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331825, 35696052, 20281100, 264905, 29331830, 264909, 265007, 33657402, 21908754, 265017, 265018, 264682, 264684, 264369, 264288, 264766, 21908765, 21908766, 21908767, 21906769, 35695917, 264691, 33657023, 264692, 35696423, 35695855, 264630, 264631, 264639, 264565
1465	87425192 (2829, 2830)	Novel Protein sim. GBank gij4589588[jb]BAA76821.1] - (AB023194) KIAA0977 protein [Homo sapiens]		glucoamylase	264488, 22278994, 56994075, 60432049, 264259, 56182181, 60432289, 29331827, 52844045, 264511, 265007, 265008, 264596, 55812038, 55811386, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21906769, 265021, 33657023, 33657182, 55811576, 264557, 18108382, 60432113
1466	87606227 (2831, 2832)	Novel Protein sim. GBank gij2245532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	264512, 265017, 264689, 264558
1467	87614326 (2833, 2834)	Novel Protein sim. GBank gij4507241[ref]NP_003137.1pSSRP - structure specific recognition protein 1		struct	264683, 264636
1468	95342862 (2835, 2836)	Novel Protein sim. GBank gij4507241[ref]NP_003137.1pSSRP - structure specific recognition protein 1			22278998, 264758, 265018, 265019, 21908769, 265020, 33657109, 22279002
1469	79236174 (2837, 2838)	Novel Protein sim. GBank gij1906586 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	18108394, 18108397, 18108398, 35696052, 29146499, 265007, 265008, 285009, 265010, 265011, 18108354, 18108365, 18108368, 18108374, 18108381, 18108382, 18108384, 18108388
1470	94990482 (2839, 2840)	Novel Protein sim. GBank gij5649170[jb]AAD43131.2[AF159092] syld709613 protein [Homo sapiens]		UNCLASSIFIED	18108394, 18108398, 56182575, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264591, 60432229, 60433356, 264595, 60434338, 264758, 33109954, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264369, 18108357, 264769, 18108358, 21906767, 21906769, 55811957, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87168518, 60432113, 264404, 22279002, 264482, 264567, 264487
1471	87826842 (2841, 2842)	Novel Protein sim. GBank gij3876146[emb]CAB01750] - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL: T01651 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	transport	29331822, 29331824, 29331825, 264828, 264603, 264689, 264693, 18108374, 55811576

1472	87756816 (2843, 2844)	Novel Protein sim. GBank gi 4680707 gb AAD27743.1 AF13298 - (AF13298) CGI-34 protein [Homo sapiens]		UNCLASSIFIED	264905, 18108351, 21906765, 264486
1473	87781609 (2945, 2946)	Novel Protein sim. GBank gi 3688780 (AF042180) - testis-specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - MHC Nucleosome assembly protein (NAP)		18108394, 22278995, 56994075, 22278999, 29331822, 29331824, 66714117, 29331825, 29331826, 35696052, 264906, 264907, 56182435, 265007, 264758, 265018, 265019, 264760, 264764, 264288, 264685, 264686, 264768, 21906769, 55811957, 265021, 264691, 264693, 264629, 55811576, 264634, 264638, 58182323, 22279002, 264566, 264486
1474	85800989 (2847, 2848)	Novel Protein sim. GBank gi 2494890 sp Q92176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - struct WD domain, G-beta repeat		264488, 35695917, 35696286, 264692, 33657023, 264693, 33657109, 35696052, 264508, 264905, 264906, 264907, 264629, 264908, 264909, 35696423, 35695855, 264511, 264910, 264632, 264634, 264635, 264636, 264637, 264558, 264557, 264639, 264758, 60432113, 264604, 264605, 264565, 264568, 264764, 264488, 264685, 264766
1475	86871935 (2949, 2950)		Contains protein domain (PF00041) - Fibronectin type III domain	UNCLASSIFIED	264681, 264682, 264288, 264566
1476	87548855 (2951, 2952)	Novel Protein sim. GBank gi 4757752 ref NP_004664.1 pANGP - angiotensin 3	Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	glycoprotein	60424179, 56181886, 29331824, 60424269, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264512, 265007, 265008, 265009, 264910, 33657402, 264595, 264596, 55812038, 265011, 264601, 264762, 18108351, 264288, 264369, 264685, 264766, 264689, 55811957, 264691, 264692, 264693, 18108370, 60431528, 18108374, 35696423, 264634, 264635, 264636, 60431850, 264555, 264638, 264557, 264639, 18108382, 18108388, 60432113, 22279002
1477	87774279 (2953, 2954)	Novel Protein sim. GBank gi 2498308 sp Q60870 DP1_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)		UNCLASSIFIED	264259, 264107, 264905, 265008, 265010, 265011, 264682, 264288, 265020, 265021, 263974
1478	11754412 (2855, 2956)				264686

1479	91640140 (2957, 2958)	Novel Protein sim. GBank gi 5499741 gb AAD43978.1 AF15296 - (AF152961) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 66714117, 264906, 264907, 56182435, 265006, 60170831, 33657402, 264758, 33108954, 21906754, 265017, 265019, 264448, 264288, 264767, 264687, 5264229, 21906764, 264689, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 18108370, 60431528, 263976, 55811576, 264556, 264557, 60170394, 87168518, 264404, 22279000, 22279002, 264563, 264482
1480	94312412 (2959, 2960)	Novel Protein sim. GBank gi 3550456 emb CAA06329.1 - (AJ005073) Alix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35696286, 56994075, 22278996, 22278997, 22278998, 22278999, 264091, 264259, 35696052, 29148499, 264103, 264105, 264108, 264907, 52644045, 264112, 265007, 265008, 265009, 60433356, 60433438, 264596, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264682, 264683, 264769, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657109, 33657182, 263972, 35695855, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	87021442 (2861, 2862)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF146793) PFT27 [Mus musculus]		MHC	265006, 265007, 265010, 18108374
1482	95320442 (2863, 2864)	Novel Protein sim. GBank gi 4585372 gb AAD25403.1 AF12292 - (AF122923) Wnt inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264908, 264910, 264758
1483	94115503 (2865, 2866)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin- like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	264259, 29331822, 52645080, 29331825, 29331826, 33656970, 29331830, 265007, 55812038, 33109954, 265017, 264288, 21906768, 21906769, 264636, 18108380, 87168518, 22279000
1484	94131544 (2867, 2868)	Novel Protein sim. GBank gi 1911774 bbs 180090 - (S83364) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 264259, 264107, 264809, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906768, 29148627, 33657023, 27486262, 18108374, 35696423, 83373044, 60432113
1485	80194441 (2869, 2870)	Novel Protein sim. GBank gi 5360129 gb AAD42883.1 AF15511 - (AF155117) NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264369, 265020, 18108374

1486	84125066 (2971, 2972)	Novel Protein sim. GBank gi 4589516 dbj BAA76780.1 - (AB023153) KIAA0938 protein [Homo sapiens]	Contains protein domain (PF00008) - Eukaryotic protein kinase domain	kinase	56182575, 22278999, 264906, 264907, 21906754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gi 5019275 emb CAB44431.1 - (AJ132751) xenobiotic/medium-chain fatty acid:CoA ligase form XL-III [Bos taurus]		synthase	21906754, 264486
1488	87732026 (2975, 2976)	Novel Protein sim. GBank gi 5712731 gb AAD47378.1 (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	tgf	264686, 264769, 264689, 264692, 264693, 264509, 264906, 264907, 18108370, 264908, 264829, 264909, 264510, 265008, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264762, 264564, 264682
1489	85104277 (2977, 2978)	Novel Protein sim. GBank gi 2497303 sp Q82786 FPRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - Immunoglobulin domain	prostaglandin	21906767, 22278999, 265022, 264259, 264693, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 66712502, 35696423, 35695855, 265007, 265008, 265009, 83373044, 21906754, 56526486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1490	87390127 (2979, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21906767, 21906768, 55811957, 60170615, 33657109, 35695855, 264635, 60170394, 56526486, 22279002, 264563
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gi 295671 (L1275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]		UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85805363 (2983, 2984)	Novel Protein sim. GBank gi 1656005 (U71205) - rt [Mus musculus]	Contains protein domain (PF00071) - Ras family	oncogene	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2985, 2986)	Novel Protein sim. GBank gij5689515jdbjBAA83041.1] - (AB029012) KIAA1089 protein [Homo sapiens]		UNCLASSIFIED	264488, 52646365, 65274572, 56182575, 22278994, 35696286, 56994075, 22278999, 60432049, 29331824, 29331828, 35696052, 264508, 284905, 264908, 52644045, 264909, 56182435, 265008, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264682, 264685, 264686, 52644229, 21906765, 21906768, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657023, 18108384, 18108365, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 264629, 18108374, 52644332, 56182323, 87168518, 22279002, 264584, 264566, 264567
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gij728832jsp39189jALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF01352) - KRAB box	kinase	264907, 265009, 264769, 18108370, 55811576, 264639, 264565, 264486
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gij4589588jdbjBAA76816.1] - (AB023189) KIAA0972 protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	22278997, 264259, 264906, 264907, 265009, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264568, 264486, 264567
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gij5420387jembjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	35696286, 264906, 265019, 264693
1497	81695428 (2993, 2994)	Novel Protein sim. GBank gij3874925jembjCAA92591] - (Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:T01018 comes from this gene; cDNA EST EMBL:D33256 comes from this gene...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264910, 264758, 265011, 264764, 264288, 264690, 264634, 264635, 56526486
1498	80934938 (2995, 2996)	Novel Protein sim. GBank gij728836jsp39193jALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		oncogene	264488, 65274572, 29331822, 265017, 265018, 21906765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	85451589 (2997, 2998)	Novel Protein sim. GBank gij2570198 (U54556) - microfilament sheath protein SHP3 [Litomosoides sigmodontis]		glucoamylase	263978, 264568
1500	80499386 (2999, 3000)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	22278999, 264769, 18108379
1501	85795297 (3001, 3002)			UNCLASSIFIED	264559
1502	80206141 (3003, 3004)				264508, 264112, 264604, 264684, 52644150, 55811576, 264632, 264556, 264638, 56182323, 284563, 264486
1503	87012701 (3005, 3006)	Novel Protein sim. GBank gij3900855 (AC004874) - similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID.g1171989) [Homo sapiens]	Contains protein domain (PF00535) - Glycosyl transferases	transferase	29331822, 265007, 264369

1504	79540051 (3007, 3008)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264693
1505	86102672 (3009, 3010)	Novel Protein sim. GBank gij475375[emb]CAB41970.1] - (AJ132545) protein kinase [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	29331826, 35696052, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 55812038, 264759, 264763, 264764, 264689, 35695917, 265022, 33657109, 18108374, 264631, 264635, 264638, 264566
1506	94143219 (3011, 3012)	Novel Protein sim. GBank gij1304201[dbj]BAA06170] - (D29766) alternatively spliced product [Rattus norvegicus]	Contains protein domain (PF00018) - SH3 domain	glycoprotein	65274572, 56182575, 56994075, 22278997, 22278998, 22278999, 264081, 264092, 60432049, 264259, 52645080, 29331822, 29331827, 264108, 29331830, 264908, 56182435, 264110, 264511, 264512, 55812038, 21906754, 87168559, 264600, 265017, 265018, 264681, 18108354, 264369, 264687, 264689, 21906765, 29148627, 21906768, 21906769, 29148629, 52644150, 33657023, 18108376, 65274791, 56182323, 264558, 264559, 18108385, 87168518, 60432113, 22279000, 264565
1507	83738250 (3013, 3014)	Novel Protein sim. GBank gij5689513[dbj]BAA83040.1] - (AB029011) KIAA1088 protein [Homo sapiens]		helicase	264639
1508	11618758 (3015, 3016)	Novel Protein sim. GBank			264593
1509	87318451 (3017, 3018)	gij5031975[ref]NP_005875.1[sp]PAK4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331828, 264591, 33109954, 264563
1510	95362643 (3019, 3020)	Novel Protein sim. GBank gij113161[sp]P28614[ACOR]ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN		UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556
1511	88318073 (3021, 3022)	Novel Protein sim. GBank gij128831[sp]P39188[ALU1]_HUMAN - III ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563
1512	95345390 (3023, 3024)	Novel Protein sim. GBank gij4559353[gb]AAD23014.1[AC006585] putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family		52645156, 18108396, 56994075, 60432289, 265006, 60433358, 60433438, 21908754, 87168474, 87168559, 265018, 264762, 264763, 264687, 21906765, 21908769, 27486262, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482
1513	87436228 (3025, 3026)	Novel Protein sim. GBank gij1330394 (U58761) - C01F1.6 gene product [Caenorhabditis elegans]			35696052, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 264766, 264689, 264692, 264629, 264636

1514	95345392 (3027, 3028)	Novel Protein sim. GBank gi14559353 gb AAD23014.1 AC006585 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	5264507, 52645156, 52646365, 52646842, 65274572, 22278994, 35698286, 58994075, 284259, 52645080, 29331822, 29331825, 35696052, 29331830, 52644045, 58182435, 265006, 60433358, 60433438, 55812038, 21906754, 52646317, 52644296, 87168474, 87168559, 284448, 52644229, 21906765, 21908766, 21908767, 21908768, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27488264, 27486265, 35695763, 18108378, 35696423, 35695855, 52644332, 18108385, 18108387, 87168518, 60432113 265020, 264639
1515	79163538 (3029, 3030)	Novel Protein sim. GBank gi13879501 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33368 comes from this gene; cDNA EST EMBL:D33365 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin	UNCLASSIFIED	
1516	88073539 (3031, 3032)	Novel Protein sim. GBank gi1498015 (L27479) - X123 [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	265008, 56182323, 22279002
1517	87793325 (3033, 3034)	Novel Protein sim. GBank gi13415134 (AF082024) - Phyb1 [Pimpinella brachycarpa]			264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gi1728838 sp P39195 ALU8_HUMAN - IIII ALU SUBFAMILY SX WARNING ENTRY IIII	tm7		66714117, 264508, 264509, 264905, 264510, 264910, 264591, 264595, 264288, 264768, 264789, 18108374, 264636, 264638, 264486
1519	94328889 (3037, 3038)	Novel Protein sim. GBank gi1526268 emb CAB45771.1 - (AL080198) hypothetical protein [Homo sapiens]			264569, 264489, 60432049, 265009, 33657402, 264598, 21908754, 265019, 264369, 21906765, 21906768, 21908769, 264891, 65274620, 33657182, 27486261, 18108374, 264557, 264638, 87168518, 22279002
1520	87592855 (3039, 3040)	Novel Protein sim. GBank gi1266216 dbj BAA23712 - (AB007800) HF0452 cDNA clone for KIAA0440 has a 438- bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	18108392, 60432049, 264259, 29331824, 265007, 60433356, 265010, 21908768, 264636
1521	86970696 (3041, 3042)	Novel Protein sim. GBank gi15052351 gb AAD38516.1 AF13542 - (AF135421) GDP- mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - Nucleotidyl transferase	synthase	18108394, 264259, 66714117, 265011, 264603, 265019, 18108364, 35696423, 264557, 264558, 18108388
1522	78960687 (3043, 3044)			UNCLASSIFIED	29331824, 265018, 265020, 265021
1523	91005151 (3045, 3046)	Novel Protein sim. GBank gi13776567 (AC005388) - Strong similarity to F2187.33 gi12809264 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]	UNCLASSIFIED	UNCLASSIFIED	55274572, 21906768, 264693
1524	80203723 (3047, 3048)			UNCLASSIFIED	264112, 21906754, 263974
1525	87799867 (3049, 3050)	Novel Protein sim. GBank gi14759040 ref NP_004283.1 pRIN1 - ras inhibitor		UNCLASSIFIED	264683, 264687, 264689, 264690, 264692, 264693

1526	95105344 (3051, 3052)	Novel Protein sim. GBank gij28850isp(P08840)AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		glycoprotein	35696286, 56182181, 60431735, 264595, 55812038, 264605, 284883, 21906785, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 284559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank gij2792496 (AF041107) - tulip 2 [Rattus norvegicus]			56182575, 264259, 60432049, 29331822, 60432289, 264908, 66712502, 60433438, 87168559, 265017, 264288, 21906768, 21906769, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)			UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264596, 265017, 265019, 264682, 264448, 264883, 264764, 264685, 284686, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 264693, 83373044, 18108385
1528	94120793 (3057, 3058)	Novel Protein sim. GBank gij406663lgb(AAD20053) - (AF131826) Unknown [Homo sapiens]		UNCLASSIFIED	264488, 263994, 56182575, 22278995, 35696286, 22278997, 264259, 29331822, 60432289, 29331827, 35696052, 264509, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 265009, 264910, 60433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264369, 264288, 264766, 18108357, 264768, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 52644150, 33657109, 264629, 35695855, 60432113, 22279002, 264563, 264564, 264486, 264567
1530	95012765 (3059, 3060)	Novel Protein sim. GBank gij2828710 (AF043642) - maltrin cydophilin [Rattus norvegicus]			264488, 264489, 35696286, 29331825, 35696052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264566, 264486
1531	95419351 (3061, 3062)	Novel Protein sim. GBank gij1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF003595) - PDZ domain (Also known as DHR or GLGF).	kinase	56182575, 35696286, 264097, 264259, 29331822, 29331825, 29331826, 29331827, 35696052, 264509, 56182435, 264510, 264511, 265007, 60433356, 55811386, 264681, 264369, 264288, 264766, 264687, 55811957, 35695917, 33657023, 35695763, 55810764, 35696423, 55811576, 283981, 60170394, 56182323, 83373044, 60432113, 264566

1532	85718224 (3063, 3064)	Novel Protein sim. GBank gll3874716[emb]CAA91265] - (Z68484) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D67438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...			UNCLASSIFIED	264689	
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gll1490324[emb]CAB01543] - (Z78141) unknown [Mus musculus]			struct	29331824, 29146489, 264907, 264112, 265008, 265011, 265017, 265018, 264762, 18108351, 263967, 20281149, 18108374, 263981, 264568	
1534	95343941 (3067, 3068)	Novel Protein sim. GBank gll81286[pir]S22697 - extensin - Vohox carterl (fragment)			UNCLASSIFIED	264905, 264807, 264766, 264637	
1535	90838732 (3069, 3070)					65274572, 22278997, 264259, 60432049, 29331822, 60432289, 29331827, 29148499, 265006, 265008, 60170831, 60433438, 33109954, 87168559, 265018, 18108357, 21908768, 29148629, 265021, 265022, 18108377, 56182323, 60432113, 22279000, 22279002	
1536	87602856 (3071, 3072)	Novel Protein sim. GBank gll106024[pir]B32891 - finger protein 2, placental - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type		transcriptfactor	264686, 18108357, 18108394, 21906767, 21906768, 29148829, 35696286, 265020, 265021, 52644150, 264693, 68714117, 29331825, 29331826, 264508, 264905, 20281149, 264909, 18108374, 35696423, 35695855, 265009, 264634, 264636, 264638, 18108385, 56526486, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766	
1537	95354556 (3073, 3074)	Novel Protein sim. GBank gll3876332[emb]CAB02096] - (Z79754) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk426f12.5 comes from this gene; cDNA EST yk342f10.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...				65274572, 56182575, 60432049, 264259, 29331826, 265006, 265007, 60433356, 60433438, 264601, 18108351, 264448, 264389, 264288, 33657023, 65274620, 33657109, 60432113	
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gll403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds], gene product [Gallus gallus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		18108394, 18108397, 264909, 265008, 265009, 265010, 18108351, 264638, 18108382, 18108385, 18108388	

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gi 321841 emb CAA19575.1 - (AL023859) SPBC19C7.07c, putative RNA splicing endonuclease ga mima subunit, len:284aa, similar eg. to YAR008W, YAH8_YEAST, P39707, YAR008W, RNA splicing endonuclease gamma subunit, (275aa), fasia scores, opt:269, E(1):6.4e-2...		nuclease	22278994, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264258, 29331822, 29331824, 60424269, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 56182435, 265009, 33657402, 60433356, 60433438, 55812038, 21906754, 87168559, 265017, 265018, 265019, 18108351, 264288, 52644229, 18108359, 21906764, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 33657023, 33657109, 27486281, 18108370, 18108376, 35696423, 55811576, 65274791, 264558, 56182323, 60170394, 83373044, 87168518, 60432113, 22278000, 22279002, 264586
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gi 5052634 gb AAD38647.1 AF14567 - (AF145672) BCDNA GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264369, 264691, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gi 5052349 gb AAD38515.1 AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264488, 264489, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264907, 264908, 264511, 264512, 264910, 264592, 264761, 264762, 264448, 264764, 264288, 264687, 21906769, 55811957, 35695917, 265020, 264691, 33657023, 264692, 33657109, 264628, 18108374, 264632, 264634, 264635, 264639, 18108385, 264563, 264564, 264565, 264586, 264486
1542	80937549 (3083, 3084)	Novel Protein sim. GBank gi 5305702 gb AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		calthepsin	18108392, 18108394, 65274572, 29331822, 264508, 265007, 265008, 265009, 265011, 264682, 18108354, 18108355, 52644150, 18108368, 264636, 18108381, 18108382
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - iiii ALU SUBFAMILY SB WARNING ENTRY iiii		nuclease	264106, 33109954, 265019, 264683, 35695917, 264690, 264692, 33657109
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gi 3493162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	nud_recpt	35686286, 56994075, 22278999, 35696052, 60433356, 60433438, 265011, 264683, 33657109, 35696423, 264631, 87168518, 22279000
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gi 1086591 (U41007) - similar to S. cerevisiae nuclear protein SNF2 (SP-P22082) in a region of gly-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	264112, 264692, 264693, 55811576
1546	79476589 (3091, 3092)	Novel Protein sim. GBank gi 2661132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	264905, 264686
1547	86999594 (3093, 3094)			UNCLASSIFIED	264258, 29331822, 66714117, 265007, 55811386, 265010, 264600, 265017, 265019, 264288, 264768, 265020, 265022, 55811576, 18108380, 264563

1548	94233065 (3095, 3096)	Novel Protein sim. GBank gi 3043682 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank gi 5689519 dbj BAA83043.1 - (AB029014) KIAA1091 protein [Homo sapiens]		eph	60424179, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35696052, 264905, 264906, 264908, 264909, 265006, 264511, 265008, 60431735, 60433356, 21906754, 55811386, 87168559, 265017, 265018, 265019, 55811150, 264682, 264288, 264389, 56181562, 264769, 21906765, 21906768, 21906769, 55811957, 265020, 264691, 33657109, 60431528, 35696423, 35695855, 56526486, 60432113, 22279002, 264563, 264566
1550	95201907 (3099, 3100)	Novel Protein sim. GBank gi 544483 sp P35350 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	Im7	65274572, 60432289, 265008, 264910, 265011, 265017, 265019, 264768, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank gi 4758566 ref NP_004798.1 pHS6S - heparan-sulfate 6-sulfotransferase		UNCLASSIFIED	22278999, 29331822, 264508, 264509, 264906, 264907, 264909, 265007, 264512, 264910, 21906754, 265018, 265019, 264681, 264764, 264766, 264688, 264769, 21906769, 264692, 35695763, 264635, 264555, 264556, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)			UNCLASSIFIED	264259, 29331828, 66712502, 264764, 264288, 264688, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank gi 4589570 dbj BAA76807.1 - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	dehydrogenase	56182575, 35696286, 29146499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274791, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233069 (3107, 3108)	Novel Protein sim. GBank gi 3043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	transferase	35696286, 22278997, 264259, 29331822, 29331824, 29331825, 29331828, 265007, 265009, 60432229, 33657402, 55812038, 265011, 265019, 264681, 264369, 264686, 264767, 264768, 21906765, 21906769, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gij2257495[dj]BAA21392] - (AB004534) p1015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 29331828, 35696052, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 264910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264769, 21908765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1556	91228268 (3111, 3112)			UNCLASSIFIED	83373044, 264758, 265022, 264600, 35696052, 264630, 35696423, 265018, 264632, 264682, 29331822, 265020, 265011
1557	87640809 (3113, 3114)	Novel Protein sim. GBank gij3328611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam: zf-C3HC4.hmm, score: 34.08); most similar to drosophila goliath protein (SW: Q06003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	60432289, 264509, 264906, 264907, 264908, 264909, 264910, 264758, 55811386, 264761, 264762, 264766, 264769, 264690, 263978, 264634, 264635, 264639, 264584, 264486
1558	94840376 (3115, 3116)	Novel Protein sim. GBank gij5360105[g]AAD42871.1[AF155105] putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			22278994, 22278996, 22278997, 22278998, 22278999, 60432048, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21908754, 265017, 265018, 264448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811576, 83373044, 87168518, 22278900, 22279002
1559	88224865 (3117, 3118)	Novel Protein sim. GBank gij112908[sp]P02750[A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 60432289, 35696052, 264107, 264110, 21908754, 33109954, 87168559, 264760, 264763, 21906764, 21908765, 21908769, 265021, 264690, 35695855
1560	94580675 (3119, 3120)	Novel Protein sim. GBank gij3880146[emb]CAA92704] - (Z68319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes from...		UNCLASSIFIED	264908, 264603, 264638
1561	86609159 (3121, 3122)			UNCLASSIFIED	264510, 264594
1562	83359682 (3123, 3124)			UNCLASSIFIED	263967
1563	85508694 (3125, 3126)			UNCLASSIFIED	264910, 264764, 264766
1564	87766371 (3127, 3128)	Novel Protein sim. GBank gij1168287[sp]P4593JACDV_RAT - ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCD)	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	18108394, 35696288, 264259, 29331822, 60432289, 35696052, 29331828, 264508, 66712502, 264908, 56182435, 265007, 264910, 60170831, 21908754, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 264688, 21906765, 21906768, 265021, 60170615, 264692, 35696423, 35695855, 264557, 56182323, 60432113, 22278902, 264482

1565	87783381 (3129, 3130)	Novel Protein sim. GBank gii129726[sp]P05307[PDI_BOVIN] - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)		isomerase	264488, 264689, 18108398, 55811957, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264636, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264596, 265011, 264603, 22279002, 18108351, 264762, 264565, 264567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gii3880445[emb]CAA20329] - (AL031266) VM106R.1 [Caenorhabditis elegans]		tnf	22278996, 22278999, 264259, 29331822, 29331824, 60432288, 29331827, 66712502, 264908, 265008, 18108351, 52644228, 21906765, 21906767, 21906768, 21906769, 33857109, 264555, 264639, 264482
1567	84999006 (3133, 3134)	Novel Protein sim. GBank gii4929689[gb]AAD34110.1[AF15187] CGI-115 protein [Homo sapiens]		UNCLASSIFIED	56182575, 21906769, 264692
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gii4827063[ref]NP_005072.1[pZNF1 - zinc finger protein 142 (clone pHZ-49)]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	29331827, 29331830, 264511, 265009, 264758, 21906767, 21908768, 264691, 264693, 22279000, 22279002
1569	90936668 (3137, 3138)	Novel Protein sim. GBank gii5689451[db][BAA83009.1] - (AB028980) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265019, 264764, 21906765, 21906769, 55811957, 60170615, 52644150, 264692, 33857023, 33857109, 18108377, 264563, 264567
1570	86943981 (3139, 3140)	Novel Protein sim. GBank gii1255430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gii4507731[ref]NP_001061.1[pTUBG - tubulin, gamma polypeptide]	Contains protein domain (PF00091) - Tubulin/FisZ family	tubulin	22278996, 35696286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264369, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384
1572	81201604 (3143, 3144)			UNCLASSIFIED	35696052, 264905, 264906, 264908, 264910, 264758, 264766, 35695917, 264637
1573	80207068 (3145, 3146)			UNCLASSIFIED	263972

1574	94216142 (3147, 3148)	Novel Protein sim. GBank gi 4758334 ref NP_004256.1 pFADS - delta-6 fatty acid desaturase	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	Cytochrome	18108394, 264887, 18108397, 18108398, 22278996, 22278997, 22278998, 264259, 29331825, 29331827, 29146498, 29146499, 264107, 264907, 264909, 52644045, 264511, 265008, 264910, 265009, 264591, 21906754, 265011, 265019, 18108351, 264882, 264763, 264764, 18108354, 264389, 264288, 264685, 264766, 264686, 264768, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 29148528, 264680, 264691, 264693, 20281069, 18108370, 18108374, 18108379, 35695855, 264634, 18108384, 18108385, 22279002, 264563, 264566
1575	95340018 (3149, 3150)	Novel Protein sim. GBank gi 3881810 emb CAA94856 - (Z70783) similar to EF-hand calcium binding protein; cDNA EST EMBL:CO8700 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00036) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 264909, 265006, 265008, 265009, 265010, 87168559, 55811150, 264448, 18108354, 264369, 264288, 18108357, 55811957, 265020, 265021, 60170615, 264691, 33657023, 33657109, 60431528, 65274791, 35695855, 18108385, 60432113, 22279002, 264482
1576	95314019 (3151, 3152)	Novel Protein sim. GBank gi 2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]		UNCLASSIFIED	264569, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 265010, 264511, 265008, 264910, 21906754, 265010, 265011, 87168559, 264761, 264762, 264288, 264768, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264638, 83373044, 264486
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gi 2499130 sp P70315 WASP_MOUSE - WISKOTT- ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)		UNCLASSIFIED	264511, 265011, 264681, 264369, 264686, 264689, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)				264259, 29331826, 265017, 264689, 264693, 60432113
1579	88085141 (3157, 3158)	Novel Protein sim. GBank gi 2978255 dbj BAA25190 - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35696286, 264908, 264909, 60433438, 55811386, 264369, 264685, 33657023, 264555, 264556, 264557, 87168518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gi 4324682 gb AAD16986 - (AF109674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278999, 35696052, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gi 2088838 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 29331822, 29331824, 29331826, 56182435, 264595, 55812038, 87168559, 265017, 264288, 21906764, 55811957, 35695917, 264692, 55811576, 264637, 56182323, 264559, 83373044, 60432113

1582	95358052 (3163, 3164)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (A)243459) proteophosphoglycan [Leishmania major]		phosphatase	264259, 60432289, 29331827, 264509, 264905, 264906, 264907, 264909, 264910, 264762, 264288, 264768, 264769, 264632, 264555, 264639, 56526486, 22279000
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gij5578959[embjCAB51351.1] - (AL050306) dJ475B7.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	60170831, 33657402, 264682, 21906766, 35695855, 264563
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gij5531815[gbjAAD44482.1] - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	- dehydrogenase	60424179, 52646842, 65274572, 56182575, 22278995, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 60424269, 60432289, 29331827, 29331828, 35696052, 29146498, 66712502, 29331830, 52644045, 56182435, 264510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811386, 52644296, 87168474, 87168559, 265018, 265019, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810764, 55811576, 35696423, 65274781, 35695855, 56182323, 83373044, 18108387, 87168518, 60432113, 22278002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gij4240132[dbjBAA74846.1] - (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	- phosphatase	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 264905, 265006, 265007, 265008, 60433356, 33109954, 87168474, 265011, 265017, 264604, 264369, 264288, 264685, 264769, 18108359, 21906765, 18108364, 18108370, 264629, 263972, 18108383, 18108388, 264482, 264564
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gij3786494 (AF098993) - No definition line found [Caenorhabditis elegans]			265017, 265018, 264689, 33657023, 263978, 264636, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gij3253159 (AF005355) - translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264907, 264908, 264511, 264910, 264591, 264594, 264629, 264631, 264563, 264483, 264567
1588	87802536 (3175, 3176)	Novel Protein sim. GBank gij1077573[pirj]S52680 - probable ribosomal protein L34, mitochondrial - yeast [Saccharomyces cerevisiae]	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	264259, 29331828, 264905, 265008, 264758, 21906754, 264761, 284762, 21906765, 21906769, 60170615, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gij2137756[pirj]I48746 - senaphorin C - mouse (fragment)		UNCLASSIFIED	65274572, 264490, 29331822, 68714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264596, 265011, 264686, 21906766, 21906768, 55811957, 27486265, 264639, 18108385, 56526486, 60432113

1590	95318825 (3179, 3180)			UNCLASSIFIED	264489, 22278996, 264259, 29331824, 29331825, 29331826, 29331827, 265006, 60433356, 21906754, 265017, 265018, 265019, 264448, 264785, 264288, 52844229, 21906765, 21906767, 21906768, 21908769, 265021, 264892, 27486285, 35695763, 56526486, 60432113, 22279000, 22279002, 264564
1591	86877160 (3181, 3182)	Novel Protein sim. GBank gi 4557749 ref NP_000237.1 pMHC2 - MHC class II transactivator		MHC	264259, 264905, 29331830, 264595, 265017, 264448, 264288, 264690, 264629, 87168518
1592	87682533 (3183, 3184)			UNCLASSIFIED	65274572, 60432049, 264509, 60433356, 21906754, 21908767, 21906768, 18108370, 35696423, 22279000, 264565, 264567
1593	94991661 (3185, 3186)			UNCLASSIFIED	264488, 29331827, 264905, 264906, 264907, 264908, 264909, 264910, 264592, 264593, 264757, 264602, 264604, 264760, 264681, 264288, 264768, 264768, 29148629, 35695917, 264692, 264628, 264629, 264630, 264632, 264634, 264635, 264636, 264639, 264563, 264564, 264566
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi 3877072 emb CAA87080 - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]		UNCLASSIFIED	29331826, 264908, 55811957
1595	78919425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	UNCLASSIFIED	
1596	79933928 (3191, 3192)	Novel Protein sim. GBank gi 5257114 gb AAD41244.1 AF09448 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - Cytochrome P450	UNCLASSIFIED	29146498, 264758, 263967
1597	86971857 (3193, 3194)			cyto450	264092, 29331824, 264508, 264682, 264369, 264686, 264630, 264563
1598	87862939 (3195, 3196)	Novel Protein sim. GBank gi 4508797 ref NP_000324.1 pSCAT - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	264259, 264634
1599	87849829 (3197, 3198)			UNCLASSIFIED	52645080, 29331824, 29331826, 264511, 265009, 265011, 264605, 264448, 264764, 265020, 264692, 264693, 18108370, 264635, 18108385
1600	80056002 (3199, 3200)				29331826, 264603, 264691, 264563
1601	15023246 (3201, 3202)			UNCLASSIFIED	264635
1602	86926987 (3203, 3204)	Novel Protein sim. GBank gi 5305704 gb AAD41780.1 AF12853 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]	Contains protein domain (PF00018) - SH3 domain	struct	29148499, 264112, 264762, 18108351, 29148627, 263974
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi 283920 prf IS27939 - tensin - chicken		collagen	264490, 29331824, 264807, 264909, 264511, 265008, 264592, 265010, 265011, 264762, 264764, 264369, 264288, 264687, 264769, 264693, 264628, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 18108385
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi 4768831 gb AAD28633.1 AF11682 - (AF116827) unknown [Homo sapiens]	ATPase-associated	ATPase-associated	263977

1605	91221129 (3208, 3210)					264905, 264509, 264906, 264907, 264908, 264909, 264604, 264768, 264788, 264892, 264693, 33657109, 264629, 35695855, 264635, 264636, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gi 4505313 ref NP_003794.1 p MYOM - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	- shud		22278996, 22278999, 264259, 33657402, 265017, 18108351, 264448, 21906767, 21906769, 52644150, 264691, 87168518
1607	10871805 (3213, 3214)	Novel Protein sim. GBank gi 5174473 ref NP_005888.1 p PPI - Intracisternal A particle-promoted polypeptide		transcriptfactor		264689
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gi 2224629 dbj BAA20802 - (AB002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED		264094, 264906, 264907, 264908, 264910, 264591, 264603, 264768, 264693, 264634, 264635, 264637, 264639
1609	94311572 (3217, 3218)	Novel Protein sim. GBank gi 4884073 emb CAB43213.1 - (AL048934) hypothetical protein [Homo sapiens]				52644507, 52645156, 52646365, 52646842, 56182575, 22278994, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29147620, 29331828, 35696052, 33656970, 284508, 264509, 264907, 52644045, 56182435, 264510, 264511, 264512, 33657402, 21906754, 52646317, 33109954, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264769, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 52645129, 27486261, 27486262, 35695763, 264628, 18108370, 18108376, 35698423, 264638, 52644332, 18108387, 87168518, 22278000, 264563, 264486
1610	85468200 (3219, 3220)	Novel Protein sim. GBank gi 283920 pir J27839 - lensin - chicken		UNCLASSIFIED		264593, 264757, 55812038, 265018, 265020, 264691, 264692, 264693, 264631, 264634, 264635, 264555, 22279000, 264564
1611	94122843 (3221, 3222)	Novel Protein sim. GBank gi 107284 pir J35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)	Contains protein domain (PF00008) - peroxidase EGF-like domain			35698288, 21906765, 264691, 35696423
1612	85746031 (3223, 3224)	Novel Protein sim. GBank gi 3874846 emb CAA94337 - (Z70307) Similarity to B. subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL:CO9951 comes from this gene; cDNA EST EMBL:CO8265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED		264488, 264509, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)			UNCLASSIFIED		264759

1614	91228634 (3227, 3228)	Novel Protein sim. GBank gi 4880673 gb AAD27726.1 AF13295 - (AF132951) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - eRF1-like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 264908, 264512, 265009, 265011, 265017, 265018, 265019, 18108351, 264683, 264288, 264766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 35696423, 35695855, 60170394, 56182323, 83373044, 264566
1615	86121909 (3228, 3230)	Novel Protein sim. GBank gi 5689485 dbj BAA83026.1 - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 284909, 56182435, 284511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 284556, 22279002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gi 3876260 emb CAB01696 - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene: cDNA EST EMBL:C07649 comes from this gene: cDNA EST EMBL:C09081 comes from this gene: cDNA EST yk399f2.3 comes from this gene: cDNA ...		UNCLASSIFIED	264488, 52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 22278996, 22278997, 22278999, 52645080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 33656970, 284905, 264909, 264594, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264448, 264684, 52644229, 21906764, 264689, 21906765, 21906766, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657349, 27486285, 35695783, 18108376, 35696423, 35695855, 264557, 52644332, 264558, 18108385, 87168518
1617	88090742 (3233, 3234)	Novel Protein sim. GBank gi 466053 sp P34679 Y041_CAEEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHHC zinc finger domain	peptidase	35696052, 264905, 264509, 264907, 284908, 264510, 264511, 264764, 264766, 264768, 264889, 264693, 18108374, 264635, 264636, 264638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gi 4240231 dbj BAA74894.1 - (AB020678) KIAA0871 protein [Homo sapiens]		struct	35696286, 22278999, 264092, 29331824, 29331825, 35696052, 33657084, 21906765, 27486264
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gi 5031763 ref NP_005515.1 pHRY - hairy (Drosophila)- homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	52646842, 65274572, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 56182435, 265007, 265008, 264910, 60170831, 60432229, 60433356, 60433438, 265019, 264448, 264288, 264686, 21906768, 265021, 60170615, 33657023, 65274620, 33657109, 18108374, 18108376, 35696423, 35695855, 56182323, 56526486
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gi 1351047 sp P45843 SCRT_DROME - SCARLET PROTEIN		UNCLASSIFIED	264684

1621	87076708 (3241, 3242)	Novel Protein sim. GBank gi 3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264910 18108392, 65274572, 18108398, 22278996, 22278997, 22278999, 29146498, 29146499, 264905, 264908, 264909, 264828, 52644045, 264592, 60433356, 21906754, 264602, 265017, 264368, 21906768, 55811957, 265021, 60170615, 264635, 264557, 60170394, 83373044, 18108385, 22279000, 22279002, 264566
1622	94741739 (3243, 3244)	Novel Protein sim. GBank gi 3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]		UNCLASSIFIED	18108398, 264259, 264909, 56182435, 87168474, 264448, 21908768, 35695917, 264691, 87168518, 264563
1623	87779106 (3245, 3246)	Novel Protein sim. GBank gi 731086[sp]P40389[uv]22_SCHPO - UV-INDUCED PROTEIN UVi22		ribosomalprot	66714117, 29331825, 264909, 265008, 264758
1624	87336178 (3247, 3248)	Novel Protein sim. GBank gi 3875666[emb]CAB05478] - (Z83104) cDNA EST EMBL:100015 comes from this gene; cDNA EST EMBL:D33665 comes from this gene; cDNA EST EMBL:D36540 comes from this gene; cDNA EST yk240f8.3 comes from this gene; cDNA EST yk387c8.3 comes from this gene; cDNA ES...		UNCLASSIFIED	
1625	95354748 (3249, 3250)	Novel Protein sim. GBank gi 4569622[dbj]BAA76833.1] - (AB023208) KIAA0989 protein [Homo sapiens]		kinase	264489, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331824, 29331825, 29331827, 29331828, 264102, 264108, 264508, 33657084, 265017, 265018, 18108351, 264683, 264369, 264288, 21906765, 21908768, 21906767, 21906769, 35695917, 265021, 264691, 65274620, 18108368, 263972, 18108376, 35696423, 264631, 264634, 22279000, 22279002
1626	94734369 (3251, 3252)	Novel Protein sim. GBank gi 5879070[gb]AAD46844.1 AF160904] BcDNA.HL05936 [Drosophila melanogaster]			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265009, 60432229, 60433356, 60433438, 21906754, 52646317, 52644296, 265011, 87168559, 264604, 265018, 264448, 264389, 264288, 264766, 52644229, 264689, 21906765, 21906768, 35695917, 265021, 265022, 52644150, 33657023, 65274620, 27486261, 27486262, 27486285, 35695763, 263972, 52644332, 60170394, 87168518, 60432113, 264567
1627	83368773 (3253, 3254)	Novel Protein sim. GBank gi 3668087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264288
1628	85708459 (3255, 3256)	Novel Protein sim. GBank gi 3668087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		eph	264288, 264686, 264767, 22279002

1629	84993841 (3257, 3258)	Novel Protein sim. GBank gi 4240175 dbj BAA74866.1 - (AB020650) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87778027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 265010, 264693, 264634, 22278002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gi 1915892 emb CAA69995 - (Y08740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811957, 264259, 33657023, 264693, 29331822, 29331824, 29331827, 29331828, 264906, 264908, 55811576, 264910, 264634, 264636, 264637, 56182323, 264559, 264758, 18108385, 264563, 264764, 264766
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gi 2558501 dbj BAA22896 - (D83850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264768, 264691, 264692, 29148499, 264509, 264905, 284907, 264511, 284512, 264482, 264681, 264763, 264682, 264683, 264488, 264259, 264907, 264908, 264909, 264628, 264629, 264631
1633	87773683 (3265, 3266)				265007, 264637, 22278002
1634	85992817 (3267, 3268)	Novel Protein sim. GBank gi 4887229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	
1635	94232600 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35696052, 52644045, 264511, 265008, 265008, 265010, 265011, 265018, 265019, 264448, 264369, 21908765, 21908768, 265021, 264690, 264482
1636	80413227 (3271, 3272)			UNCLASSIFIED	22278995, 264594, 264763, 265020
1637	80070435 (3273, 3274)	Novel Protein sim. GBank gi 455751 ref NP_001339.1 pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264558
1638	87101854 (3275, 3276)	Novel Protein sim. GBank gi 3420051 AC004680 - unknown protein [Arabidopsis thaliana]			21906765, 21906767, 22278998, 35696286, 22278999, 264259, 264692, 264693, 29331824, 33657109, 264508, 264906, 18108370, 264629, 265007, 33657402, 21908754, 264602, 264604, 264764, 264683, 264566, 264288
1639	94322194 (3277, 3278)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35696052, 264908, 56182435, 264112, 265006, 265008, 264757, 264758, 55811386, 264603, 264760, 18108351, 264764, 264288, 264766, 264768, 21906767, 55811957, 264691, 33657023, 65274620, 18108370, 55810764, 55811576, 264558, 264639, 83373044, 18108385, 87168518

1640	94143185 (3279, 3280)	Novel Protein sim. GBank gjl2842469jemb CAA16847.1 - (AL021747) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56994075, 35696286, 60432049, 60432289, 29331827, 35698052, 52644045, 56182435, 264510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21906765, 21906766, 21906768, 35695917, 265021, 60170615, 52644150, 33657023, 33657109, 33657349, 18108374, 35696423, 65274791, 35695855, 264632, 264555, 56182323, 22279000
1641	87625160 (3281, 3282)			UNCLASSIFIED	29146489, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1642	94312557 (3283, 3284)	Novel Protein sim. GBank gjl1575333 (U60416) - myr 6 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - struct DIL domain	struct	22278999, 29147620, 29331826, 29331828, 33658970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 56182323, 18108388, 87168518, 22279002, 264564, 29331825, 29331827, 29331828, 21906754, 265019, 264288, 264693, 33657349, 18108370, 18108376, 264555, 83373044, 22279002, 264482
1643	94131766 (3285, 3286)				264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1644	88095125 (3287, 3288)			UNCLASSIFIED	264685, 264693
1645	95013858 (3289, 3290)	Novel Protein sim. GBank gjl1076802 pir ISA9915 - extensin like protein - maize		UNCLASSIFIED	22278994, 56994075, 35696286, 264259, 29331824, 29331825, 29331826, 60432289, 264508, 60433356, 60433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486261, 27486265, 33657349, 60432113, 264563, 264564
1646	95362691 (3291, 3292)				29331822, 264806, 264908, 264369, 21906768, 60170615, 264639, 22279000
1647	94278428 (3293, 3294)	Novel Protein sim. GBank gjl5002573 emb CAB44338.1 - (Y17466) alpha-N-acetylgalactosamine alpha-2,6-sialyltransferase [Fugu rubripes]		UNCLASSIFIED	265009, 264686, 55811957, 35695917, 55810764, 264556, 56182323, 264558, 18108385
1648	87642098 (3295, 3296)		Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	

1649	95347628 (3297, 3298)	Novel Protein sim. GBank gij1854065[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35696286, 22278998, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 66712502, 264908, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264596, 55812038, 21906754, 265011, 264601, 264602, 265017, 265018, 265019, 264682, 264448, 264764, 264683, 264288, 264768, 264685, 264687, 264768, 264688, 264769, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265021, 265022, 52644150, 264692, 33657023, 33657109, 20281149, 18108370, 264628, 18108374, 18108376, 35695423, 35695855, 264632, 264634, 264635, 264636, 18108380, 264639, 264556, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22279000, 22279002, 264482, 264555, 264566, 264487, 265011, 264602, 21906767, 18108374, 18108377, 18108385
1650	87418539 (3299, 3300)	Novel Protein sim. GBank gij3647335[emb CAA21059] - (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]			
1651	81639773 (3301, 3302)	Novel Protein sim. GBank gij4884278[emb CAB43247.1] - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108397, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21906754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264888, 21906765, 21906766, 21906768, 21906769, 265022, 264692, 264693, 264629, 35695855, 264556, 264637, 264557, 264559, 83373044, 56526486, 22279000, 22279002, 264564, 22278997, 29146498, 56182435, 21906754, 264369, 21906765, 21906768, 21906769, 265020, 52644150, 33657109, 22279000, 22279002
1652	86598622 (3303, 3304)	Novel Protein sim. GBank gij1657837 (U73200) - p116Rip [Mus musculus]	Contains protein domain (PF00169) - PH domain	si-rucd	18108398, 22278995, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264909, 265006, 265009, 60432229, 60433356, 60433438, 21906754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108364, 55274791, 18108384, 60432113, 264567, 33657109, 264565
1653	94255993 (3305, 3306)	Novel Protein sim. GBank gij3776054[emb CAA06273] - (AJ004999) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	
1654	79756471 (3307, 3308)			UNCLASSIFIED	

1655	86689346 (3309, 3310)	Novel Protein sim. GBank gij3355717[embjCAA73496] - (Y13053) seryl-tRNA synthetase [Zea mays]		synthase	52644507, 35696286, 22278998, 22278999, 29331824, 29331825, 29331828, 33658970, 264908, 52644045, 264511, 264910, 52646317, 264288, 52644229, 33657023, 33657109, 52644332, 264557, 56182323, 56526486, 604332113
1656	79862297 (3311, 3312)	Novel Protein sim. GBank gij1890141[dbijBAA18947] - (D83206) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771994 (3313, 3314)	Novel Protein sim. GBank gij4557645[refjNP_001524.1]pHNRP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331827, 265009, 21906766, 21906767, 265020, 265022, 33657109, 264638, 56526488, 264482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gij3877072[embjCAA87060] - (Z48937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal prokaryotic L21 protein	UNCLASSIFIED	52646365, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 264905, 264908, 52644045, 265006, 60433356, 264757, 60433438, 21906754, 265011, 18108351, 264448, 264369, 264288, 264766, 264768, 21908765, 21906767, 21906768, 21906769, 29148629, 265021, 265022, 18108362, 263969, 263971, 18108374, 35696423, 18108383, 22279000, 264482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gij539218[pirjS38038] - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52646317, 21906766, 21906767, 21906768, 87168518, 22278996, 265020, 22278999, 87168559, 264603, 265017, 264631, 265018, 265019, 22279002, 264482, 264635, 264565, 264488, 35696286, 264259, 35696052
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gij2497012[spjQ10010]YSV4_CAEEL - HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265009, 264910, 264592, 264598, 265010, 264600, 264602, 265017, 265018, 264605, 264760, 264764, 264288, 264766, 264688, 264768, 264689, 21906766, 35695917, 264690, 33657023, 264693, 33657109, 264628, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264639, 264559, 18108385, 18108388, 264563, 264483, 264564, 264565, 264566, 264486, 264567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi 4759100 ref NP_004759.1 pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 22278998, 264259, 29331824, 29331826, 29331827, 29331828, 264509, 66712502, 29331830, 264908, 52644045, 265007, 264512, 60433356, 60433438, 55812038, 21906754, 265019, 264448, 264766, 264768, 264769, 21908768, 21906769, 265020, 33657023, 33657109, 65274791, 87168518, 264482, 264563, 264564, 264565, 264567
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi 1730502 sp P52875 PF27_MOUSE - TRANSMEMBRANE PROTEIN PF27			18108392, 29331822, 29331828, 20281100, 264106, 265006, 265007, 265008, 18108348, 21906766, 18108365, 18108366, 18108374, 83373044, 18108385
1663	94217146 (3325, 3326)	Novel Protein sim. GBank gi 4894136 emb CAB43275.1 - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	kinase	52645156, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331826, 29331827, 29331828, 33656970, 29331830, 264908, 56182435, 264511, 60433356, 33657402, 33109954, 87168474, 87168559, 265017, 265018, 264605, 18108351, 264764, 264288, 264766, 264768, 21906765, 21908766, 21906767, 21908768, 21908769, 265021, 265022, 264691, 33657023, 264693, 263987, 33657109, 264630, 52644332, 83373044, 87168518, 80432113, 22279000
1664	94234076 (3327, 3328)	Novel Protein sim. GBank gi 3043682 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35696286, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 60170831, 264591, 264592, 264595, 87168474, 265011, 264600, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264766, 264687, 264768, 264769, 21906764, 21908765, 21908767, 35695917, 265021, 264534, 60170615, 264690, 264691, 264692, 33657109, 33657182, 264628, 18108370, 264629, 35698423, 35695855, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264566, 264486

1665	91225852 (3329, 3330)	Novel Protein sim. GBank gjl1083506[ipr]S50065 - sialoadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	immunoglob	264488, 29331826, 29331828, 264509, 264906, 264907, 264909, 264510, 264511, 264910, 264592, 264593, 264595, 264758, 264596, 264600, 264760, 264762, 264764, 264766, 264768, 264629, 264630, 264634, 264636, 83373044, 264564, 264566, 264567, 264486
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gjl3913431[sp]O42643[DDX8_SCHPO - PUTATIVE PRE-MIRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	helicase	58994075, 22278999, 264259, 29331824, 29331826, 29331827, 29146498, 265009, 33109954, 87168559, 265010, 264288, 264688, 21906767, 21906769, 264691, 33657182, 18108370, 18108374, 18108385, 22279002
1667	91228655 (3333, 3334)	Novel Protein sim. GBank gjl5689535[jdb]BAAB3051.1] - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transport	264259, 29331822, 29331826, 264905, 264906, 264908, 264510, 265009, 264595, 264758, 265011, 87168559, 265017, 265018, 265019, 264448, 264768, 264686, 21906765, 21906767, 21906769, 265020, 265021, 60170615, 264690, 264692, 264693, 18108368, 18108370, 263972, 55810764, 264555, 83373044, 60432113, 22279000, 22279002
1668	88095135 (3335, 3336)	Novel Protein sim. GBank gjl2076894[gb]AAB53983.1] - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]		kinase	66714117, 264508, 264509, 264906, 264907, 264908, 264511, 264910, 264764, 264687, 264689, 33657109, 35695423, 35695855, 264632
1669	91227846 (3337, 3338)	Novel Protein sim. GBank gjl387537[emb]CAA85414.1] - (Z36948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor UZAF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes fr...		UNCLASSIFIED	29331825, 33109954, 264369, 264767, 264689, 33657109, 83373044
1670	87628009 (3339, 3340)			UNCLASSIFIED	264259, 29331824, 29331827, 60433438, 265022, 264636
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gjl462451[sp]P34244[KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35696286, 22278997, 29331825, 264909, 21906754, 265017, 265018, 265019, 264682, 264683, 264768, 264688, 21908768, 21906767, 21906768, 21906769, 264691, 264555, 264556, 22279000, 264566
1672	88291834 (3343, 3344)	Novel Protein sim. GBank gjl1814270 [U74586] - double-stranded RNA specific adenosine deaminase [Rattus norvegicus]		deaminase	264906, 264909, 264632, 18108381

1673	88095137 (3345, 3346)	Novel Protein sim. GBank gjl2076894[gbjAAB53983.1] - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	264488, 264568, 18108394, 56994075, 22278996, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264764, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264690, 33657023, 264692, 264693, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264639, 264563, 264482, 264564, 264565, 264566, 264567, 264486
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gjl5262467[embjCAB45693.1] - (AL080062) hypothetical protein [Homo sapiens]		kinase	29331822, 29331824, 264906, 52644045, 60433358, 87168559, 264448, 264288, 264888, 264691
1675	87606466 (3349, 3350)	Novel Protein sim. GBank gjl3128366 (AF010496) - 50S ribosomal protein l9 [Rhodobacter capsulatus]		UNCLASSIFIED	56181686, 35696286, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 66712502, 264764, 264288, 264686, 264687, 35695917, 265020, 264690, 264693, 35695763, 18108370, 35696423, 35695855, 264637, 264639, 18108385, 264564
1676	95358086 (3351, 3352)	Novel Protein sim. GBank gjl4164065[gbjAAD05327] - (AF111091) latrophilin 3 splice variant bba1 [Bos taurus]		UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21906765, 265020, 265022, 35695855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gjl3327046[dbjBAA31591] - (AB014516) KIAA0616 protein [Homo sapiens]		UNCLASSIFIED	264908
1678	86866829 (3355, 3356)	Novel Protein sim. GBank gjl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	UNCLASSIFIED - carboxylase	29331824, 264102
1679	91214108 (3357, 3358)	Novel Protein sim. GBank gjl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]			264488, 18108392, 18108394, 52646842, 18108397, 18108398, 35696286, 29331824, 265006, 265007, 265008, 265009, 18108348, 265011, 18108351, 264883, 18108354, 18108358, 18108359, 21906765, 29148627, 29148629, 264690, 18108361, 18108362, 18108364, 18108365, 18108368, 264628, 18108379, 35696423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	91005372 (3359, 3360)	Novel Protein sim. GBank gjl2394478 (AF024500) - No definition line found [Caenorhabditis elegans]		transport	65274572, 22278994, 22278999, 66714117, 29331827, 56182435, 21806754, 265018, 264288, 21906769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gjl5689537[dbjBAA83052.1] - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	22278996, 29331822, 264908, 264593, 264604, 265019, 264683, 55811957, 264690, 33657023, 35696423, 83373044, 264563
1682	86042710 (3363, 3364)			UNCLASSIFIED	264909, 265017, 264605

1683	94316213 (3365, 3366)	Novel Protein sim. GBank gi 5031717 ref NP_005704.1 pGPBP - goodpasture antigen- binding protein	Contains protein domain (PF01852) - START domain	UNCLASSIFIED	263994, 35696286, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264910, 264593, 264756, 265010, 265011, 264760, 264761, 264762, 264763, 264764, 264369, 264766, 264768, 35695917, 264892, 33657109, 35696423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 264486
1684	80063409 (3367, 3368)			UNCLASSIFIED	264563, 264566
1685	94323182 (3369, 3370)	Novel Protein sim. GBank gi 1255371 (U53147) - coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00625) - Guanylate kinase	UNCLASSIFIED	60424179, 52646842, 22278994, 35696286, 22278998, 264259, 52645080, 29331824, 29331826, 265007, 33657084, 265018, 264681, 264448, 264683, 264369, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 65274620, 33657109, 27486262, 264635, 52644332, 56182323, 22279000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gi 2244707 dbj BAA21115.1 - (AB005287) thrombospondin 1 [Bos taurus]		UNCLASSIFIED	56182375, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 264512, 265009, 264910, 264758, 265010, 265011, 264605, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 264630, 264631, 264634, 264635, 264637, 264638, 264639, 264565, 264486, 264587
1687	94719400 (3373, 3374)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	35659517, 264906, 264907, 264908, 264510, 265006, 265007, 264910, 264556, 18108381, 18108383, 265011
1688	82158442 (3375, 3376)			UNCLASSIFIED	264905, 264910, 264760, 264629, 264555
1689	94325049 (3377, 3378)	Novel Protein sim. GBank gi 4240193 dbj BAA74875.1 - (AB020659) KIAA0852 protein [Homo sapiens]		UNCLASSIFIED	264559, 35696286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 264448, 264764, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gi 3800736 (AF031572) - seven- pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00028) - Cadherin domain	cadherin	18108374, 65274791, 83373044, 264089 264369, 21906766, 264692, 264639, 87188518
1691	88095223 (3381, 3382)	Novel Protein sim. GBank gi 2773208 (AF039713) - No definition line found [Caenorhabditis elegans]			264768, 33657109, 29331827, 29148629, 264510, 264105, 264910, 264109, 264508, 60170831, 264563, 264905, 264564, 264691, 264637, 264628, 264807, 264908, 33657023, 264567, 264766, 263974
1692	86106709 (3383, 3384)				264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gi 121271 sp P02207 GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	UNCLASSIFIED	29331826, 264508, 264905, 264907, 264595, 265010, 265011, 21906768, 33657023, 264629, 263978, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gi 5453932 refNP_008225.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01183) - RNA polymerases L / 13 to 16 kDa subunit	mapolymerase	35698286, 22278998, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331828, 35696052, 29148499, 264905, 264908, 52844045, 264511, 265006, 265007, 265009, 264592, 60433356, 21906754, 265010, 265011, 18108351, 264763, 264682, 264448, 264683, 264288, 264768, 264689, 21906768, 60170615, 264691, 264692, 264693, 18108370, 18108374, 263978, 35698423, 35695855, 264556, 18108381, 18108385, 87168518, 264482, 264486 264634
1695	94719325 (3389, 3390)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gi 4220517 emb CAA22990 - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278997, 264259, 265010, 18108351, 264764, 21906766, 18108370
1697	85740963 (3393, 3394)	Novel Protein sim. GBank gi 505662 (U10362) - GP36b glycoprotein [Homo sapiens]		glycoprotein	264682
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gi 5052031 gb AAD38411.1 AF15573 - (AF155739) axolotrin [Mus musculus]			56994075, 22278998, 22278999, 264509, 33657402, 264758, 87168474, 87168559, 265017, 265018, 264448, 264687, 29148627, 21906769, 29148629, 265020, 265022, 33657023, 264558, 87168518, 22279002
1699	87424783 (3397, 3398)	Novel Protein sim. GBank gi 543344 pir J S41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED nucl_rept	35696286, 264635 29331824, 52644045, 265008, 265009, 263969, 263971
1700	87859161 (3399, 3400)	Novel Protein sim. GBank gi 3877439 emb CAA96652] - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		UNCLASSIFIED MHC	22278995, 22278997, 264092, 29146498, 29146499, 264107, 264508, 264907, 264110, 264112, 265009, 60170831, 21906754, 265011, 265017, 264762, 18108351, 264288, 21906765, 35695917, 265021, 60170815, 263967, 33657109, 18108370, 263972, 263974, 18108374, 263976, 35695855, 264555, 263981, 60170394, 18108385, 56528486, 87168518, 60432113
1701	86570488 (3401, 3402)	Novel Protein sim. GBank gi 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264909, 265017, 264628, 264629, 264638
1702	87795092 (3403, 3404)	Novel Protein sim. GBank gi 1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	264369
1703	79588651 (3405, 3406)	Novel Protein sim. GBank gi 4519621 db BAA75670.1] - (AB017614) OASIS protein [Mus musculus]			264569, 35696286, 264907, 265010, 264687, 264768, 264692, 264693, 264636, 264566 22278996, 22278998, 264259, 264509, 265018, 264764, 264685, 264686, 21906768, 21906769, 265022, 264691, 264558, 22279000
1704	86622978 (3407, 3408)	Novel Protein sim. GBank gi 3123034 sp Q15011 Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			
1705	87795175 (3409, 3410)	Novel Protein sim. GBank			
1706	87790967 (3411, 3412)	Novel Protein sim. GBank			

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gij4321684[gbjAAD15797] - (AF055470) ZNF258 [Homo sapiens]		UNCLASSIFIED	18108396, 22278997, 264259, 29147620, 29331826, 29146498, 264905, 264906, 265008, 264593, 264595, 264758, 264596, 265018, 264760, 18108351, 264764, 264766, 264689, 264693, 18108370, 35698423, 55811576, 264558, 87168518, 60432113, 264567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gij5174591[refjNP_005947.1]pMTHF - 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	Contains protein domain (PF01268) - Formate-tetrahydrofolate ligase	Synthase	56182575, 22278996, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146499, 29331830, 265009, 60170831, 33657402, 33109954, 87168559, 265018, 18108351, 264448, 21906765, 21906767, 21906768, 29148627, 29148629, 29148784, 60170615, 52644150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264563, 264107, 55811957, 263974, 263976, 263977, 263981
1709	80222563 (3417, 3418)			UNCLASSIFIED	264556
1710	20754572 (3419, 3420)	Novel Protein sim. GBank gij5031735[refjNP_005760.1]pHEC - N-acetylglucosamine 6-O-sulfotransferase		UNCLASSIFIED	65274572, 29331824, 29331826, 264768, 60431528, 35696423, 60432113, 264563
1711	91013729 (3421, 3422)	Novel Protein sim. GBank gij5454168[refjNP_008453.1]pXAP4 - HBV associated factor	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	kinase	56994075, 264093, 264259, 29331822, 264099, 29331824, 29331827, 264107, 264110, 264511, 264592, 265011, 265018, 264683, 264686, 264689, 265020, 33657023, 263967, 33657109, 263974, 35696423, 35695855, 264630, 264636, 264558, 264566
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gij5454168[refjNP_008453.1]pXAP4 - HBV associated factor		UNCLASSIFIED	22278995, 264508, 264758, 18108351, 18108370, 263974, 18108374, 264634, 56182323, 83373044, 60432113
1713	94143453 (3425, 3426)	Novel Protein sim. GBank gij160409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278997, 264757, 21906765, 265020, 265021, 264692, 56526486
1714	87420048 (3427, 3428)				265021, 264692, 56526486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gij5689537[dbj]BAA83052.1] - (AB028023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	264509, 264905, 264906, 264807, 264908, 264909, 264910, 264591, 265011, 264766, 264768, 264769, 264691, 264692, 264632, 264634, 264635, 264636, 264637, 264556, 264639, 264564
1716	87400449 (3431, 3432)	Novel Protein sim. GBank gij4589468[dbj]BAA76761.1] - (AB012808) mBOCT [Mus musculus]		transport	56182575, 29331824, 60432289, 264109, 264909, 265007, 264600, 265019, 264686, 265020, 264693, 55811576, 264558, 60432113, 22279002

1717	87563223 (3433, 3434)	Novel Protein sim. GBank gij2765411[embjCAA74749] - (Y14391) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264569, 264259, 29331825, 29331826, 29331828, 35696052, 264508, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264592, 264758, 264759, 265017, 264681, 264764, 264766, 264688, 18108357, 35695917, 264690, 264692, 264693, 264628, 264629, 35696423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108388, 18108391
1718	87032628 (3435, 3436)	Novel Protein sim. GBank gij2833262[spjQ14999]Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)		UNCLASSIFIED	265011, 264681, 264682, 264684, 264688, 264689, 21906765, 265021, 264691, 33657023, 264693, 18108370, 35695855, 264632, 264634, 264636, 18108388, 22279002
1719	94315259 (3437, 3438)	Novel Protein sim. GBank gij4505197[refjNP_003473.1]pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108398, 65274572, 35696286, 22278997, 60432049, 56182181, 66714117, 60432289, 29331828, 35696052, 29331828, 264906, 29331830, 56182435, 264592, 60431735, 60433438, 55812038, 264759, 265010, 264600, 264601, 265017, 264448, 264764, 264288, 264769, 21906766, 21906769, 55811957, 265020, 265021, 52644150, 33657023, 33657109, 33657182, 27486262, 33657349, 35695763, 18108370, 60431528, 18108374, 35696423, 55811576, 35695855, 264631, 56182323, 264559, 264584, 264486
1720	94853063 (3439, 3440)	Novel Protein sim. GBank gij2129478[pirj]S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	56182575, 22278999, 264259, 29331824, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21906754, 265011, 264601, 264760, 264762, 264288, 264766, 264886, 18108357, 264689, 21906765, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274791, 264630, 20281071, 264634, 264635, 264638, 264637, 264556, 264638, 264639, 56182323, 87168518
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gij4886461[embjCAB43381.1] - (AL050280) hypothetical protein [Homo sapiens]		UNCLASSIFIED	22278994, 22278999, 29331822, 265006, 265007, 265008, 55812038, 21906754, 60174639, 265011, 87168559, 18108351, 18108354, 21906765, 21906766, 21906768, 21906769, 265020, 33657109, 18108370, 18108374, 264556, 60170394, 83373044, 18108385, 264488
1722	94134549 (3443, 3444)	Novel Protein sim. GBank gij5689375[dbj]BAA82968.1] - (AB030644) tudor repeat associator with PCTAIRE 2 [Rattus norvegicus]	Contains protein domain (PF00567) - Tudor domain	kinase	56994075, 29331824, 29331828, 265009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044

1723	95358181 (3445, 3446)	Novel Protein sim. GBank gi4426962[gb]AAD20633] - (AF126062) Art-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264488, 264687, 264769, 21906767, 21906768, 56182575, 55811957, 22278997, 22278998, 265020, 264259, 264692, 33657023, 29331822, 29331824, 29331825, 60432289, 33657182, 33856970, 33857349, 29146499, 264508, 264907, 18108370, 264628, 264908, 264909, 18108374, 55811576, 264510, 265006, 264511, 265007, 284910, 264632, 264591, 60432229, 264592, 60433356, 264594, 60433438, 264595, 83373044, 55812038, 33109954, 33657084, 87168518, 87168474, 265010, 265011, 87168559, 264600, 60432113, 264604, 265019, 264563, 264448, 264682, 264586, 264764, 264288, 264587, 264486, 264369, 264766
1724	87713806 (3447, 3448)	Novel Protein sim. GBank gi2340162 (AF005083) - dsRBP-ZFa [Xenopus laevis]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	284905, 18108359, 284693, 264628, 264631, 264636, 264555, 264558, 264558, 264559, 35696286, 264259, 29331822, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264910, 265009, 264591, 264601, 264760, 18108351, 264681, 264764, 264288, 264766, 264768, 21906769, 35695917, 264628, 35696423, 264630, 264631, 264632, 264635, 264636, 264638, 87168518, 264586
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gi3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - homeobox Ank repeat	homeobox	264508, 264509, 264905, 264906, 264907, 264908, 264909, 264910, 265009, 264591, 264601, 264760, 18108351, 264681, 264764, 264288, 264766, 264768, 21906769, 35695917, 264628, 35696423, 264630, 264631, 264632, 264635, 264636, 264638, 87168518, 264586
1726	85754255 (3451, 3452)			UNCLASSIFIED	29146498, 264683, 264689
1727	85296382 (3453, 3454)	Novel Protein sim. GBank gi4689348[gb]AAD27851.1[AF13256 - (AF132562) BcDNA.LD14270 [Drosophila melanogaster]		UNCLASSIFIED	264905, 265011, 264689, 21906768

1728	95349515 (3455, 3456)	Novel Protein sim. GBank gij408549[gbjAAD20027] - (AF131738) Unknown [Homo sapiens]	UNCLASSIFIED	60424179, 18108397, 56182575, 22278995, 56994075, 35698286, 22278997, 22278998, 22278999, 264094, 60432049, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35696052, 264905, 264906, 264907, 29331830, 66712502, 264908, 56182435, 264511, 265008, 265009, 60432229, 60433356, 33657402, 60433438, 264759, 21908754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 5581150, 264681, 264448, 264682, 264763, 264683, 264288, 264684, 264368, 264685, 264766, 264687, 264769, 21908764, 264689, 21908765, 21908766, 21908767, 21908768, 35695917, 265020, 265021, 265022, 264535, 264691, 264692, 33657023, 264693, 33657109, 18108370, 264628, 263972, 264629, 18108374, 18108376, 55810784, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264564, 264566
1729	81227948 (3457, 3458)	Novel Protein sim. GBank gij854065[embjCAA58337] - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	264906, 264907, 264908, 264511, 264555, 83373044, 264596, 264566
1730	85483474 (3459, 3460)		UNCLASSIFIED	29331822, 29331825, 29331828, 264907, 264908, 264909, 265011, 264764, 264629
1731	88266068 (3461, 3462)	Novel Protein sim. GBank gij831600[piljS47094 - hypothetical protein - rabbit]	UNCLASSIFIED	52648842, 264907, 264909, 56182435, 55811386, 87168559, 265018, 265019, 264760, 52644229, 55811576
1732	81218878 (3463, 3464)	Novel Protein sim. GBank gij4240231[dbjBAA74894.1] - (AB020678) KIAA0871 protein [Homo sapiens]	struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265019, 21908768, 21908769, 35695917, 265020, 265021, 264636, 56182323
1733	87617178 (3465, 3468)	Novel Protein sim. GBank gij1575756 (U70674) - m-Numb [Mus musculus]	Contains protein domain (PF00640) - synthase Phosphotyrosine interaction domain (PTB/PID).	264907, 264910, 33657402, 265010, 264681, 264683, 264684, 264688, 264769, 264691, 264692, 264693, 264628, 264636, 264556, 264693
1734	87795261 (3467, 3468)			

1735	88318638 (3469, 3470)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF146793) PF127 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016	264488, 18108394, 18108398, 22278998, 60432049, 264259, 29331822, 264908, 265006, 265007, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 264689, 21906765, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 52644150, 18108384, 18108385, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264563, 18108390, 284490, 264259, 66714117, 66712502, 56182435, 265008, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1738	95362884 (3471, 3472)	Novel Protein sim. GBank gi 4885647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component	UNCLASSIFIED	264490, 264259, 66714117, 66712502, 56182435, 265008, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gi 2143607 pir S568695 - BIK protein - rat	kinase	29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gi 2225941 emb CAA69714 - (Y08460) Mdes protein [Mus musculus]	UNCLASSIFIED	264908, 264909, 265008, 264910, 264566
1739	87328576 (3477, 3478)		UNCLASSIFIED	35696052, 264603, 264557
1740	83592939 (3479, 3480)	Novel Protein sim. GBank gi 4809 emb CAA44309 - (X62452) YCR601 [Saccharomyces cerevisiae]	traffic	264604, 21906764, 18108364, 264629, 35695855, 264638
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gi 488388 gb AAD31695.1 AF13042 - (AF130420) serine protease-like protein isoform [Homo sapiens]	UNCLASSIFIED	60432289, 29331827, 264509, 265009, 60432229, 264759, 265017, 264767, 264688, 264689, 21906769, 265020, 33657109
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gi 4505183 ref NP_003667.1 pMLD - membrane fatty acid (lipid) desaturase	UNCLASSIFIED	264908, 264910, 264758, 265011, 264631, 264638, 264566
1743	86966475 (3485, 3486)			265017, 265020, 264692
1744	81224003 (3487, 3488)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	UNCLASSIFIED	22278998, 264508, 264907
1745	20290075 (3489, 3490)		UNCLASSIFIED	264558
1746	84326110 (3491, 3492)	Novel Protein sim. GBank gi 731756 sp P38873 YHY6_YEAST - HYPOTHETICAL 175.8 KD PROTEIN IN GND1-IK1 INTERGENIC REGION	UNCLASSIFIED	65274791, 264639, 264559
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gi 1658503 (U75467) - ALU (Drosophila melanogaster)	transcription factor	52646842, 29331824, 29331825, 52644045, 56182435, 265007, 52646317, 87168474, 265018, 18108351, 264369, 264769, 264689, 35695917, 60170615, 264691, 33657023, 65274791, 35695855, 60170394, 22279000, 264482

1748	88003580 (3495, 3498)	Novel Protein sim. GBank gi 4504511 ref NP_001530.1 phsJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00684) - eph DnaJ central domain (4 repeats)	264489, 56182575, 29331824, 56182435, 264112, 265007, 265019, 264764, 21906768, 265020, 264691, 55811576, 264635, 264555, 264556, 264557, 264559 264106
1749	83363091 (3497, 3498)	Novel Protein sim. GBank gi 5650780 gb AAD45948.1 AF151968) RGS protein RGS-17 (Gallus gallus)	Contains protein domain (PF00615) - oncogene Regulator of G protein signaling domain	
1750	94321664 (3499, 3500)	Novel Protein sim. GBank gi 4996894 gb AAC28444.2 - (AF065164) hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]		33657402, 264288, 52644150, 2633974, 83373044
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gi 2760161 gb BAA24184 - (AB010054) outer arm dynein light chain 2 [Anihocdatis crassigalina]	Contains protein domain (PF00560) - ATPase-associated Leucine Rich Repeat	265010, 264369
1752	86456530 (3503, 3504)	Novel Protein sim. GBank gi 3915482 sp P74346 YG29_SYNY3 - HYPOTHETICAL 36.0 KD PROTEIN SLR1629	Contains protein domain (PF00849) - deaminase RNA pseudouridylate synthase	264510, 264593, 264682, 21906765, 18108370
1753	94235159 (3505, 3506)	Novel Protein sim. GBank gi 2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - phosphatase Acyltransferase	56994075, 22278996, 264908, 60170831, 264682, 264764, 264369, 264288, 264685, 264687, 21906766, 264692, 264693, 65274620, 65274791, 35695855, 264637, 264564
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gi 731421 sp P39981 YE44_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION	transport	264488, 35696286, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 264604, 264762, 264763, 264685, 264766, 264691, 264628, 35696423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264564, 264565, 264566, 264567 264686
1755	79470282 (3509, 3510)	Novel Protein sim. GBank gi 1176422 (U43194) - rhophilin [Mus musculus]	UNCLASSIFIED	
1756	92862614 (3511, 3512)	Novel Protein sim. GBank gi 4432860 gb AAD20708 - (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]		52646842, 22278994, 22278995, 56994075, 22278996, 22278997, 264259, 29331822, 60432289, 29331827, 33656970, 265006, 265009, 60432229, 60433356, 60433438, 33109954, 21908754, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264558, 18108388, 87168518, 60432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gi 5441615 emb CAB46856.1 - (AJ388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00096) - dna_rna_bind Zinc finger, C2H2 type	22278997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21908768, 65274620, 18108385, 60432113, 264566, 264487

1758	87612971 (3515, 3516)	Novel Protein sim. GBank gij3881040[emb]CAA16403] - (AL021497) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33656970, 264508, 265006, 265007, 265009, 264591, 33657402, 33109954, 87168474, 264600, 265017, 265018, 21906769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695855, 264632, 52644332, 22278002, 264583
1759	36894372 (3517, 3518)			UNCLASSIFIED	264759
1760	87328716 (3518, 3520)	Novel Protein sim. GBank gij3262749[emb]CAB45688.1] - (AJ131320) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432049, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264910, 60432229, 264592, 264595, 55812038, 264758, 264762, 18108351, 264764, 264766, 264768, 264769, 21806765, 55811957, 35695917, 264690, 264692, 264628, 264629, 55811576, 35698423, 264632, 264634, 264636, 264557, 264639, 60432113, 264565, 264486
1761	87408586 (3521, 3522)	Novel Protein sim. GBank gij127749[sp]P10569[MYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00618) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 264910, 264685, 264686
1762	95319887 (3523, 3524)	Novel Protein sim. GBank gij3169158 (AC004770) - BC269730_2 [Homo sapiens]	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	desaturase	22278999, 264259, 264905, 264907, 60170831, 265010, 265011, 265017, 264448, 21906765, 21906766, 21906767, 21906768, 265021, 264690, 33657109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gij4809026[gb]AAD30062.1] - (AF132856) suppressor of G2 allele of skp1 homolog [Homo sapiens]			56181686, 29331825, 35696052, 264905, 264906, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35696423, 264634
1764	87757687 (3527, 3528)	Novel Protein sim. GBank gij1360869[pr]ICGHUV - collagen alpha 1(V) chain precursor - human	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	22278998, 264259, 35696052, 29331828, 56182435, 265008, 265017, 265018, 264448, 264288, 21906766, 21906767, 29148627, 35695917, 264691, 33657023, 60432113, 22279002
1765	81230091 (3528, 3530)	Novel Protein sim. GBank gij486806[pr]IS35503 - finger protein neutralized - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264907, 264511, 265007, 265008, 264910, 265009, 21806754, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264369, 264288, 264766, 18108359, 21906766, 21906767, 29148627, 29148629, 35695917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi2499087 sp Q09332 UGG_DROME - UDP- GLUCOSE-GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	52645156, 87168559, 60170615, 33657023, 264693, 33657109, 27486261, 264555, 83373044
1767	87755998 (3533, 3534)	Novel Protein sim. GBank gi1152042 sp P00736 C1R_HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR		UNCLASSIFIED	265017, 265019, 264686, 264768, 265020, 264692
1768	80253216 (3535, 3536)			UNCLASSIFIED	29331824, 29331825, 264591, 56182323
1769	87388988 (3537, 3538)			UNCLASSIFIED	264563
1770	95413144 (3539, 3540)	Novel Protein sim. GBank gi1152042 sp P00736 C1R_HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin	complement	264488, 264768, 264769, 56182575, 55811957, 264690, 264691, 35696052, 264905, 264509, 264906, 264907, 264628, 264908, 264909, 264910, 264634, 264635, 264636, 264556, 264757, 264758, 55812038, 65274444, 264760, 264563, 264762, 264764, 264684, 264766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi3914191 sp P56558 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAc TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00515) - TPR Domain	transferase	264758, 264600, 264369, 55811957, 265020, 83373044, 22278000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi4959442 gb AAD34351.1 AF12136 - (AF121360) DNZDHCNEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHC zinc finger domain		22278998, 29331828, 33109954, 265018, 265019, 264764, 21906765, 265020, 265021, 264556
1773	94116824 (3545, 3546)	Novel Protein sim. GBank gi3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	potassium_channel	65274572, 56182575, 22278996, 35696286, 22278999, 264259, 29331824, 60424269, 29331825, 60432289, 35686052, 264106, 264509, 264906, 264907, 29331830, 264908, 52644045, 264511, 265006, 265007, 265008, 60170831, 60433438, 264758, 55811388, 87168559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906768, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52644150, 264691, 33657023, 264692, 264693, 60431528, 35696423, 35695855, 264636, 56182323, 18108387, 56526486, 22278000, 22279002, 264563, 264564, 264565, 264566, 264567
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi2495699 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109954, 21908754, 265017, 21908767, 21908768, 21908769, 265020, 264691, 264636, 56182323, 22279002

1775	95359330 (3549, 3550)	Novel Protein sim. GBank gll1469199[dbj]BAA094871 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696286, 22278997, 29331822, 29331826, 60432289, 29331828, 35696052, 29331830, 66712502, 264828, 56182435, 264511, 265007, 265009, 60170831, 60432229, 60433438, 55812038, 21906754, 85658542, 87168559, 264601, 265017, 265018, 265019, 264762, 264448, 264288, 264889, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 265022, 264691, 33657023, 264692, 33657109, 27486261, 33657349, 18108370, 18108377, 35696423, 55811576, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264486, 264910
1776	94133756 (3551, 3552)	Novel Protein sim. GBank gll4589676[dbj]BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gll3219939[sp]P87115[YDK9_SCHPO - HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1	nucl_rept		56994075, 29331826, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181562, 264689, 21906765, 21906768, 21906769, 35695917, 264690, 33657023, 35695763, 60431528, 35696423, 55811576, 35695855, 22279000, 22279002, 264564
1778	94851624 (3555, 3556)	Novel Protein sim. GBank gll3875648[emb]CAA91454.1] - (Z66561) Similarity to Human rab13 protein (PIR Acc. No. A49647). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL.M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9...	UNCLASSIFIED		29331826, 29331827, 35696052, 264512, 265007, 265009, 265017, 265019, 264762, 18108351, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gll4589676[dbj]BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]	UNCLASSIFIED		29148627, 35696286, 29147620, 265006, 265007, 265008, 18108385, 65274727, 264482, 264369, 264766
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56526486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264906, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gll729225[sp]P41237[CTXN_RAT] - CORTEXIN			264259, 29331822, 264508, 264905, 264906, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264288, 264768, 264769, 264635, 264636, 264637, 264639, 264553
1783	85717905 (3565, 3566)	Novel Protein sim. GBank gll2257543[dbj]BAA214361 - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]	interferon		264768

1784	95187093 (3567, 3568)	Novel Protein sim. GBank gij1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - struct PH domain	35696286, 264259, 35696052, 264508, 264905, 264908, 264907, 66712502, 264908, 264909, 265007, 265008, 265009, 264910, 264591, 264594, 264757, 264758, 264759, 265010, 265011, 264601, 264602, 264604, 264605, 18108351, 264762, 264763, 264764, 264389, 264766, 264687, 264768, 264688, 21908768, 35695917, 264690, 264691, 264692, 264693, 264628, 18108374, 35696423, 264631, 264632, 264635, 264637, 264638, 264639, 18108385, 22279000, 22279002, 264565, 264566, 264488
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gij4589552[dbj]BAA76798.1] - (AB023171) KIAA0954 protein [Homo sapiens]	UNCLASSIFIED	65274572, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 264905, 264906, 264908, 66712502, 56182435, 264511, 265007, 60433356, 55811150, 264683, 264369, 264687, 52644229, 21908767, 52644150, 33657023, 65274620, 33657182, 65274791, 35695855, 264555, 65274727, 22279002
1786	85296485 (3571, 3572)	Novel Protein sim. GBank gij117788[sp]P26770[CYAA_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)]	UNCLASSIFIED	264908, 35696423, 264636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gij3877175[emb]CAA90338.1] - (Z50028) cDNA EST vk321h8.5 comes from this gene; cDNA EST EMBL:D68896 comes from this gene; cDNA EST vk395f9.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264905, 264908, 264909, 264595, 264764, 264766, 264692, 60431528, 264629, 264636, 264564, 264566
1788	91228779 (3575, 3576)		UNCLASSIFIED	264488, 83373044
1789	88094529 (3577, 3578)	Novel Protein sim. GBank gij2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]	UNCLASSIFIED	264488, 29331828, 264909, 18108351, 264288, 265021, 264555, 264636
1790	82489734 (3579, 3580)			35696052, 264905, 264906, 264907, 264908, 264909, 265008, 264910, 264758, 265011, 265019, 264764, 264766, 264769, 264628, 264635

1791	95197259 (3581, 3582)	Novel Protein sim. GBank gij2114321dbj BAA200371 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	264488, 264686, 264687, 264768, 18108394, 264769, 18108397, 264259, 264691, 264692, 33657023, 264693, 264509, 264905, 264906, 264628, 264907, 264629, 264908, 264909, 264510, 265008, 264511, 265008, 264630, 265009, 264631, 264910, 264632, 264634, 264635, 264555, 264636, 264592, 264637, 264593, 264638, 18108381, 264639, 264758, 265010, 265011, 264602, 22279000, 264604, 264760, 264564, 264681, 264762, 264565, 264763, 264683, 264566, 264764, 264288, 264684, 264567, 18108354, 18108391, 264685, 264766
1792	87792690 (3583, 3584)	Novel Protein sim. GBank gij4337106 gb AAD180821 - (AF129756) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	22278997, 264259, 264508, 265007, 33657402, 87168559, 264369, 33657023, 35695855, 20281071, 264559, 18108387, 87168518
1793	95337877 (3585, 3586)	Novel Protein sim. GBank gij5579331 gb AAD45504.1 AF145732 - (AF145732) endoplasmic reticulum alpha-mannosidase I [Homo sapiens]	Contains protein domain (PF01532) - Glycosyl hydrolase family 47	ATPase-associated	65274572, 22278995, 22278996, 22278997, 22278998, 264093, 264259, 29331824, 66714117, 60432289, 29331827, 29331828, 264103, 264105, 29331830, 265007, 264910, 265009, 60170831, 60433356, 21906754, 265010, 265017, 265019, 264681, 264682, 264288, 52644229, 21906765, 21906766, 21908767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 52644150, 33657023, 33657109, 18108370, 18108374, 65274791, 20281071, 60432113, 22278000, 264482, 264564
1794	87759808 (3587, 3588)	Novel Protein sim. GBank gij4914604 emb CAB43577.1 - (AL050369) hypothetical protein [Homo sapiens]	Contains protein domain (PF01788) - Putative snoRNA binding domain	UNCLASSIFIED	18108394, 22278995, 22278999, 264259, 29331822, 29331824, 29331825, 29146498, 29146499, 264508, 264905, 52844045, 264112, 265006, 265008, 264910, 60433356, 264757, 55812038, 87168474, 265011, 265017, 18108351, 264763, 264448, 264683, 264389, 21906765, 21906766, 21906767, 21906769, 29148784, 35695917, 60170815, 33657023, 264629, 18108374, 18108376, 35696423, 35695855, 264556, 264557, 264638, 264558, 18108385, 264564, 264632, 264635, 264636, 264595, 264596, 264907, 264566, 264909
1795	79747856 (3589, 3590)			UNCLASSIFIED	
1796	86598486 (3591, 3592)	Novel Protein sim. GBank gij585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)		glycoprotein	264488, 264907, 264909, 264594, 264595, 264766, 264687, 21906765, 21906767, 264628, 264630, 264559

1797	91223219 (3593, 3594)	Novel Protein sim. GBank gii1842111 (U87586) - decoy (Arabidopsis thaliana)		ribosomalprot	22278996, 22278997, 22278998, 22278999, 29331822, 264910, 60170831, 21906754, 52644229, 21906765, 21906768, 21906769, 35695917, 265022, 52644150, 264691, 33657023, 263967, 33657109, 22279000
1798	91221276 (3595, 3596)	Novel Protein sim. GBank gii2832806(dbi)BAA24608.1] - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 56994075, 22278997, 22278998, 22278999, 264259, 29331826, 60432289, 29331828, 33656970, 265008, 60432229, 264757, 60433438, 21906754, 33657084, 87168559, 265017, 18108351, 264682, 264448, 264288, 21906765, 21906768, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 33657182, 27486261, 27486265, 33657349, 263973, 18108374, 55811576, 35695855, 18108385, 87168518, 22279000, 264488
1799	86321713 (3597, 3598)	Novel Protein sim. GBank gii5689541(dbi)BAA83034.1] - (AB029025) KIAA1102 protein [Homo sapiens]		teph	264908, 21906754, 21906767, 21906769, 265020, 33657023, 264692, 264693, 264404, 22279000
1800	87080116 (3599, 3600)	Novel Protein sim. GBank gii4680679(gbi)AAD27729.1]AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	264691, 264558, 264566
1801	95060723 (3601, 3602)	Novel Protein sim. GBank gii134920(sp)P21997(SSGP VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			52644045, 265007, 264632
1802	8771012 (3603, 3604)	Novel Protein sim. GBank gii134920(sp)P21997(SSGP VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			35696286, 66714117, 264508, 264509, 58182435, 264512, 18108351, 264688, 55811957, 264692, 55811576, 35695855, 264486
1803	85060725 (3605, 3606)	Novel Protein sim. GBank gii4680679(gbi)AAD27729.1]AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			264686, 264488, 264687, 264489, 264768, 264769, 264689, 21906769, 35696286, 35695917, 264259, 264691, 264692, 264693, 20281099, 18108364, 35696052, 264508, 264509, 264905, 264906, 18108370, 264628, 264907, 66712502, 264908, 264909, 18108374, 18108376, 35696423, 35695855, 264510, 264511, 265008, 265007, 264512, 265008, 264910, 264631, 264632, 264634, 264635, 264591, 264638, 264637, 264592, 264638, 264593, 264639, 264594, 83373044, 264758, 264598, 18108385, 18108387, 265011, 264760, 264563, 18108351, 264762, 264564, 264448, 264585, 264763, 264683, 264764, 264566, 264288, 264486, 264567, 264765, 264766

1804	87770203 (3607, 3608)	Novel Protein sim. GBank gij3879914[embjCAA98538.1]- (Z74043) predicted using GeneFinder: cDNA EST EMBL:C13850 comes from this gene: cDNA EST EMBL:C11575 comes from this gene: cDNA EST yk3434.5 comes from this gene [Caenorhabditis elegans]			5264565, 22278997, 22278999, 264905, 264908, 264909, 264910, 21906754, 264766, 21906765, 21906768, 35695917, 265020, 265022, 264691, 264637, 264639, 22279000, 264564, 264566
1805	95330375 (3608, 3610)	Novel Protein sim. GBank gij5453644[refINP_006461.1]pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644229, 35696423, 264636, 60432113
1806	94133762 (3611, 3612)	Novel Protein sim. GBank gij4589676[jdbjBAA76857.1]- (AB023230) KIAA1013 protein [Homo sapiens]	struct		264094, 264105, 264908, 35696423, 265006, 265007, 265008, 264555, 264592, 265011, 265016, 264369
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gij4884079[embjCAB43235.1]- (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264488, 35696286, 66714117, 35696052, 66712502, 264592, 60433438, 52644296, 265010, 264683, 264369, 264689, 55811957, 35695917, 33657109, 35695763, 55810764, 18108379, 35696423, 35695855, 56182323, 264563, 264564, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gij1916927 (U87965) - putative G protein [Mus musculus]	UNCLASSIFIED		264594, 55811150, 264686, 29148629, 29148784, 264690, 264629, 18108374, 264556, 264557, 264558
1810	88096316 (3618, 3620)	Novel Protein sim. GBank gij1352944[spjP47179]YJP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264488, 35696052, 264905, 264906, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33657402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264686, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264486, 264567
1811	88086272 (3621, 3622)	Novel Protein sim. GBank gij2134984[pirj j37275 - death-associated protein kinase (EC 2.7.1.-) - human	kinase Antk repeat	Contains protein domain (PF00023) -	264488, 264259, 264508, 264509, 264905, 264908, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264766, 264686, 264769, 264534, 60170615, 33657023, 264629, 264631, 264639, 264563, 264482, 264483
1812	79245772 (3623, 3624)				29331822, 29331824, 265019, 18108351, 21906769

1813	86090972 (3625, 3626)	Novel Protein sim. GBank gi 5051636 gb AAD38326.1 AF07372 - (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 264259, 29331824, 66714117, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 265007, 264910, 264591, 264593, 55812038, 265011, 265018, 264760, 264682, 264764, 264683, 264369, 264766, 264768, 264769, 21906768, 21906768, 264691, 264693, 18108374, 35695855, 264634, 264635, 264637, 264639, 264559, 22278000, 22279002, 264566
1814	86178047 (3627, 3628)	Novel Protein sim. GBank gi 3843608 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 35696286, 22278998, 264092, 264094, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264107, 52644045, 56182435, 265009, 60432229, 60433356, 87168474, 87168559, 264369, 264288, 21906765, 35695917, 265021, 265022, 33657023, 33657109, 18108374, 35696423, 264638, 55526486, 264482
1815	85296473 (3629, 3630)	Novel Protein sim. GBank gi 117788 sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)		sinucl	22278999, 264508, 264509, 264907, 264908, 264910, 265011, 264760, 264766, 264634, 264636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gi 1176623 sp P41846 YO96_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 264509, 264907, 264908, 264909, 265009, 264591, 265011, 265017, 264687, 264688, 265022, 264691, 18108362, 18108368, 18108370, 18108374, 18108379, 264635, 264557, 264564, 264567, 264488, 22278997, 22278999, 60432049, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644229, 21906765, 21906767, 21906768, 52644150, 33657023, 33657109, 27486262, 18108370, 18108374, 60170394, 56182323, 22279002
1817	86095268 (3633, 3634)	Novel Protein sim. GBank gi 3766377 emb CAA21429 - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	histone	35696286, 60433356, 264758, 264369, 264686, 21906769, 264693, 264632
1818	85806775 (3635, 3636)	Novel Protein sim. GBank gi 3879121 emb CAA94370 - (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:TO1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	22278995, 22278997, 22278999, 264259, 29331826, 264908, 265007, 265008, 265009, 60432229, 265017, 265018, 265019, 264448, 264288, 21906768, 21906769, 265020, 18108381, 18108384, 22279000, 22279002, 264567
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gi 5031865 ref NP_005771.1 pLHFP - lipoma HMGIC fusion partner		UNCLASSIFIED	

1820	87769455 (3839, 3840)				284905, 284907, 284594
1821	80431510 (3841, 3842)				284907, 264768, 263978
1822	91221523 (3843, 3844)	Novel Protein sim. GBank gii4884130[emb]CAB43272.1] - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 35698052, 29331828, 264908, 29331830, 60170831, 264591, 264593, 60433356, 264598, 265017, 265019, 18108351, 264763, 264683, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33857023, 18108364, 18108370, 35695855, 22278900, 22279002
1823	85522330 (3845, 3846)			UNCLASSIFIED	264488, 264259, 264511, 264288, 264768, 264693, 35698423, 284634, 18108385, 264486
1824	86612025 (3847, 3848)	Novel Protein sim. GBank gii477072[pir]IA48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	284907, 264908, 264909, 284511, 264631, 264634, 264635, 264637, 264638, 264639, 264758, 264568
1825	87430125 (3849, 3850)	Novel Protein sim. GBank gii3036803[emb]CAA18493] - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60432049, 264910, 264487
1826	91723612 (3851, 3852)	Novel Protein sim. GBank gii4680885[gb]AAD27732.1]AF13295 - (AF132957) CGI-23 protein [Homo sapiens]		ATPase-associated	52644507, 52645156, 52646842, 22278994, 22278996, 56994075, 264259, 60432049, 52645080, 35698052, 66712502, 52644045, 265008, 265009, 60432229, 60433356, 60433438, 52646317, 52644296, 265011, 87168559, 264448, 264288, 264369, 264688, 52644229, 264689, 21906765, 21906768, 265020, 60170615, 52644150, 33657023, 27486262, 27486264, 27486265, 35695763, 35698423, 35695855, 83373044, 87168518, 264404, 22279002
1827	81647212 (3853, 3854)				264758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank gi 4503571 ref NP_001419.1 pENO1 - endolase 1, (alpha)	Contains protein domain (PF00113) - Endolase	oncogene	284488, 52646842, 56182575, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264907, 66712502, 52644045, 56182435, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 60432229, 264593, 60433356, 60433438, 264758, 33109954, 21906754, 87169474, 265010, 265011, 87168559, 265017, 265019, 264761, 264762, 264448, 264764, 264683, 264288, 264369, 18108355, 264768, 18108357, 18108358, 264688, 264769, 264689, 21906768, 21906769, 35695917, 265021, 60170615, 33657023, 33657349, 263972, 35811578, 35695855, 264635, 264555, 264558, 264638, 264557, 87168518, 22279000, 22279002, 264563, 264482, 264565, 264484, 264567
1829	80197720 (3657, 3658)				264508, 264634, 284509, 264482, 29331827, 264908, 265009, 264910
1830	94312942 (3659, 3660)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease	52645156, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 29331822, 29331825, 35696052, 52646317, 52644296, 87168559, 265019, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 35695763, 263974, 35698423, 35695855, 52644332
1831	94138063 (3661, 3662)			UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 264758, 265010, 265019, 265022, 264693, 65274791
1832	84521663 (3663, 3664)	Novel Protein sim. GBank gi 1330345 (U58755) - coded for by C. elegans cDNA yk46b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....			264602

1833	85314184 (3665, 3666)	Novel Protein sim. GBank gi 517413 ref NP_006028.1 pCDC4 - CDC42-binding protein kinase beta (DMPK-like)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 35686052, 29148499, 264508, 264509, 264808, 264907, 66712502, 264908, 52844045, 264909, 264512, 265008, 264591, 264593, 60433356, 21906754, 33857084, 265011, 265017, 264604, 265018, 265019, 264881, 18108351, 264683, 264288, 264885, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 265020, 265021, 264690, 264892, 33657023, 65274820, 33657182, 27486264, 33657349, 65274791, 264634, 264635, 264556, 264557, 264558, 264559, 18108385, 56528486, 87168518, 60432113, 22279000, 22279002, 264563
1834	80562760 (3667, 3668)				264259, 264907, 264689, 22279000, 22279002
1835	94135718 (3669, 3670)			UNCLASSIFIED	22278998, 29331822, 29331826, 87168474, 264603, 21908768, 263976, 35685855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gi 4759286 ref NP_004268.1 pUCP4 - uncoupling protein 4	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331825, 264908, 265019, 264764, 264686, 21906765, 264635
1837	94234297 (3673, 3674)	Novel Protein sim. GBank gi 3334400 sp Q24574 UBPE_DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	22278995, 29148499, 265006, 265008, 265009, 265010, 264683, 21906765, 29148627, 29148629, 265020, 265021, 265022, 65274620, 18108370, 18108374, 264556, 18108385
1838	94324369 (3675, 3676)	Novel Protein sim. GBank gi 1362599 pir J55154 - Abi substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain		29331822, 265017, 264760, 265020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gi 2117310 emb CAB09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 264601, 21906765, 21906766, 265021, 33657109, 264556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank gi 127560 sp P23249 MV10_MOUSE - PROTEIN MOV-10		UNCLASSIFIED	264693
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gi 4572464 gb AAD23834.1 AF123655 (AF123653) FEZ1 [Homo sapiens]			56182575, 29331824, 29331826, 60433356, 264764, 264288, 33657023, 263987, 18108370, 18108374, 264631, 264555, 264556, 264639

1842	90992645 (3683, 3694)	Novel Protein sim. GBank gi1326268 (U58728) - C54H2.1 gene product [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 29331822, 29331824, 29331825, 66714117, 29331826, 29331827, 264907, 264909, 52644045, 56182435, 264510, 265006, 265007, 265009, 264910, 60433356, 264757, 60433438, 55812038, 265017, 18108354, 264686, 264769, 33657023, 264693, 18108364, 33657109, 18108368, 264628, 55810764, 56182323, 18108384, 264563, 264564
1843	95292692 (3685, 3686)			UNCLASSIFIED	264488, 56182435, 264769, 29331826, 29331828, 264511, 265006, 265007, 264910, 264631, 264509, 264690, 264636, 264564, 264691, 60432229, 60432049, 264259, 264629, 33657023, 264486, 264909, 264567, 264595, 264768
1844	87444764 (3687, 3688)	Novel Protein sim. GBank gi2496887[sp]Q09232[YO22 CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III]		UNCLASSIFIED	264908, 265022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank gi1175494[sp]Q09819[YAC5 SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I]	Contains protein domain (PF00628) - PHD-finger	transcriptfactor	264259, 29331824, 264907, 264908, 66712502, 264510, 265007, 265008, 55812038, 265018, 21906765, 52644150, 33657109, 264555, 264556, 264557, 56182323, 18108382, 83373044, 18108385, 264564
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gi3881080[emb]CAA21739] - (AL032657) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h6.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk467g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264905, 264908
1847	87821497 (3693, 3694)	Novel Protein sim. GBank gi5059323[gb]AAD38967.1[AF151522] hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	22278997, 264259, 29331824, 264909, 18108351, 263974, 22279002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gi5701854[emb]CAB52191.1] - (AJ245417) G5b protein [Homo sapiens]		im7	29331825, 29331826, 29331827, 265017, 264883, 264288, 264768, 264768, 21906767, 21908768, 264692, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gi4503665[ref]NP_001989.1[pFBLN - fibulin 2 precursor	Contains protein domain (PF00008) - EGF-like domain	ATPase_associated	56182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gi4589582[db]BAA76813.1] - (AB023186) KIAA0969 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	strucd	60432049, 264908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gi220637[db]BAA01471] - (D10827) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331824, 35696052, 264910, 60433438, 264888, 35695917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gi 5174629 refNP_005090.1 pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35696286, 22278996, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52844045, 265007, 264910, 60432229, 60433358, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 284448, 264686, 264687, 21906765, 21906767, 21906769, 265021, 265022, 52844150, 264693, 33657109, 18108370, 18108374, 55811578, 35695855, 56182323, 60432113, 22279002, 264563 264687, 264768, 52644507, 264769, 21906765, 21906767, 21906768, 22278995, 56994075, 22278999, 52844150, 264259, 264692, 29331822, 29331824, 52645129, 29331827, 33656970, 33657349, 35695763, 264508, 264906, 264628, 264907, 264629, 264909, 35696423, 35695855, 264510, 265006, 264511, 264512, 264630, 265009, 264631, 264910, 264634, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52646317, 52644296, 87168518, 87168559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264567, 264288, 264369, 264766
1853	81222287 (3705, 3706)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264592
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gi 2072964 (U93569) - putative p150 [Homo sapiens]	nuclease		
1855	81221459 (3709, 3710)	Novel Protein sim. GBank gi 4539520 emb CAB39994.1 - (AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - nucl_recpt Kelch motif		18108392, 52646365, 65274572, 56182575, 22278994, 58994075, 22278998, 35696286, 22278999, 264259, 60432049, 264908, 264510, 265007, 265008, 265009, 264595, 21906754, 87168474, 265011, 87168559, 264681, 264288, 264768, 18108359, 21906764, 21906768, 29148627, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108372, 18108374, 18108376, 35696423, 264631, 264636, 18108381, 264482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gi 3954978 emb CAA06945 - (AJ008278) acetylglucosaminyltransferase-like protein [Mus musculus]	UNCLASSIFIED		56994075, 264259, 29331828, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gi 4322670 gb AAD16120 - (AF094508) dentin phosphoryn [Homo sapiens]	ATPase_associated		22278999, 264259, 264906, 60170831, 264448, 264686, 265020, 265022, 33657109, 60170394, 83373044

1858	87628311 (3715, 3716)	Novel Protein sim. GBank gij4381903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	264757	
1859	84407464 (3717, 3718)	Novel Protein sim. GBank gij4240317 gb BAA74937.1 - (AB020721) KIAA0914 protein [Homo sapiens]		22278996, 29331824, 265007, 33109954, 265019, 264369, 21906768, 29148784, 27486261, 52644332, 22279002 265019	
1860	17829308 (3719, 3720)	Novel Protein sim. GBank gij4009522 (AF099731) - connexin 31.1 [Homo sapiens]			
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gij2143637 pir B4505 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase	264887, 264259, 29331822, 29331824, 29331825, 265007, 265009, 264591, 33109954, 265010, 265019, 264369, 264288, 264688, 264691, 264693, 27486284, 18108370, 18108374, 263977, 55811576, 56182323, 264639, 22279000, 22279002, 264482	
1862	87372823 (3723, 3724)	Novel Protein sim. GBank gij125493 sp P07313 KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35696286, 264259, 87168474, 264369, 21906766, 264558, 264583	
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gij3820909 emb CAA09299 - (AJ010642) Dof protein [Drosophila melanogaster]	UNCLASSIFIED	264601, 264766, 29148627, 29148629, 264692, 264629, 264835	
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gij4322263 gb AAD15985 - (AF077738) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	22278999, 264259, 264907, 265018, 18108370, 264634, 264635, 264555, 264556, 264638, 18108387	
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gij2495727 sp Q93073 Y256_HUMAN - HYPOTHETICAL PROTEIN KIAA0256		22278999, 264490, 29331822, 66714117, 66712502, 265006, 265007, 265008, 265009, 264591, 60433438, 265010, 265019, 264760, 264448, 264768, 29148627, 29148628, 265020, 265022, 18108385, 60432113	
1866	87266816 (3731, 3732)	Novel Protein sim. GBank gij5282617 emb CAB45748.1 - (AL080157) hypothetical protein [Homo sapiens]	kinase	18108374, 264769, 18108377, 21906765, 21906766, 35696423, 56182575, 21906769, 29148629, 35696286, 35695917, 265021, 264510, 264511, 264512, 264534, 264535, 60170831, 52644150, 264555, 264691, 264259, 264556, 264692, 264557, 33657023, 60433358, 29331822, 264559, 264595, 29331824, 18108385, 21906754, 33657182, 29331827, 35696052, 33656970, 87168518, 265017, 60431602, 22279000, 264508, 264509, 18108351, 264907, 264682, 264567, 18108372, 264765, 264486	
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gij3859830 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]	UNCLASSIFIED	264094	

1868	87357459 (3735, 3738)	Novel Protein sim. GBank gi 3881525 emb CAA93884 - (Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357110.5 comes from this gene [Caenorhabditis elegans]		nuclease	264489, 22278997, 22278999, 29331825, 29331828, 265008, 265009, 33657402, 87168474, 18108351, 21906765, 21906768, 21906769, 285020, 265021, 60170615, 27486264, 264628, 18108374, 264631, 18108385, 87168518, 22279000, 22279002, 264566, 264567
1869	86977292 (3737, 3738)	Novel Protein sim. GBank gi 4826772 ref NP_004961.1 pIGFA - insulin-like growth factor binding protein, acid labile subunit	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264508, 264509, 264906, 264908, 264909, 264910, 264591, 264600, 18108351, 264663, 264766, 264769, 35695855, 264634, 264558, 264639, 18108385, 264563, 264486
1870	95349488 (3739, 3740)	Novel Protein sim. GBank gi 1869859 emb CAB06722 - (Z86099) very large tegument protein [human herpesvirus 2]		UNCLASSIFIED	29331824, 60424269, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264766, 264686, 264688, 21906768, 21906769, 35695917, 60170615, 264692, 18108368, 35695763, 35698423, 65274791, 264638, 264639, 56526486
1871	80234464 (3741, 3742)			UNCLASSIFIED	264509, 264905, 264595, 264768, 264635, 264636, 264563, 264486
1872	80235355 (3743, 3744)	Novel Protein sim. GBank gi 2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	264510, 264594, 264565
1873	80213890 (3745, 3746)				264509, 264512, 265009, 265011, 18108351, 264687, 264691, 18108370, 18108374, 264635
1874	95351136 (3747, 3748)		Contains protein domain (PF00293) - Bacterial mutT protein	UNCLASSIFIED	264488, 35695917, 264259, 264905, 264907, 264908, 264909, 263978, 264511, 264635, 264636, 264637, 264638, 33657402, 264558, 18108385, 264600, 264604, 264764, 264567, 264766
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gi 4589520 db BAA76782.1 - (AB023155) KIAA0938 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264828, 264592, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gi 263810 bbs 122920 - collagen alpha chain [Riftia pachyptila=tube worms, Peptide, 1027 aa]		UNCLASSIFIED	264259, 29331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264769, 18108376, 264556, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gi 3983356 gb AAC83924.1 - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	264767, 264686, 264768, 263978, 264693, 264639, 285010, 264563, 264905, 264906, 264907

1878	95351056 (3755, 3756)	Novel Protein sim. GBank gi 4510345 gb AAD21434.1 - (ACO06921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264569, 264488, 35696266, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 29146498, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 33857402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264764, 264389, 264288, 264766, 264687, 264768, 264769, 21906766, 35695917, 265021, 60170615, 33657023, 264692, 264693, 33657109, 27486265, 264628, 18108370, 264629, 18108374, 35686423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 56526486, 87168518, 264563, 264564, 264568, 264488, 264567, 264905, 264907, 264908, 265007, 264565, 264566
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gi 4929643 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gi 1550785 emb CAA69283 - (Y08026) Immune associated protein 38 [Mus musculus]		UNCLASSIFIED	264766, 264691, 264692, 83373044
1881	80214949 (3761, 3762)	Novel Protein sim. GBank gi 93144 pir JB40505 - hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhouser or Becker)		UNCLASSIFIED	264509, 264905, 264908, 264909, 264910, 264762, 264687, 33657023, 264632
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gi 2384956 (AF022985) - No definition line found [Caenorhabditis elegans]			264908, 21806766, 18108370, 263974, 87168518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	264908, 264910, 87168559, 21906766, 264636

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gi 4929643 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108394, 56181686, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264512, 265009, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811386, 265010, 265011, 87168559, 264600, 265017, 264604, 265019, 264605, 264760, 5581150, 264761, 264882, 264763, 264683, 264764, 264288, 264369, 264766, 264686, 264768, 264769, 29148784, 35695917, 264690, 264691, 33657023, 264692, 264693, 33657109, 18108370, 264628, 60431528, 264629, 263973, 18108374, 55810764, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264486, 264567
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gi 2507155 sp P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	56182575, 264259, 264905, 264909, 265008, 264596, 264766, 265020, 264628, 60431528, 264634, 56526486, 264080, 264563
1886	86674062 (3771, 3772)	Novel Protein sim. GBank gi 2854158 gb AAC02577.1 - (AF045641) No definition line found [Caenorhabditis elegans]			22278998, 22278999, 60432049, 264910, 265018, 264766, 21906768, 29148629, 264690, 264693, 264628, 264555, 264488
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gi 5174421 ref NP_006023.1 pCPNE - copine VI (neuronal)	Contains protein domain (PF00168) - C2 domain	ATPase-associated	29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 264681, 264768, 29148627, 264693, 18108364, 35696423, 65274791, 35695855, 264632, 56182323, 264639, 264563
1888	87622804 (3775, 3776)	Novel Protein sim. GBank gi 3319931 emb CAB10841 - (Z88046) dJ1409.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gi 1083308 pir J A56559 - enhancer-trap-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	264906, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21906765, 21906768, 21906769, 265021, 33657023, 33657109, 56182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gi 4240185 dbj BAA74876.1 - (AB020680) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108398, 29147620, 264907, 265009, 264600, 265018, 18108351, 264288, 264689, 21906765, 21906768, 21906769, 264691, 264692, 264693, 264628, 18108370, 264638, 264558, 264404

1891	87013895 (3781, 3782)			UNCLASSIFIED	264686, 264768, 264687, 264692, 264693, 29331822, 29331824, 264508, 264905, 264906, 18108370, 264628, 264907, 264908, 264909, 18108379, 265007, 265008, 264910, 264632, 264591, 264639, 264596, 18108384, 265010, 265011, 264601, 264605, 264563, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gi 5689535 dbj BAA83051.1 - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	struct	22278995, 264509, 87168559, 18108351, 264448, 264682, 265020, 264693, 18108374, 22279000
1893	88533826 (3785, 3786)			laminin	264569, 65274572, 22278997, 22278999, 264259, 29331822, 29331824, 68714117, 29331828, 264906, 265008, 265009, 264592, 265018, 264681, 264448, 264683, 18108354, 264369, 264684, 264685, 264768, 264687, 264689, 21906768, 265020, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 264628, 18108374, 35695855, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22279000
1894	86989120 (3787, 3788)				264508, 264905, 264906, 264907, 264594, 264684, 264690, 264692, 264630, 264635, 264636, 264639, 264563
1895	87631891 (3789, 3790)	Novel Protein sim. GBank gi 5262574 emb CAB45729.1 - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat		56182575, 264259, 60432289, 29331826, 264107, 264905, 264908, 264910, 60170831, 264758, 265010, 265018, 264448, 264288, 264768, 33657109, 264628, 55810784, 18108379, 264634, 56182323, 56526486
1896	85673555 (3791, 3792)		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264907, 265008, 264682, 264686, 21906768, 264629, 264631, 264634, 264555, 264259
1897	80585589 (3793, 3794)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - III ALU SUBFAMILY SP WARNING ENTRY III		cadherin	
1898	87617637 (3795, 3796)	Novel Protein sim. GBank gi 127560 sp P23249 MV10_MOUSE - PROTEIN MOV-10		helicase	22278996, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35696052, 29331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 55810784, 22279000
1899	86673097 (3797, 3798)	Novel Protein sim. GBank gi 2809819 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]	Contains protein domain (PF00909) - Ammonium Transporter Family	glycoprotein	264259, 264508, 264909, 60432229, 264769, 21906765, 21906769
1900	87641858 (3799, 3800)	Novel Protein sim. GBank gi 4102881 (AF017250) - vitellogenin precursor [Oreochromis aureus]		UNCLASSIFIED	264683

1901	95196847 (3801, 3802)	Novel Protein sim. GBank gjl585959lsplP38378IS61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52644507, 52645156, 18108396, 52646365, 52646842, 18108397, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278998, 264490, 60432049, 264259, 29331822, 52645080, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 29146498, 264906, 264907, 29331830, 264908, 52644045, 264909, 264112, 265006, 264512, 265008, 264910, 265009, 60170831, 60432229, 60433356, 33657402, 60433438, 55812038, 264758, 33109954, 21908754, 33657084, 52644296, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 52644229, 21908765, 21908766, 21906767, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 18108362, 33657023, 264693, 263987, 33657109, 33657182, 27486264, 33657349, 35695763, 18108370, 18108376, 55811576, 35696423, 35695855, 60431850, 264636, 263981, 52644332, 60170394, 83373044, 18108385, 87168518, 60432113, 264584 264107, 263978
1902	80202013 (3803, 3804)	Novel Protein sim. GBank gjl4426613lgb/AAD204511- (AF098796) SLM-1 [Mus musculus]		dna_rna_bind	
1903	87776554 (3805, 3806)	Novel Protein sim. GBank gjl3747107 (AF095741)- unknown [Rattus norvegicus]		UNCLASSIFIED	264759, 29331825, 29331827, 264508, 264907, 265008, 60170831, 60433356, 60433438, 264759, 21908754, 264448, 264288, 265021, 265022, 33657023, 264693, 55811576, 264555, 264556, 22279000
1904	80434213 (3807, 3808)	Novel Protein sim. GBank gjl1352911lsplP47147YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	264509, 264905, 264906, 264907, 264908, 265007, 264910, 264686, 264768, 264687, 264769, 264693, 264628, 18108374, 264634, 264636, 264637, 264585
1905	85351140 (3809, 3810)	Novel Protein sim. GBank gjl3043714[d]BAA255211- (AB011167) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00293) - Bacterial mutT protein		264488, 264768, 264769, 264689, 29148629, 35695917, 35696286, 264259, 264692, 18108362, 33657023, 29331824, 33657109, 29146499, 264508, 264509, 264905, 264906, 264907, 66712502, 264908, 264909, 35696423, 35695855, 264510, 264511, 264512, 264910, 264634, 264635, 264637, 264638, 33657402, 264758, 85658542, 264602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264566, 264288, 264766
1906	12763822 (3811, 3812)			UNCLASSIFIED	264637

1807	95351144 (3813, 3814)	Novel Protein sim. GBank gi 4929595 gb AAD34053.1 AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - hydrolase alpha/beta hydrolase fold	UNCLASSIFIED	65274572, 22278996, 35696286, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 60424269, 29331828, 35696052, 264593, 60433356, 21906754, 55811386, 85658542, 87168559, 265018, 264681, 264682, 264684, 264288, 21906765, 21906766, 21906768, 265020, 265022, 264890, 52644150, 264692, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1808	95313641 (3815, 3816)	Novel Protein sim. GBank gi 3986770 (AF109906) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331826, 29331827, 29331828, 29146499, 264905, 264906, 264907, 264908, 86712502, 264909, 56182435, 264510, 264511, 265008, 264810, 60170831, 264592, 60433356, 33657402, 264594, 60433438, 264596, 55812038, 33109954, 52646317, 265011, 265017, 264604, 265018, 265019, 264605, 55811150, 264681, 264448, 264288, 264688, 264688, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148629, 35695917, 265020, 265022, 264691, 264692, 18108364, 65274620, 33657109, 33657349, 35695763, 18108374, 263978, 55810764, 55811576, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22279000, 22279002, 264566, 264486
1809	85514505 (3817, 3818)	Novel Protein sim. GBank gi 2224653 db BAA20813 - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 264511, 264910, 264593, 264758, 264764, 264766, 18108370, 264634, 264637, 264486
1910	94216821 (3819, 3820)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	35696286, 22278996, 22278999, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265007, 264512, 264910, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264768, 264768, 264687, 264769, 35695917, 265021, 52644150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486

1811	91725345 (3821, 3822)	Novel Protein sim. GBank gi 4809339 gb AAD30184.1 AC006530 - (AC006530) hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331826, 29331827, 33656970, 264906, 265007, 264591, 55812038, 87168559, 264448, 264389, 21906765, 21906768, 265022, 264691, 264693, 18108385, 55811576, 264556, 18108385, 18108388
1812	95413519 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA83003.1 - (AB028974) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181686, 22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 66714117, 35696052, 264605, 264906, 264907, 264908, 52644045, 56182435, 265007, 265008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264681, 264369, 264684, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264692, 33657023, 264693, 18108376, 55811576, 35696423, 65274791, 264637, 56182323, 83373044, 56526486, 22279002, 264563, 264566
1813	95305546 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_005685.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278994, 22278995, 56994075, 22278996, 22278998, 22278999, 29331826, 29331827, 265006, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264369, 264288, 264685, 264686, 264769, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265022, 264691, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1814	83423982 (3827, 3828)	Novel Protein sim. GBank gi 4589604 dbj BAA76824.1 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35696052, 264906, 264908, 264828, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1815	95340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA82991.1 - (AB028962) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 29331826, 29331827, 264508, 264909, 265009, 265017, 265019, 264768, 264769, 264689, 264628, 264635, 264637, 264639, 83373044, 264585
1816	79640761 (3831, 3832)				264693, 264639

1917	87821680 (3833, 3834)	Novel Protein sim. GBank gi15669391 dbj BAA82979.1 - (AB028950) KIAA1027 protein [Homo sapiens]		struct	284769, 284688, 21806765, 21806768, 22278996, 264259, 264691, 264693, 29331824, 29331825, 29331826, 29331828, 264905, 264908, 264628, 264907, 264908, 264809, 264510, 264630, 264910, 264634, 264635, 264838, 264637, 264638, 263981, 264639, 264758, 18108385, 21806754, 265011, 264604, 264583, 18108351, 264762, 264763, 264568, 264764, 264766
1918	95302785 (3835, 3836)	Novel Protein sim. GBank gi15281517 gb AAD41524.1 AF154831 - (AF154831) PV-1 [Rattus norvegicus]		struct	264488, 18108392, 18108357, 21806765, 21906767, 21906768, 56182575, 21906769, 22278994, 35896286, 35895917, 22278996, 22278997, 265021, 265022, 264534, 264690, 264691, 264692, 33857023, 264693, 29331824, 29331825, 33857109, 29331826, 52645129, 35696052, 29331828, 27486262, 27486264, 35895783, 284508, 264905, 264509, 264908, 264628, 264907, 18108370, 264908, 264629, 264909, 18108372, 18108374, 263978, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264631, 265009, 264910, 264634, 264635, 264555, 264636, 264556, 264637, 264557, 264593, 264638, 264594, 60170394, 264595, 264559, 264596, 83373044, 264758, 52646317, 18108385, 52644286, 56526486, 87168518, 265010, 265011, 87168559, 264600, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 264760, 264761, 264482, 264564, 18108351, 264762, 264682, 264565, 264448, 264764, 264566, 264486, 264567, 264389, 264288, 264766, 264487, 264685
1919	94143847 (3837, 3838)	Novel Protein sim. GBank gi13878584 emb CAB01237 - (Z77667) cDNA EST EMBL:C08125 comes from this gene; cDNA EST EMBL:C08753 comes from this gene [Caenorhabditis elegans]	oxidase		22278997, 29331822, 265007, 60170831, 60432229, 60433438, 264448, 264682, 264288, 55811957, 33857023, 33857109, 65274791, 56182323, 22279002, 264510, 264511, 264512, 264566
1920	91229853 (3839, 3840)	Novel Protein sim. GBank gi11809231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838495) and H12868 (NID:g877688) [Homo sapiens]	UNCLASSIFIED		
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gi14580997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED		264693

1922	87641863 (3843, 3844)	Novel Protein sim. GBank gij138593spP02845VIT2, CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVI)]; YGP40]		UNCLASSIFIED	264686, 264688, 264490, 18108370, 264909, 18108374, 265008, 264557, 264564, 18108351
1923	94323589 (3845, 3846)	Novel Protein sim. GBank gij119110spP03211[EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278995, 264094, 264259, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264908, 264511, 264512, 265007, 264910, 265009, 264591, 264592, 264593, 264594, 264595, 264758, 264596, 264759, 265011, 265017, 265018, 265019, 55811150, 264681, 264762, 264448, 264764, 264288, 264369, 264766, 264767, 264686, 264687, 264768, 264769, 56181562, 264689, 21908766, 264691, 33657023, 264693, 65274620, 33657109, 18108370, 264628, 264629, 35698423, 264630, 264631, 264632, 264634, 264555, 264635, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264564, 264565, 264566, 264567
1924	87338925 (3847, 3848)	Novel Protein sim. GBank gij387655[embCAA96657] - (Z72511) possible zinc finger protein; cDNA EST EMBL: M89115 comes from this gene; cDNA EST EMBL: D71533 comes from this gene; cDNA EST EMBL: D72314 comes from this gene; cDNA EST EMBL: D75164 comes from this gene; cDNA EST EMBL: C1...	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		29331826, 264906, 264908, 264595, 265017, 265018, 265019, 265021, 264691, 264693, 264637, 18108385, 264565
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gij4981903[gbAAD36415.1]AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomal prot	22278995, 22278996, 22278997, 264259, 29331824, 66714117, 29146499, 264909, 52644045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264692, 33657109, 18108374, 60170394
1926	88094739 (3851, 3852)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		strud	264905, 264906, 264907, 264910, 264593, 265018, 264760, 264764, 264288, 264692, 264693, 263978, 264631, 264634, 264637, 264563
1927	85654657 (3853, 3854)	Novel Protein sim. GBank gij3043632[dbjBAA25480] - (AB011126) KIAA0554 protein [Homo sapiens]			264689, 264631
1928	87788054 (3855, 3856)	Novel Protein sim. GBank gij166576[dbjBAA13377] - (D87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00193) - Inf Extracellular link domain	Inf	264489, 264259, 265017, 265021, 264692
1929	86997236 (3857, 3858)	Novel Protein sim. GBank gij5001993[gbAAD37247.1]AF13432 - (AF134321) chimeric AFGPtypsinogen-like serine protease precursor [Dissostichus mawsoni]		UNCLASSIFIED	264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639

1830	87889128 (3859, 3860)	Novel Protein sim. GBank gi 1709230 sp P52963 NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35698286, 29331828, 264905, 264907, 264908, 264909, 264511, 264910, 264758, 264601, 265017, 265019, 264605, 264760, 264764, 264766, 264688, 264769, 265022, 35698423, 264638, 60432113
1831	87797279 (3861, 3862)	Novel Protein sim. GBank gi 404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264906, 264908, 60432229, 264758, 264764, 264288, 265020, 264692, 264634, 264637, 264684, 264691, 264635
1832	15030972 (3863, 3864)			UNCLASSIFIED	264595
1833	11613668 (3865, 3866)	Novel Protein sim. GBank gi 4115748 gb BAA36494 - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		struct	56182575, 56182435, 264510, 264757, 264758, 55812038, 55811388, 265018, 55811150, 21906765, 264681, 264631, 264635, 264637
1835	87752511 (3869, 3870)			UNCLASSIFIED	264688, 265011, 264511, 264905, 18108351, 264564, 264681, 264259, 18108370, 264566, 264764, 264359, 264595
1836	85414336 (3871, 3872)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit			60432289, 265007, 265010, 265011, 265018, 33657109, 18108374
1837	84847141 (3873, 3874)	Novel Protein sim. GBank gi 543187 pir S37771 - ankryn, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	85658542, 21906767, 35695917, 60170615, 264683, 33657109
1838	87403277 (3875, 3876)	Novel Protein sim. GBank gi 4544431 gb AAD22340.1 AC006955 - (AC006955) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00888) - Cullin family	collagen	264488, 29146498, 264905, 264559
1839	91004976 (3877, 3878)	Novel Protein sim. GBank gi 500858 dbj BAA03210 - (D14168) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	85274572, 22278999, 60432289, 56182435, 60433356, 265017, 21906765, 21906766, 21906768, 55811957, 27486264, 35698423, 60432113, 264584
1840	87348810 (3879, 3880)	Novel Protein sim. GBank gi 1946300 emb CAA73132 - (Y12529) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	264488, 29331822, 264448, 264683, 264288, 265020, 33657023, 264631
1841	94147177 (3881, 3882)	Novel Protein sim. GBank gi 4208386 (AF060570) - rig-1 protein [Mus musculus]		UNCLASSIFIED	56994075, 22278998, 264259, 29331824, 29331827, 264905, 265008, 33657084, 265017, 265018, 264288, 264687, 21906765, 21906766, 21906767, 265020, 52644150, 27486264, 83373044, 18108387, 60432113, 22279002, 264565
1842	87641870 (3883, 3884)	Novel Protein sim. GBank gi 4927204 gb AAD33049.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 18108398, 29331825, 27486261, 264509, 18108370, 18108374, 264482
1843	94325298 (3885, 3886)	Novel Protein sim. GBank gi 3122952 sp O15736 TIPD_DICD1 - TIPD PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	22278998, 29331822, 29331827, 35696052, 264511, 265009, 264592, 60432229, 265017, 265018, 265019, 264684, 264692, 33657109, 65274791, 264638

1844	94232958 (3887, 3888)	Novel Protein sim. GBank gi 1799570 dbj BAA13432 - (D87671) TIP120 [Rattus norvegicus]	UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 264259, 52645080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264910, 60170831, 60432229, 60433358, 33657402, 60433438, 264586, 33109954, 21906754, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264369, 264686, 264768, 21906765, 21906768, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 264692, 33657023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264563, 264488, 22278996, 264510, 264511, 18108351, 264683, 264486, 264567
1845	87641872 (3889, 3890)	Novel Protein sim. GBank gi 4927204 gb AAD33048.1 AF13391 - (AF133911) ARL-6 interacting protein-4 [Mus musculus]	UNCLASSIFIED	60432289, 29331827, 35696052, 265007, 265008, 60433356, 60433438, 264389, 56181562, 21906767, 52844150, 264693, 27486264, 264637, 87168518, 264563
1846	87443980 (3891, 3892)	Novel Protein sim. GBank gi 2498104 sp Q27969 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN	UNCLASSIFIED	22278998, 264905, 264906, 264908, 264909, 264512, 264758, 264762, 264682, 264683, 264764, 264288, 264768, 264688, 21906768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002, 264909, 60170831, 264591, 264594, 235010, 265011, 264764, 264369, 264689, 264631, 264638
1847	86438862 (3893, 3894)	Novel Protein sim. GBank gi 3914801 sp O54888 RPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)	mapolymerase	264369
1848	85189174 (3895, 3896)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243458) proteophosphoglycan [Leishmania major]	struct	264488, 264768, 264688, 264689, 264259, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264583, 55811150, 18108351, 264369, 264288, 18108354
1849	7640129 (3897, 3898)	Novel Protein sim. GBank gi 3876766 emb CAA93466.1 - (Z69637) predicted using GeneFinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	UNCLASSIFIED	56182575, 22278997, 52645080, 29331824, 29331825, 29331827, 55812038, 52646317, 265018, 265019, 264369, 21906765, 21906767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 58182323, 22279002
1850	87788531 (3899, 3900)	(269637) predicted using GeneFinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	Contains protein domain (PF00857) - Isochorismatase family	264591, 264593, 264594, 264595, 264555, 264556, 264557, 264558, 264565
1851	86988253 (3901, 3902)	Novel Protein sim. GBank gi 2626753 dbj BAA23424 - (AB008782) sulfate transporter [Arabidopsis thaliana]	transport	
1852	87069775 (3903, 3904)	Novel Protein sim. GBank gi 4929633 gb AAD34077.1 AF15184 - (AF151840) CGI-82 protein [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase reductase	

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gi 168715 sp P31721 C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR Novel Protein sim. GBank gi 4240271 dbj BAA74914.1 - (AB020698) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00386) - C1q domain	complement	264259, 264558 264488, 263994, 18108394, 35696286, 22278998, 29331822, 66714117, 29331826, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 265007, 265008, 264910, 265009, 60170831, 60432229, 265011, 265017, 264603, 264604, 265019, 18108351, 264685, 264766, 264769, 35895917, 265020, 265021, 264691, 33637023, 264692, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264564, 264566, 264488, 264567
1954	91226025 (3907, 3908)		Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	
1955	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181686, 22278994, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 35696052, 264508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264766, 21906765, 21906766, 21906767, 55811957, 265020, 265021, 52645129, 33657109, 27486264, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gi 1665821 dbj BAA134071 - (D87469) Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278996, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21906769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002, 264563, 264564

1957	94326510 (3913, 3914)	Novel Protein sim. GBank gij4589674[dbj BAA76856.1] - (AB023229) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52648642, 56182575, 22278997, 22278998, 22278999, 29331824, 66714117, 29331827, 29146498, 264593, 33657402, 33109954, 87168474, 265018, 264448, 264369, 264288, 264766, 21906766, 21908767, 21906768, 21906769, 265020, 265021, 264692, 65274620, 27486264, 33657349, 27486265, 33695855, 22279002, 264482
1958	95313902 (3915, 3916)	Novel Protein sim. GBank gij4240227[dbj BAA74892.1] - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278998, 264092, 264084, 264259, 60432048, 29331824, 56182181, 86714117, 264107, 264109, 264909, 264511, 60170831, 60432229, 21906754, 265010, 21906769, 33695917, 265022, 65274620, 263967, 263976, 35698423, 264631, 264632, 264634, 264635, 18108385, 22279000, 22279002, 264593, 265019
1959	85701470 (3917, 3918)	Novel Protein sim. GBank gij2281983[emb CAB10860] - (Z98056) hyppothetical protein [Schizosaccharomyces pombe]		ubiquitin	
1960	80308608 (3919, 3920)	Novel Protein sim. GBank gij2274851[dbj BAA21515] - (D64159) 3-7 gene product [Homo sapiens]		struct	264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264595, 265017, 264604, 265018, 18108351, 264764, 264369, 264766, 264768, 21906765, 18108368, 264629, 18108379, 264635, 264636, 264637, 264638, 264486
1961	16292607 (3921, 3922)				264635
1962	91008385 (3923, 3924)			UNCLASSIFIED	65274572, 264592, 264593, 265019, 264691
1963	80936017 (3925, 3926)	Novel Protein sim. GBank gij3721653[dbj BAA33581] - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		eph	65274572, 18108398, 35695286, 29331825, 60432289, 29331827, 264828, 265006, 265009, 60433356, 60433438, 21906754, 265020, 265021, 33657023, 33657109, 27486265, 35695855, 264555
1964	94317605 (3927, 3928)	Novel Protein sim. GBank gij5262638[emb CAB45757.1] - (AL080169) hypothetical protein [Homo sapiens]		cadherin	264488, 264092, 264259, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 265009, 264910, 264592, 264593, 264594, 264595, 264758, 264600, 264603, 264604, 264605, 264760, 264762, 264448, 264764, 264288, 264685, 264766, 264768, 264769, 21906766, 264691, 264692, 264693, 18108370, 264628, 264629, 18108374, 264630, 264631, 264634, 264636, 264637, 264638, 18108382, 83373044, 18108385, 264483, 264564, 264565, 264566, 264486, 264567
1965	94317445 (3929, 3930)	Novel Protein sim. GBank gij4107017[dbj BAA36294] - (AB001773) PEM-6 [Ciona savignyi]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264488, 264510, 264760, 264768, 264486

1866	84192058 (3931, 3932)	Novel Protein sim. GBank gi 4929707 gb AAD34114.1 AF15187 - (AF15187) CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - Uncharacterized protein family	glycoprotein	22278999, 264092, 264259, 29331826, 29331828, 29146488, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264685, 264686, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264486, 264587
1867	87396123 (3933, 3934)	Novel Protein sim. GBank gi 2957270 (AF044576) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, x domain	esterase	29331824, 265010, 265017, 264288, 21906764, 263981, 56526486
1868	88095641 (3935, 3936)	Novel Protein sim. GBank gi 2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264805, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264764, 264685, 264766, 264767, 264689, 264691, 264693, 264628, 264629, 35698423, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264564, 264565, 264566, 264587
1869	84328529 (3937, 3938)	Novel Protein sim. GBank gi 2911274 (U20329) - spidroin 1 [Nephila clavipes]		UNCLASSIFIED	22278995, 22278996, 35696052, 264906, 264908, 18108351, 264482
1870	80596049 (3939, 3940)	Novel Protein sim. GBank gi 4050087 (AF109907) - S164 [Homo sapiens]		UNCLASSIFIED	264908, 264288, 264766, 264636
1871	94843914 (3941, 3942)	Novel Protein sim. GBank gi 134206 sp P09593 SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR		collagen	264488, 264489, 22278998, 264259, 60432049, 68714117, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264508, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21906765, 33657023, 264692, 18108370, 264629, 35696423, 65274791, 35695855, 264632, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 60432113, 22278000, 264583, 264584, 264585, 264586, 264486
1872	87645444 (3943, 3944)	Novel Protein sim. GBank gi 4519623 dbj BAA75671.1 - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain		22278999, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265006, 264511, 265008, 52644296, 265018, 265019, 264761, 264689, 21906768, 21906769, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1873	86395533 (3945, 3946)			UNCLASSIFIED	28331826, 264692, 35696423, 264631, 264555, 264556, 264557, 264558, 264559
1874	80396629 (3947, 3948)	Novel Protein sim. GBank gi 3309543 (AF036382) - MLL [Fugu rubripes]		UNCLASSIFIED	264682, 264764, 264563

1975	94316479 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 29331826, 29331828, 56182435, 265006, 264757, 55812038, 265010, 265017, 264369, 55811957, 65274781, 35695855, 56182323, 60432113, 264259, 35696052, 265018, 265020, 265021, 33657109, 56526486
1976	95358914 (3951, 3952)			UNCLASSIFIED	264259, 35696052, 265018, 265020, 265021, 33657109, 56526486
1977	94852664 (3953, 3954)	Novel Protein sim. GBank gij2499526[spIQ07782]NASU_RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)		homeobox	264908, 264596, 265021, 264566
1978	87447645 (3955, 3956)	Novel Protein sim. GBank gij103421[pir]A33471 - transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment)		transcription factor	60170831, 264568
1979	87627709 (3957, 3958)	Novel Protein sim. GBank gij2244815[emb]CAB10238.11 - (Z97338) hypothetical protein (Arabidopsis thaliana)		UNCLASSIFIED	29331826, 28146498, 264905, 264907, 265007, 265009, 265010, 265018, 264686, 18108359, 21908768, 35695917, 265020, 60170615, 264693, 18108358, 18108370, 264631, 264635, 264556, 264558, 18108384, 22279000, 264565
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gij4759290[ref]NP_004642.1[p]USP1 - Ubiquitin carboxyl-terminal hydrolase, X-linked		ubiquitin	264489
1981	87606974 (3961, 3962)	Novel Protein sim. GBank gij4406683[gb]AAD200601 - (AF131849) Unknown (Homo sapiens)		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331825, 29331828, 29146498, 29146499, 264107, 264908, 264910, 264595, 21906754, 265010, 265017, 265018, 265019, 264448, 264288, 21908767, 33657023, 27486264, 18108370, 18108374, 18108376, 264630, 264631, 264635, 18108385, 87168518, 22279000, 264482, 264564
1982	90995367 (3963, 3964)	Novel Protein sim. GBank gij5689523[dbj]BAA83045.11 - (AB029016) KIAA1093 protein (Homo sapiens)			65274572, 29331825, 35696052, 33656970, 264909, 265008, 55811386, 264780, 264686, 264691, 27486264
1983	95098688 (3965, 3966)	Novel Protein sim. GBank gij3417297 (AC002310) - Unknown gene product (Homo sapiens)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	22278996, 35696286, 264259, 29331822, 20281099, 29331824, 60432289, 29331827, 264509, 264905, 264906, 264907, 66712502, 264908, 52844045, 264909, 264510, 264512, 264910, 265009, 264591, 264592, 60433356, 60433438, 264758, 265010, 264600, 264603, 264604, 264760, 264762, 264763, 264764, 264768, 264687, 264768, 264769, 21908765, 55811957, 35695917, 264690, 264692, 264693, 264628, 264629, 263978, 18108379, 35696423, 35695855, 20281071, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 83373044, 18108385, 22279000, 22279002

1884	85760989 (3867, 3968)	Novel Protein sim. GBank gij2896695[embjCAA17174.1] - (AL021887) fadD14 [Mycobacterium tuberculosis]		synthase	264688, 21906766, 55811957, 56994075, 265020, 265021, 22278999, 265022, 264259, 29331822, 33657182, 29148499, 264628, 18108370, 264908, 264629, 55811576, 35695855, 265006, 265007, 264591, 21908754, 33657084, 265010, 265017, 265019, 264288
1885	85636897 (3968, 3970)	Novel Protein sim. GBank gij5712131[gbjAAD47379.1]AF12049 - (AF120499) DEM1 protein [Homo sapiens]		glycoprotein	264760, 264288, 263978, 55811576, 264637, 56182323, 18108385, 264564
1886	80200507 (3971, 3972)			UNCLASSIFIED	264488, 264629
1887	87011117 (3973, 3974)	Novel Protein sim. GBank gij4868443[gbjAAD31319.1]AF14457 - (AF144573) Mx-interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00089) - Eukaryotic protein kinase domain		22278999, 29331830, 265007, 265018, 21906768, 33657023, 264692, 264693, 18108377, 264635, 60170394, 22279002
1888	94122108 (3975, 3976)			UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264910, 264591, 264593, 264758, 264764, 264686, 264768, 265021, 264692, 264628, 264629, 35695855, 264630, 264635, 264636, 264637, 264638, 264639, 264483
1889	91225225 (3977, 3978)	Novel Protein sim. GBank gij2801701 (AF042379) - spindle pole body protein spc97 homolog GCP2 [Homo sapiens]		tubulin	60432049, 60432289, 52644045, 56182435, 264112, 265007, 33657402, 52644229, 21906765, 21906768, 21906769, 55811957, 33657023, 263967, 33657109, 18108370, 22279000, 22279002
1890	85699888 (3979, 3980)	Novel Protein sim. GBank gij5701727[dbjBAA83074.1] - (AB024729) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			264508, 264757, 264764, 18108381
1891	95353114 (3981, 3982)	Novel Protein sim. GBank gij4240287[dbjBAA74922.1] - (AB020706) KIAA0899 protein [Homo sapiens]	Contains protein domain (PF01602) - Adaptin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35696286, 56994075, 22278997, 22278999, 29331822, 29331824, 29331825, 60432289, 29331828, 264508, 264906, 264907, 264908, 56182435, 264510, 265007, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264762, 18108351, 264763, 264683, 264369, 264286, 264685, 264766, 264687, 264769, 21906765, 21906768, 21906769, 55811957, 265020, 60431528, 263974, 18108379, 35695855, 264555, 264557, 264639, 83373044, 18108384, 87168518, 60432113, 22279000, 22279002, 264564, 264488
1892	95317232 (3983, 3984)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struc	28331827, 264906, 264907, 264909, 265007, 264603, 264766, 264688, 264768, 21906768, 264628, 264635, 264636, 18108385, 56526486, 264566, 264567
1893	80054763 (3985, 3986)	Novel Protein sim. GBank gij2565091 (U80761) - CTG26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	264592, 35696423

1994	94328114 (3987, 3988)	Novel Protein sim. GBank gi15630077 gb AAD45822.1 AC00601 - (AC006017) similar to ALR; similar to AAC51735 (PID:g2358287) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	mapolymerase	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 264908, 265008, 60432229, 33657402, 60433356, 264757, 60433438, 264758, 33109954, 265011, 265017, 265018, 265019, 264684, 264369, 264685, 264686, 264768, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 18108362, 264693, 85274620, 18108370, 264635, 264555, 264556, 264557, 56182323, 83373044, 56526485, 22279000, 22279002, 264564
1995	95414353 (3989, 3990)	Novel Protein sim. GBank gi4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit		UNCLASSIFIED	264488, 18108396, 22278994, 56984075, 22278996, 35686286, 22278997, 22278999, 264259, 29147620, 56182181, 29331824, 60432289, 29331826, 29331827, 35696052, 29146499, 264905, 264907, 66712502, 56182435, 265006, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 85658542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 56181562, 264689, 21906765, 21906768, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265020, 265021, 264690, 18108361, 264693, 27486262, 27486264, 27488265, 18108370, 60431528, 18108374, 18108377, 35696423, 55811578, 65274791, 35695855, 264631, 264634, 264635, 264555, 264636, 60431850, 264557, 264558, 264559, 83373044, 20788451, 87188518, 264404, 60432113, 264567 264564
1996	80254186 (3991, 3992)	Novel Protein sim. GBank gi1791146 emb CAA60020 - (XB6028) extensin-like protein [Vigna unguiculata]		UNCLASSIFIED	
1997	87028423 (3993, 3994)	Novel Protein sim. GBank gi12642034 (AF034547) - protein phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	phosphatase	264908, 264909, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gi14589634 dbj BAA76839.1 - (AB023212) KIAA0995 protein [Homo sapiens]		UNCLASSIFIED	264113, 264685, 264555, 264567

1999	94324903 (3997, 3998)	Novel Protein sim. GBank gij5225312igb/AAD40846.1(AF072441) calchectin binding protein cabin 1 (Homo sapiens)	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35696286, 50424269, 29331827, 29331828, 35696052, 265006, 264512, 55811388, 265010, 265018, 265019, 5581150, 18108351, 264763, 264682, 264369, 264685, 264686, 56181582, 265020, 264691, 33657023, 264693, 33657109, 27486264, 18108370, 18108379, 35695855, 264634, 264635, 264636, 264555, 264557, 56182323, 18108382, 264559, 83373044, 60432113, 22279000, 264563, 264564, 264566
2000	95413705 (3999, 4000)	Novel Protein sim. GBank gij1723232ispjQ10155YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME 1		UNCLASSIFIED	52646365, 52646842, 22278994, 22278995, 22278998, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331828, 29331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21906754, 52644296, 265017, 265018, 265019, 264761, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 65274620, 52645129, 27486261, 27486262, 27486264, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526488, 22279002, 264566, 264567
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gij107560[pri]B38637 - Ras inhibitor (clone JC265) - human (fragment)		UNCLASSIFIED	264769, 52644229, 65274572, 21906768, 22278996, 35696286, 35695917, 265020, 22278999, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274791, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108385, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gij729433ispjP38637IER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P58)	Contains protein domain (PF00085) - Thioredoxin	isomerase	264907, 265006, 264910, 264603, 264692, 264629, 18108374, 264556, 264557
2003	80074449 (4005, 4006)	Novel Protein sim. GBank gij86388[pri]A27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264905, 264906, 264908, 264910, 264596, 265017, 18108351, 264692, 264629, 264634, 264565

2004	95317318 (4007, 4009)	Novel Protein sim. GBank gj4884249[embjCAB43230.1] - (AL048996) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	52645156, 52646842, 52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331824, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 264908, 264592, 60433356, 33657402, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264763, 264683, 264288, 52644229, 21906768, 21906769, 35695917, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486282, 33657349, 27486265, 35695763, 18108374, 18108376, 18108377, 35696423, 35695855, 264631, 52644332, 264558, 18108385, 56526486, 87168518, 60432113, 264483
2005	87400864 (4009, 4010)	Novel Protein sim. GBank gj3879501[embjCAA87795] - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	264488, 264906
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gj4106673[embjCAA22613] - (AL035064) queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424269, 66714117, 35696052, 264906, 66712502, 264909, 264510, 60433356, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 29148627, 21906769, 29148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810764, 55811576, 35695855, 87168518, 60432113, 264563, 264482
2007	94325556 (4013, 4014)	Novel Protein sim. GBank gj2682161[dbjBAA23712] - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265007, 264910, 264592, 264595, 264758, 265011, 264760, 264762, 264764, 264766, 264685, 264767, 264768, 264769, 55811957, 35695917, 265020, 264691, 264693, 264628, 264629, 65274791, 35695855, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 264566
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gj1550703[embjCAA69257] - (Y07960) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264909, 264768, 35695855

2009	85748240 (4017, 4016)	Novel Protein sim. GBank gi 3882305 dbj BAA34512.1 - (AB018335) KIAA0792 protein [Homo sapiens]	UNCLASSIFIED	22278998, 264259, 264810, 264591, 265017, 264881, 264683, 21906768, 264691, 33657182, 33657349, 264631, 87168518, 264404, 22279002, 264563
2010	85422458 (4019, 4020)	Novel Protein sim. GBank gi 5262629 emb CAB45753.1 - (AL080164) hypothetical protein [Homo sapiens]	eph Contains protein domain (PF00057) - Low-density lipoprotein receptor domain class A	52644507, 52645156, 52646365, 52646842, 18108397, 65274572, 22278994, 58994075, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432229, 60433356, 21906754, 52646317, 33109954, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264685, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 264691, 264692, 33657023, 263987, 52645129, 35695763, 18108376, 35696423, 65274791, 35695855, 264631, 264634, 60431850, 264637, 264638, 52644332, 60170394, 18108385, 87168518, 22279002, 264564, 264565, 264566, 264567
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gi 3347953 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]	UNCLASSIFIED	56182575, 56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35696052, 264906, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 264681, 264448, 264683, 264369, 264288, 264685, 264766, 264687, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 65274620, 33657109, 264629, 264557, 264559, 83373044, 87168518, 60432113, 22279002
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gi 1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87168559, 265019, 264682, 264288, 264686, 21906764, 265020, 265022, 33657023, 264693, 33657109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264567
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gi 450785 ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pZ-17)	dna_rna_bind Contains protein domain (PF00096) - Zinc finger, C2H2 type	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21906767, 265020, 264692
2014	87347840 (4027, 4028)	Novel Protein sim. GBank gi 127720 sp P20938 MYPO_HETFR - MYELIN P0 PROTEIN PRECURSOR	UNCLASSIFIED	264488, 29331826, 264807, 264636, 264555, 264639, 264558

2015	88094922 (4029, 4030)	Novel Protein sim. GBank gij181286 pir S22697 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	56182575, 35696286, 264259, 35696052, 264508, 264906, 264907, 264510, 264512, 87168474, 265010, 264681, 264288, 264689, 264628, 35698423, 35698585, 264639, 264563, 264564
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gij285046 pir S26413 - t-complex protein Tcp-10 - mouse		struct	264102, 264508, 264110, 265009, 33108954, 21906768, 265021, 33657109, 27486282, 263972, 18108374, 263976, 264555, 264564
2017	79464293 (4033, 4034)	Novel Protein sim. GBank gij124735 sp P18175 INVO_PIG - INVOLUCRIN		UNCLASSIFIED	264685, 264636
2018	79637067 (4035, 4036)	Novel Protein sim. GBank gij21439 0 pir S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat		phosphatase	264107, 264110, 264112, 265017, 263976
2019	87787800 (4037, 4038)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycoprotein AFGP precursor [Boreogadus salda]		UNCLASSIFIED	264259, 264508, 264591, 265018, 264682, 264288, 264688, 22278002
2020	84674476 (4039, 4040)	Novel Protein sim. GBank gij585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 264593, 33109954, 21906754, 21906768, 33657023, 33657109, 27486261, 87168518
2021	85718818 (4041, 4042)	Novel Protein sim. GBank gij4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			264757, 264767, 60170615, 18108385
2022	95295665 (4043, 4044)	Novel Protein sim. GBank gij5410230 gb AAD2982.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]			18108394, 22278999, 264259, 264905, 264906, 264908, 264595, 264762, 264769, 264634, 264636, 87168518, 60432113, 22279000, 264482, 264565
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gij5410230 gb AAD2982.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	60433438, 265017, 264686, 264692, 264693, 264636
2024	87896443 (4047, 4048)	Novel Protein sim. GBank gij4755188 gb AAD29055.1 AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	22278997, 264509, 264906, 264909, 55812038, 265017, 265021, 265022, 60170615, 264556
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gij165589 emb CAA69032 - (Y07752) perlecanin-5 [Volvox carteri]		UNCLASSIFIED	56994075, 60432049, 264508, 66712502, 264112, 60170831, 87168559, 264288, 264688, 264689, 21906766, 33657109, 18108370, 264638, 18108385, 60432113, 22279000, 22279002, 264564, 264566, 264567
2026	84122114 (4051, 4052)	Novel Protein sim. GBank gij165589 emb CAA69032 - (Y07752) perlecanin-5 [Volvox carteri]			263978, 264634, 264486
2027	80249001 (4053, 4054)			UNCLASSIFIED	

2028	94699884 (4055, 4056)	Novel Protein sim. GBank gi 1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - HECT-domain (ubiquitin-transferase).	ubiquitin	52644507, 52645156, 52646842, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331828, 29331827, 29331828, 35696052, 264906, 264907, 264808, 29331830, 52644045, 56182435, 265006, 265009, 60432228, 33657402, 264595, 264757, 55812038, 21906754, 52646317, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264369, 264766, 52644228, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 65274820, 33657109, 52645129, 18108368, 27486261, 27486262, 27486264, 27486265, 35695763, 264629, 55811576, 35696423, 35695855, 264635, 264636, 52644332, 264558, 83373044, 56526486, 22279000, 22279002, 264563, 265009, 264595, 85658542, 264555, 264556, 264557, 264558, 83373044
2029	85362032 (4057, 4058)	Novel Protein sim. GBank gi 3599940 (AF017368) - facio-genital dysplasia protein 2 [Mus musculus]	Contains protein domain (PF00621) - RhoGEF domain	UNCLASSIFIED	18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21906769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gi 5630080 [gb AAD45825.1]AC00489 - (AC004890) similar to HUB1; similar to BAA24380 (PID:g2789430) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	264591, 55811957, 18108365, 264557, 264558, 18108382, 18108384
2031	80245281 (4061, 4062)				55274572, 35696286, 29331824, 264908, 265009, 264593, 265018, 264288, 264686, 264769, 21906768, 21906767, 29146627, 264628, 35696423, 264634, 264556, 18108381, 60170394, 264559, 83373044, 18108385, 264482, 264484
2032	91232607 (4063, 4064)	Novel Protein sim. GBank gi 5689491 [dbj BAA83029.1] - (AB029000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase	56181562, 264628, 264632, 264555, 264556
2033	95000809 (4065, 4066)	Novel Protein sim. GBank gi 2494828 [sp Q64686]CAG7_RAT - ALPHA-N-ACETYLGLACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNACIII) (STY)		synthase	
2034	91232529 (4067, 4068)	Novel Protein sim. GBank gi 4826984 [ref NP_005147.1]PROD1 - UNKNOWN	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278998, 22278999, 264907, 29331830, 265008, 265018, 264681, 264682, 264684, 21906767, 21906768, 21906769, 33657109, 83373044, 56526486

2035	83553451 (4069, 4070)				264369, 264686, 265022, 56526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264369, 29148627, 60432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]	UNCLASSIFIED		65274572, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331826, 29331828, 35696052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 264584, 55812038, 33109954, 21906754, 87168559, 265017, 265018, 265019, 264762, 264369, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264563
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gi 3880625 emb CAB07859 - (Z93785) predicted using GeneFINDER; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	UNCLASSIFIED	Contains protein domain (PF01412) - Putative GTP-ase activating protein (for Arf)	22278995, 22278996, 56994075, 264259, 29331824, 35696052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264389, 264768, 264767, 264686, 18108358, 21906765, 21906769, 52644150, 33657023, 264692, 18108362, 33657109, 27485262, 18108370, 18108374, 18108379, 35698423, 65274791, 264632, 264636, 18108383, 83373044, 18108385, 87168518, 22279000, 22279002, 264563, 264584, 264566
2039	85514626 (4077, 4078)	Novel Protein sim. GBank gi 2224653 dbj BAA20813 - (AB002354) KIAA0356 [Homo sapiens]	UNCLASSIFIED	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265009, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35698423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168518, 264486
2040	95308417 (4079, 4080)		UNCLASSIFIED		264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gi 2500825 sp P70700 JRP2 MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)	mapolymerase		264488, 22278998, 35696052, 264805, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264766, 264769, 21906766, 265021, 265022, 264692, 33657109, 264628, 264629, 35698423, 35695855, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gi 4406590 gb AAD20040 - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 264259, 29331826, 35696052, 29331828, 264508, 264509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 264595, 265017, 265019, 264681, 264764, 264369, 264765, 264684, 264288, 264766, 264686, 52644229, 264769, 21908765, 35695917, 264535, 52644150, 264691, 264692, 18108365, 27486281, 27486282, 27486285, 18108374, 35696423, 65274791, 35695855, 264555, 264558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264563, 264564, 264566
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gi 5052554 gb AAD38607.1 AF14563 - (AF145632) BCDNA GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264488, 52644507, 52646365, 56894075, 22278997, 22278999, 20281171, 264259, 29331822, 29331824, 66714117, 29331826, 29331828, 33656970, 29146498, 264509, 264908, 52644045, 56182435, 265006, 33657402, 21908754, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21908766, 21906767, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35695763, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264567
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264093, 29331827, 264905, 66712502, 264592, 264889, 21908765, 21908769, 265020, 264692, 264482, 264566
2045	79635532 (4089, 4090)	Novel Protein sim. GBank gi 4406688 gb AAD20062 - (AF131852) Unknown [Homo sapiens]			264692
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gi 4406688 gb AAD20062 - (AF131852) Unknown [Homo sapiens]			264259, 264906, 264683, 22279002
2047	84578801 (4093, 4094)	Novel Protein sim. GBank gi 4101720 (AF006466) - lymphocyte specific formin related protein [Mus musculus]			22278999, 29147620, 29331824, 29146498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148629, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2048	84606378 (4095, 4096)	Novel Protein sim. GBank gi 4589656 db BAA76850.1 - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264909
2049	88094690 (4097, 4098)	Novel Protein sim. GBank gi 4589656 db BAA76850.1 - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264763, 21906767, 21906768, 264629, 264634, 264637, 22279002, 264564, 264565, 264566, 264567

2050	79633835 (4089, 4100)			UNCLASSIFIED	264693	264488, 264259, 264509, 264906, 264907, 264769, 18108374, 35696423, 264563, 264586, 264488
2051	87780168 (4101, 4102)			UNCLASSIFIED		
2052	88086393 (4103, 4104)	Novel Protein sim. GBank gi 4529889 gb AAD21812.1 - (AF134726) G9A [Homo sapiens]	Contains protein domain (PF00856) - SET domain	kinase		264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264766, 264686, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264584, 264566, 264488, 264567
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gi 2995449 emb CAA75113 - (Y14848) midline 1 protein [Mus musculus]		UNCLASSIFIED		22278996, 22278997, 264259, 29331822, 264102, 264508, 35695917, 263972, 264482
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gi 3876326 emb CAB02090 - (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain			60424179, 264094, 264259, 29331825, 60424269, 264908, 60433356, 87168559, 265019, 264760, 264288, 264686, 21906769, 33657023, 264693, 55810764, 55811576, 264635, 56182323, 60432113
2055	88259449 (4109, 4110)	Novel Protein sim. GBank gi 5353746 gb AAD42226.1 AF15913 - (AF159133) SIR2-like protein [Oryza saliva subsp. indica]		UNCLASSIFIED		264488, 29331826, 60432289, 29331828, 60433358, 265019, 264683, 264684, 265021, 33657109, 18108374, 264637, 18108385, 87168518, 60432113, 22279000, 264584

2056	88177396 (4111, 4112)	Novel Protein sim. GBank gij4828980refNP_005042.1lpQARS - glutamine-IRNA synthetase	Contains protein domain (PF00749) - IRNA synthetases class I (E and Q)	- synthase	264488, 52645156, 56182575, 22278994, 35696286, 56994075, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 60432289, 29331827, 29331828, 33656970, 264104, 264908, 264908, 265006, 265008, 60170831, 264591, 60432229, 60433438, 18108348, 21908754, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 264760, 18108351, 264681, 264682, 264448, 264683, 264369, 264288, 264685, 264687, 264688, 264689, 21908765, 21906766, 21908767, 21908769, 55811957, 35695917, 265022, 33657023, 18108362, 33657109, 18108368, 33657182, 27486261, 27486264, 27486265, 33657349, 264628, 18108370, 264629, 18108374, 18108377, 18108379, 35696423, 55811576, 20281152, 264636, 264952, 18108385, 18108388, 87168518, 264482, 264565, 264586, 264567
2057	87877905 (4113, 4114)	Novel Protein sim. GBank gij728850spIP08640JAMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		UNCLASSIFIED	52646842, 52646365, 56182575, 35696286, 22278996, 22278997, 22278998, 264093, 52645080, 35696052, 29331828, 33656970, 265009, 52646317, 55811386, 52644296, 52644229, 21908769, 35695917, 265021, 60170615, 52644150, 33657109, 33657182, 27486261, 27486262, 35695763, 35696423, 35695855, 52644332
2058	86276896 (4115, 4116)	Novel Protein sim. GBank			265007, 265008, 264591
2059	79866684 (4117, 4118)	gij119714spIP13983JEXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	29331825, 264682, 264686, 264691, 264693, 22279002
2060	83050800 (4119, 4120)	Novel Protein sim. GBank gij2811122 (U87318) - NaDC-2 [Xenopus laevis]		UNCLASSIFIED	56182575, 29331824, 29331826, 264910, 55811957, 18108370, 55811576

2061	95362204 (4121, 4122)	Novel Protein sim. GBank gi 2496947 sp Q09298 YQO9_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29331828, 264906, 66712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265009, 264910, 264591, 33657402, 21906754, 85658542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264556, 264557, 264558, 18108382, 264559, 83373044, 18108384, 56528486, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gi 4502091 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Ank repeat	strut	264905, 264628, 264907, 264629, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264563, 18108351, 264762, 264565, 264764, 264487, 264766
2063	87601272 (4125, 4126)	Novel Protein sim. GBank gi 4589562 db BAA76803.1 - (AB023176) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	oncogene	22278994, 22278999, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811576, 18108384, 22279002, 264482, 264563, 264564, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gi 1754515 db BAA13413.1 - (D87515) aminopeptidase-B [Rattus norvegicus]		hydrolase	264488, 52646365, 56994075, 35696286, 22278997, 22278998, 264259, 29331826, 60432289, 29331827, 29331828, 35696052, 264509, 265007, 265008, 60432229, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264761, 18108351, 264682, 264369, 264288, 52644229, 21906765, 21906767, 21906768, 35695917, 33657109, 18108368, 18108374, 35696423, 35695855, 52644332, 264559, 60432113, 22279000, 22279002, 264566, 264486
2065	95092238 (4129, 4130)	Novel Protein sim. GBank gi 2507144 sp Q04205 TENS_CHICK - TENSIN		kinase	264569, 18108394, 56182181, 60432289, 29331826, 264905, 264906, 264908, 60431735, 60433356, 55811386, 85658542, 265018, 55811150, 264681, 264766, 264692, 60431528, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002
2066	85793402 (4131, 4132)	Novel Protein sim. GBank gi 160171 (M58295) - circumsporozoit protein [Plasmodium yoelii]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	56182575, 264259, 264906, 264764, 264288, 56182323, 264567

2067	95303892 (4133, 4134)				35696286, 22278997, 22278998, 60432049, 264259, 60432289, 60433438, 264682, 264448, 264369, 264288, 18108355, 21906765, 21906768, 265022, 33657109, 35696423, 35695855, 264558, 264404, 264553, 264486
2068	84344754 (4135, 4136)		UNCLASSIFIED		264687
2069	94319177 (4137, 4138)	Novel Protein sim. GBank gj 3152682 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat		60424179, 56182575, 22278995, 22278996, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33656870, 264509, 264905, 56182435, 265009, 60433358, 87168559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 33657109, 263976, 264555, 264557, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gj 5712131 gb AAD47379.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]	UNCLASSIFIED		35695917, 264905, 264628, 264908, 264638
2071	86946116 (4141, 4142)	Novel Protein sim. GBank gj 3551531 dbj BAA33016 - (AB017437) avena [Gallus gallus]	Contains protein domain (PF00568) - WH1 domain		18108398, 265006, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108368, 264634, 18108381, 18108385, 18108388, 18108391
2072	91718428 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophyseal hormones, C-terminal Domain		22278995, 35696286, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 265008, 33657402, 21906754, 265011, 265019, 18108351, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264680, 264692, 35696423, 264555, 264556, 264558, 22279000
2073	27825664 (4145, 4146)	Novel Protein sim. GBank gj 1504026 dbj BAA13212 - (D86978) similar to C.elegans protein (Z37093) [Homo sapiens]	UNCLASSIFIED		264556
2074	94324767 (4147, 4148)	Novel Protein sim. GBank gj 4240317 dbj BAA74937.1 - (AB020721) KIAA0914 protein [Homo sapiens]			29331822, 264909, 264511, 265008, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264567

2075	94314886 (4149, 4150)	Novel Protein sim. GBank gj15138930[gb AAD40382.1] - (AF093880) transcription factor 11B [Homo sapiens]			18108394, 22278994, 22278996, 35696286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35698052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265009, 33657084, 264760, 264448, 264288, 264766, 264767, 264689, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 33657023, 27486262, 27486265, 35696423, 35695855, 264631, 264634, 264639, 87168518, 22279002, 264563, 264488, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385
2077	11389877 (4153, 4154)			UNCLASSIFIED	264592
2078	87539364 (4155, 4156)	Novel Protein sim. GBank gj14220590[dbj BAA74579] - (D87908) nuclear protein np95 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	ubiquitin	29331825, 265017, 265018, 264288, 265020, 265021, 264634, 56526486
2079	88085916 (4157, 4158)	Novel Protein sim. GBank gj14240255[dbj BAA74906.1] - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	264768, 22278997, 265021, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264908, 264907, 264628, 20281069, 264909, 265007, 265009, 264632, 264638, 264591, 264592, 264639, 264758, 264759, 33108954, 264604, 265018, 265019, 22279002, 264563, 264584, 264448, 264694, 264567, 264685
2080	94136689 (4159, 4160)	Novel Protein sim. GBank gj12408021[emb CAB18219.1] - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	56182575, 264092, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94847186 (4161, 4162)	Novel Protein sim. GBank gj15524734[gb AAD44360.1]AF166350 ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - CUB domain	eph	22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85658542, 265011, 265018, 265019, 21906767, 21906768, 264693, 18108385, 22279000, 22279002
2082	87628629 (4163, 4164)	Novel Protein sim. GBank gj13880558[emb CAA94234] - (Z70271) predicted using GeneFinder; similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	264907, 265019
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gj12352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278996, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264593, 21906754, 265018, 265019, 264448, 264288, 264685, 21906769, 265020, 265022, 264691, 18108370, 65274791, 264631, 264555, 264563
2084	95199298 (4167, 4168)	Novel Protein sim. GBank gj1728638[sp P39193]ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	94989476 (4169, 4170)	Novel Protein sim. GBank gi 1655699 emb CAA69032 - (Y07752) perophorin-S [Volvox carter]	UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264763, 264369, 264686, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gi 3875032 emb CAA88936 - (Z49125) similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21837); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D36149 come...	UNCLASSIFIED	35696286, 264259, 35696052, 264906, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35698423, 35698585, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264486
2087	21435337 (4173, 4174)		UNCLASSIFIED	264489
2088	84111527 (4175, 4176)	Novel Protein sim. GBank gi 3880930 emb CAA16334.1 - (AL021481) similar to Phosphoglucosylase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36188 comes from this gene; cDNA EST EMBL:D70897 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...		264488, 22278994, 35696286, 22278996, 29331827, 35696052, 33657402, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264448, 264683, 264369, 264685, 264687, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35698423, 35698585, 83373044, 87168518, 22279000, 264587
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gi 4758118 ref NP_004623.1 pDAP3 - Death associated protein 3	cadherin	18108392, 264488, 52644507, 18108394, 18108397, 52648842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264259, 29331822, 20281099, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33658970, 29146498, 29146499, 264102, 264106, 264107, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 264828, 52644045, 264909, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264592, 264593, 60433356, 33657402, 80433438, 264595, 55812038, 264758, 21906754, 33657084, 55811386, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264766, 264686, 264687, 264768, 52644229, 264688, 18108358, 56181562, 264769, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 29148629, 29148784, 35695917, 265020, 265021, 265022, 60170815, 264690

2090	88222470 (4179, 4180)				22278995, 22278998, 22278999, 264259, 29331826, 35696052, 264910, 33657402, 60433438, 33109954, 87168474, 87168559, 265018, 265019, 264681, 264684, 264686, 264687, 264688, 264689, 21908765, 21908766, 21906767, 21906769, 35695917, 265022, 60170615, 33657023, 35696423, 35695855, 264952, 18108387, 22279000, 263984, 264905, 264908, 264511, 264512, 265008, 264910, 55811386, 264288, 264768, 56181562, 21906765, 21906768, 21906769, 265022, 264628, 264563, 264567
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gi 4580997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED	homeobox	22278997, 22278999, 66712502, 87168559, 264683, 265021, 264486
2092	88223605 (4183, 4184)			Contains protein domain (PF00153) - Mitochondrial carrier proteins	264905, 264906, 264907, 264908, 264510, 265008, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gi 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Cryptotagus cuniculus]		MHC	35696286, 265017, 265018, 265019, 18108388
2094	91230928 (4187, 4188)	Novel Protein sim. GBank gi 4929551 gb AAD34036.1 AF15179 - (AF151799) CGI-40 protein [Homo sapiens]	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_ma_bind	35696286, 52644045, 265006, 265007, 265008, 87168559, 18108351, 21906769, 29148784, 265020, 33657023, 27486262, 18108374, 18108388
2095	95351526 (4189, 4190)	Novel Protein sim. GBank gi 1363238 pir JA57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264488, 264489, 65274572, 56182575, 22278996, 22278997, 22278999, 264259, 60432289, 29331826, 35696052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433356, 60433438, 264758, 264596, 55812038, 21906754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264687, 264768, 264769, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 52644150, 264691, 264692, 33657023, 264693, 27486261, 35695763, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264637, 263981, 264638, 264639, 264563, 264483, 264565, 264566, 264486, 264567
2096	94119760 (4191, 4192)	Novel Protein sim. GBank gi 3834423 (AF070689) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]			

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gi15174501 ref NP_006051.1 pLYF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170615, 264692, 33657109, 18108370, 264636, 264483 56994075, 264259, 264288, 265020, 264563
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gi1758209 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase Vh1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	
2099	95412827 (4197, 4198)	Novel Protein sim. GBank gi12695659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDP1 [Bos taurus]		phosphatase	65274572, 264905, 65274444, 264691, 264636, 264555
2100	95332656 (4199, 4200)	Novel Protein sim. GBank gi13881189 emb CAB16514 - (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337 comes from this gene; cDNA EST EMBL: C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nucl_recpt	56182575, 22278995, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 29146488, 264909, 265008, 265009, 264910, 264591, 60432229, 60433356, 33657402, 264758, 21906754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264762, 264448, 264369, 264288, 18108355, 264686, 21908765, 21908767, 21908768, 21908769, 265020, 265021, 33657023, 18108374, 35896423, 264558, 83373044, 87168518, 60432113, 22279000, 22279002 264091, 29331824, 264105, 265007, 265010, 18108380
2101	87762604 (4201, 4202)	Novel Protein sim. GBank gi14589468 dbj BAA76761.1 - (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gi13874149 emb CAA97423.1 - (Z73103) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264489, 35696286, 264259, 35696052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433356, 264758, 264601, 264605, 264760, 18108351, 264448, 264764, 264288, 264767, 264788, 21908769, 35695917, 18108374, 264634, 264555, 264559, 264563, 264482, 264486
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gi14240159 dbj BAA74858.1 - (AB020842) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	65274572, 56994075, 22278999, 264259, 29331824, 29331825, 35696052, 29331828, 66712502, 265009, 60170831, 264595, 33109954, 85658542, 87168559, 265017, 265019, 264448, 21906765, 21906768, 265022, 33657023, 27486262, 33657349, 35695763, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264584
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22279000

2105	94848080 (4209, 4210)	Novel Protein sim. GBank gi 1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....		UNCLASSIFIED	264488, 56182575, 22278994, 56894075, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264508, 264905, 264509, 264907, 29331830, 52644045, 264510, 264511, 265007, 264512, 265009, 60170831, 60432229, 33657402, 60433356, 264595, 60433438, 264758, 33657084, 87168474, 265010, 87168559, 265017, 265018, 265019, 264762, 18108351, 264684, 18108354, 264288, 264686, 52644229, 18108359, 21806765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170815, 52644150, 264692, 33657023, 264693, 33657109, 60431528, 18108374, 65274791, 35695855, 264635, 60170394, 264639, 264558, 18108385, 18108387, 56526486, 87168518, 60432113, 264564, 264566, 264567
2106	83365475 (4211, 4212)				265006, 265019
2107	79822662 (4213, 4214)	Novel Protein sim. GBank gi 3881524[emb]CAA93883] - (Z70038) ZK1067.4 [Caenorhabditis elegans]			264906, 264639
2108	842333976 (4215, 4216)	Novel Protein sim. GBank gi 3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]		UNCLASSIFIED	264905, 264806, 264907, 264908, 264909, 264758, 265011, 264600, 264601, 264764, 264766, 264767, 264768, 264769, 264693, 264629, 35695855, 264632, 264634, 264635, 264638, 264639, 83373044, 264488
2109	80478719 (4217, 4218)			UNCLASSIFIED	18108348, 264769, 18108370, 18108374, 264555, 264556, 264557, 264558
2110	87729075 (4219, 4220)	Novel Protein sim. GBank gi 481043 pir S37671 - bat2 protein - human		UNCLASSIFIED	264564
2111	87818419 (4221, 4222)	Novel Protein sim. GBank gi 2143638 pir 56542 - calmodulin-binding protein - rat		UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2112	87283783 (4223, 4224)	Novel Protein sim. GBank gi 4426629 gb AAD20459] - (AF100980) protocadherin [Rattus norvegicus]	Contains protein domain (PF00069) - struct		264508, 264806, 264591, 264682, 22279002
2113	78841388 (4225, 4226)	Novel Protein sim. GBank gi 3327184 dbj BAA31660] - (AB014585) KIAA0685 protein [Homo sapiens]	Eukaryotic protein domain (PF00028) - cadherin		265006
2114	87889342 (4227, 4228)		Cadherin domain		66714117, 29331826, 29331827, 60433438, 55812038, 265017, 265019, 264689, 21906769, 55811957, 265020, 265021, 33657109, 60170394, 264558
2115	90993785 (4229, 4230)	Novel Protein sim. GBank gi 4757890 ref NP_004328.1 pC8OR - chromosome 8 open reading frame 1		UNCLASSIFIED	65274572, 264689, 264691, 264692, 60432113

2116	88259387 (4231, 4232)	Novel Protein sim. GBank gij2246532 (U83872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	35656286, 22278999, 56182181, 29331824, 29331825, 29331827, 35696052, 284907, 56182435, 265008, 264591, 55812038, 55811386, 87168559, 264288, 264389, 21906769, 29148629, 33657023, 35695763, 55811576, 35698423, 18108385
2117	87788904 (4233, 4234)	Novel Protein sim. GBank gij2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	29331824, 264511, 265009, 33109954, 265017, 265018, 264288, 264689, 265020, 264692, 56526486, 264482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gij1079307 [p1] [B56573 - nuclear pore complex glycoprotein p62 - African clawed frog]		glycoprotein	264259, 264905, 264907, 264908, 264510, 264511, 265009, 264910, 265010, 264602, 264288, 264768, 264693, 263987, 263972, 264638, 264559
2119	86999317 (4237, 4238)	Novel Protein sim. GBank gij4321407 [gb] [AAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	264693, 18108385
2120	87789395 (4239, 4240)	Novel Protein sim. GBank gij4885527 [ref] [NP_005480.1] pNSP3 - novel SH2-containing protein 3	Contains protein domain (PF00017) - eph Src homology domain 2	eph	264091, 264259, 29331826, 29331828, 265017, 264604, 264288, 264685, 265020, 264691, 18108370, 55810764, 264555, 264636, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gij4757728 [ref] [NP_004886.1] pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	264601, 264766, 263978
2122	81230931 (4243, 4244)	Novel Protein sim. GBank gij4929551 [gb] [AAD34036.1] [AF151799] CGI-40 protein [Homo sapiens]			18108394, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 264907, 56182435, 265007, 264910, 265010, 265018, 264686, 265020, 55811576, 264555, 264637, 18108382, 83373044, 18108383, 18108384, 56526486, 264565, 264567
2123	86787898 (4245, 4246)	Novel Protein sim. GBank gij2244551 [dbj] [BAA20764] - (AB002303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	struct	18108386, 264757, 265011, 18108351, 264691, 264634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gij5689455 [dbj] [BAA83011.1] - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - PKD domain	transport	29331822, 264906, 264907, 264591, 264639, 264563
2125	95354041 (4249, 4250)	Novel Protein sim. GBank gij728831 [sp] [P39188] [ALU1_HUMAN - III] ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	264259, 264509, 264907, 264511, 85658542, 264763, 21906765, 35695917, 264636, 264486
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gij4539264 [emb] [CAB39853.1] - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264488, 264489, 29331827, 35696052, 264905, 264509, 264908, 264909, 264510, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264596, 264758, 264601, 264603, 265018, 264604, 264605, 264760, 264681, 264762, 264683, 264764, 264684, 264288, 264685, 264689, 60170615, 33657023, 33657109, 55810764, 264635, 264636, 264637, 264638, 264639, 83373044, 264564, 264566

2127	81118652 (4253, 4254)	Novel Protein sim. GBank gij4868435[gb AAD31315.1 AF143236) apoptosis related protein APR-2 [Homo sapiens]			35696286, 29331826, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 265008, 264511, 264512, 265007, 265009, 264910, 264758, 265011, 264600, 264601, 264604, 264762, 264763, 264766, 264687, 264768, 264769, 264689, 35695917, 264690, 264691, 264692, 264693, 264629, 18108374, 35695855, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264567, 56182575, 35696288, 56182181, 29331824, 60432289, 35696052, 264905, 264907, 66712502, 264908, 264909, 264510, 264512, 265009, 264910, 264591, 55812038, 265018, 264764, 264288, 264369, 264687, 264768, 55811957, 264692, 18108368, 264628, 264632, 264634, 264635, 264637, 56182323, 264639, 18108384, 18108388, 264563, 264567
2128	87414262 (4255, 4256)				56714117, 264628, 264595, 55812038, 55811150, 55811957, 264693, 18108374, 263978, 65274791, 18108381, 83373044, 22278000
2129	95102089 (4257, 4258)		UNCLASSIFIED		263981
2130	95417144 (4259, 4260)	Novel Protein sim. GBank gij2649255 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]	UNCLASSIFIED		
2131	85723065 (4261, 4262)	Novel Protein sim. GBank gij1086886 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)		35696052, 264909, 264768, 35695917
2132	95361096 (4263, 4264)	Novel Protein sim. GBank gij5689373[dbj BAA82973.1 - (AB028944) KIAA1021 protein [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase		264488, 22278999, 264259, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264910, 264591, 264592, 264595, 264758, 21906754, 33109954, 87168474, 265011, 264600, 264601, 264605, 265019, 264760, 18108351, 264681, 264762, 264764, 264288, 264684, 264766, 264686, 264687, 264768, 264769, 264688, 21908769, 264690, 52644150, 264691, 264693, 18108370, 264628, 264629, 18108372, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264636, 264555, 264637, 18108380, 264639, 264558, 56182323, 56526486, 264564, 264565, 264566, 264567

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gij4220489 (AC006069) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60424179, 52646365, 52646842, 56994075, 35696286, 22278997, 22278998, 60432049, 56182181, 66714117, 60424269, 29331826, 29331828, 35696052, 264905, 264906, 264907, 66712502, 29331830, 58182435, 265006, 264512, 265008, 60431735, 60433356, 33657402, 55812038, 33109954, 21906754, 55811386, 265010, 264603, 265017, 265018, 265019, 55811150, 18108351, 264682, 264369, 264288, 52644229, 56181562, 21906785, 21908766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 33657023, 33657109, 60431528, 18108374, 35696423, 65274791, 35695855, 264634, 60431850, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264563, 264566
2134	95412697 (4267, 4268)	Novel Protein sim. GBank gij3875351[emb](CAB09415) - (Z96047) DY3.6 [Caenorhabditis elegans]			56181686, 35696286, 21906754, 55811386, 265011, 265017, 18108351, 264765, 264766, 264688, 21906768, 35695917, 265020, 33657023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	88079813 (4269, 4270)	Novel Protein sim. GBank gij5689559[dbj](BAA83063.1) - (AB029034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22278999, 29331828, 35696052, 264906, 264908, 264910, 265009, 264591, 264758, 52646317, 265011, 8718859, 264601, 18108351, 284448, 264683, 264684, 264689, 18108359, 264691, 33657023, 264692, 35695763, 264629, 35695855, 264631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264584
2136	84346479 (4271, 4272)	Novel Protein sim. GBank gij2662167[dbj](BAA23715) - (AB007903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gij4884110[emb](CAB43262.1) - (AL050090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264569, 264909, 33109954, 264763, 21906768, 60170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gij5174779[gb](AAD40686.1) - (U87804) 50 kDa protein [Caulobacter crescentus]		ATPase_associated	264259, 29331828, 35696052, 264909, 265006, 265017, 265018, 18108351, 264288, 21906768, 33657023, 33657109, 264628, 18108374, 35695855, 264634, 264555, 264556, 264557, 264558, 264559
2139	94843882 (4277, 4278)	Novel Protein sim. GBank gij3850821[emb](CAA77135) - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]			264905, 264910, 264591, 55812038, 55811386, 8568542, 264760, 18108351, 18108359, 55811957, 265020, 265021, 33657023, 18108364, 55811576, 83373044, 18108385, 56526486, 264482

2140	87645655 (4279, 4280)	Novel Protein sim. GBank gij4417293jgb/AAD20418] - (AC007018) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264509, 265006, 264759, 265018, 264448, 264288, 21908768, 55811957, 265021, 33657023, 27488265, 35696423, 264636, 264556, 264557, 264559, 264566
2141	79623988 (4281, 4282)		UNCLASSIFIED	265020, 264693
2142	80041222 (4283, 4284)		UNCLASSIFIED	263978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank gij2135766jprj/S53362 - mucin 5AC (clone JER47) - human (fragment)	UNCLASSIFIED	22278997, 29331827, 264907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank gij2076483 (U43200) - antifreeze glycoprotein AFGP polyprotein precursor [Boreogadus saida]	UNCLASSIFIED	66274572, 264259, 29331824, 29331827, 264906, 264908, 264591, 265011, 87168559, 264600, 265019, 264288, 264768, 21906765, 21906767, 55811576, 35696423, 65274791, 22279002
2145	20564305 (4289, 4290)		UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank gij1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR:S28503) [Caenorhabditis elegans]	UNCLASSIFIED	264908, 60433356, 264686
2147	80432911 (4293, 4294)	Novel Protein sim. GBank gij3080398jembjCAA18718.1] - (AL022603) putative protein [Arabidopsis thaliana]	UNCLASSIFIED	264907, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank gij28837jpiP39194JALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY IIII	UNCLASSIFIED	264593
2149	87362022 (4297, 4298)	Novel Protein sim. GBank gij119863jpiP20693jFCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	glycoprotein	29331824, 29331826, 35696052, 264756, 87168474, 265018, 52644150, 33657109
2150	94140059 (4299, 4300)	Novel Protein sim. GBank gij5420387jembjCAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	22278998, 29331822, 29331824, 29331828, 264764, 264769, 21906766, 264486
2151	95353241 (4301, 4302)	Novel Protein sim. GBank gij5689407jdbjBAA82987.1] - (AB028958) KIAA1035 protein [Homo sapiens]		22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 29331828, 264508, 264511, 60433356, 264758, 264596, 33109954, 60174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264689, 21906765, 21906768, 21908768, 265020, 60170615, 33657109, 33657182, 33657349, 18108370, 264635, 264557, 60170394, 18108385, 87168518, 22279000, 18108397, 18108398, 265007, 264591, 265011, 18108351, 18108366, 18108374, 18108388
2152	79321640 (4303, 4304)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase	

2153	88313371 (4305, 4306)	Novel Protein sim. GBank gi14758704[refNP_004216.1]pMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263994, 52646842, 22278996, 22278998, 22278999, 264259, 29331822, 3568052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87168474, 87168559, 265017, 265019, 264760, 264288, 264359, 264766, 264687, 264769, 52644229, 21906768, 21908768, 35695917, 33657023, 33657109, 35695855, 264631, 264632, 264635, 264636, 264639, 18108385, 264483, 264554, 264488
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gi225150[prf1209265U - chorion protein B11 [Bombyx mori]		UNCLASSIFIED	56994075, 264094, 265009, 265019, 264288, 21908767, 35695917
2155	87424072 (4309, 4310)			UNCLASSIFIED	18108392, 18108398, 22278996, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264686, 265020, 264693, 264628, 56182323
2156	84295205 (4311, 4312)	Novel Protein sim. GBank gi3970966 (AC004974) - spa-1- (like, similar to AF026504 (PID:g2555183) [Homo sapiens])			265007, 264694
2157	87316344 (4313, 4314)	Novel Protein sim. GBank gi1076211[pir1S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]		UNCLASSIFIED	264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gi4650844[dbj BAA77027.1] - (AB026190) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_rna_bind	264596
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gi2879925[dbj BAA24826] - (AB007897) KIAA0437 [Homo sapiens]			29331822, 264112, 265009, 264691, 33657023, 264634
2160	16283674 (4319, 4320)				264634
2161	87739131 (4321, 4322)	Novel Protein sim. GBank gi1504006[dbj BAA13202] - (D88868) simliarto human ZFY protein. [Homo sapiens]		UNCLASSIFIED	265008
2162	94318526 (4323, 4324)			UNCLASSIFIED	65274572, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264596, 264758, 265011, 264600, 264762, 264763, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 264688, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264566, 264567
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gi3876537[emb CAA98270] - (Z73974) cDNA EST yk291f5.3 comes from this gene; cDNA EST yk291f5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278996, 264093, 264683, 33657023, 65274620, 60432113
2164	80559456 (4327, 4328)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	collagen	264503, 264637, 264565

2165	84329169 (4329, 4330)	Novel Protein sim. GBank gj1086794 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 29331830, 56182435, 265009, 21906754, 33657084, 265011, 265019, 264448, 264288, 264369, 21906765, 21906768, 21908769, 265020, 265021, 264691, 264692, 33657023, 65274620, 35695855, 264556, 60170394, 83373044, 60432113, 22279002, 264567
2166	87619934 (4331, 4332)	Novel Protein sim. GBank gj2706522[emb]CAA75816] - (Y15885) ubiquitin activating enzyme [Drosophila melanogaster]	ubiquitin		52645156, 22278994, 22278998, 66714117, 29331828, 52644045, 265018, 265019, 264369, 21906765, 21906767, 21906768, 21906769, 265021, 265022, 264693, 27486262, 35695763, 18108376, 56526486, 87168518, 264567
2167	87716864 (4333, 4334)	Novel Protein sim. GBank gj2224713[dbj]BAA20840] - (AB002384) KIAA0386 [Homo sapiens]	UNCLASSIFIED		56182575, 35696286, 29331824, 29331826, 29146488, 56182435, 265008, 265009, 264592, 264593, 33657402, 33109954, 265011, 265017, 265018, 18108351, 264369, 21906764, 21906765, 21906768, 29148627, 21906769, 52644150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 264567
2168	86999334 (4335, 4336)	Novel Protein sim. GBank gj4321407[gb]AAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	Contains protein domain (PF00664) - ABC transporter transmembrane region.	transport	66714117, 29331827, 264907, 264511, 264591, 265018, 264764, 264683, 264766, 264768, 264568
2169	87886937 (4337, 4338)	Novel Protein sim. GBank	UNCLASSIFIED		264629, 264555, 264559
2170	94141033 (4339, 4340)	gj5106521[gb]AAD39741.1[AF10536] K-CI cotransporter KCC4 [Homo sapiens]			65274572, 56182575, 22278997, 22278998, 264259, 29331825, 264509, 264908, 56182435, 60433438, 55812038, 264596, 55811386, 265019, 264762, 264763, 264448, 264764, 264684, 264288, 264766, 264685, 56181562, 264689, 55811957, 265020, 264535, 264691, 33657109, 60431528, 18108374, 35696423, 55811576, 65274791, 264634, 264639, 264558, 87168518, 60432113, 264564
2171	80194050 (4341, 4342)		UNCLASSIFIED		264369, 265020, 264558
2172	85452460 (4343, 4344)		UNCLASSIFIED		264259, 264558
2173	87036740 (4345, 4346)	Novel Protein sim. GBank gj4309681[gb]AAD15478] - (AC008930) R33423.1 [Homo sapiens]	UNCLASSIFIED		264369
2174	95003288 (4347, 4348)	Novel Protein sim. GBank gj2493778[sp]Q08456[YQ35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5]			264908, 35695855, 264555, 264557

2175	94325850 (4349, 4350)	Novel Protein sim. GBank gi1263287 (U47855) - fibronin-3 (Araneus diadematus)		UNCLASSIFIED	264488, 35696286, 20281099, 29331826, 60432289, 35696052, 264109, 284508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264598, 264758, 55812038, 265011, 264600, 264603, 264760, 264762, 264448, 264764, 284288, 264766, 264688, 264687, 21906768, 55811957, 35695917, 265020, 265022, 264691, 264692, 33657023, 264693, 264628, 264629, 55811576, 35696423, 65274791, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 284558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264486, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gi1728837 sp P39184 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00805) - oncogene Pentapeptide repeats (8 copies)	oncogene	52644507, 52646842, 22278994, 35696286, 22278996, 22278999, 29331828, 29331827, 35696052, 29331828, 33656970, 29331830, 264910, 33657402, 264758, 52644296, 87168559, 265018, 264688, 21906765, 21906767, 21906769, 35695917, 52644150, 264690, 33657023, 33657109, 52645129, 33657182, 27486261, 27486262, 33657349, 18108376, 18108377, 35695855, 87168518, 60432113, 264404, 22279000, 264486
2177	94128942 (4353, 4354)	Novel Protein sim. GBank gi15454072 ref NP_006416.1 pSLU7 - step II splicing factor SLU7		kinase	18108392, 22278997, 22278999, 264093, 33657402, 265019, 264448, 264766, 264689, 21906767, 21906768, 21906769, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gi1473407 (U08215) - NST-1 (Mus musculus)	Contains protein domain (PF00012) - eph Hsp70 protein	eph	264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644296, 87168474, 18108370, 35695855, 22279002
2179	87316275 (4357, 4358)			UNCLASSIFIED	60424269, 264760, 264628, 264632

2180	95351397 (4359, 4360)	Novel Protein sim. GBank gi 3122317 sp P90648 KMH_B_DICD1 - MYOSIN HEAVY CHAIN KINASE B (MHCK B)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 22278994, 35698286, 22278997, 22278999, 284259, 52845080, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 284508, 264509, 264908, 29331830, 264909, 264510, 265008, 265007, 33657402, 55812038, 21906754, 87168474, 87168559, 265017, 265018, 265019, 264763, 264682, 264683, 264684, 264288, 264686, 21908765, 21908768, 21908769, 265020, 265021, 265022, 52644150, 33657023, 33657109, 27486265, 33657349, 18108374, 35698423, 35698555, 263981, 60170394, 18108385, 58528486, 87168518, 60432113, 22279000, 264482, 264566, 264567, 264486 29331827, 264369, 18108376, 264564
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gi 3024689 sp Q15542 T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII-100) (TAFII100)		kinase	
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278996, 22278997, 22278999, 264259, 29331822, 56182435, 264112, 264764, 264288, 21906767, 21908768, 21906769, 33657109, 18108376, 60170394, 22279000, 22279002 264760
2183	85460649 (4365, 4366)	Novel Protein sim. GBank gi 3873406 gb AAC77482.1 - (U17129) unknown [Rhodococcus erythropolis]		Inf	29331822, 29331825, 29331826, 56182435, 265011, 264685, 264686, 21906768, 18108370, 264629, 264631, 264636, 264557
2184	87760690 (4367, 4368)	Novel Protein sim. GBank gi 3114713 (AF061346) - Edp1 protein [Mus musculus]			29331824, 264907, 66712502, 264757, 265019, 264288, 264692, 56526486
2185	87826463 (4369, 4370)	Novel Protein sim. GBank gi 5106956 gb AAD39906.1 AF11361 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]		ATPase associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264760, 264766, 55811957, 33657023, 55811576, 56182323, 264563
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gi 2864625 emb CAA16972 - (AL021811) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	35696052, 264905, 264908, 264907, 264908, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264681, 264766, 264789, 35695917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264586, 264486 18108398, 56994075, 264259, 29331824, 29331825, 66714117, 29331827, 264908, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2187	87388173 (4373, 4374)			UNCLASSIFIED	
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gi 5107816 gb AAD40129.1 AF14941 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gi 3452357 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01596) - O-methyltransferase		22278996, 264259, 29331826, 21906754, 264369, 264288, 263967

2180	87639197 (4379, 4380)	Novel Protein sim. GBank gij132575 sp P29315 RINI_RAT - RIBONUCLEASE INHIBITOR		nucleaseinhib	22278996, 22278999, 29331822, 29331824, 29331826, 265008, 264910, 60170831, 55812038, 52644296, 265010, 265018, 264685, 264688, 56181562, 21906769, 35695917, 265022, 60170394, 22279000
2181	95198928 (4381, 4382)	Novel Protein sim. GBank gij5327002 emb CAB46272.1 - (Y18503) XAP-5-like protein [Homo sapiens]			29331825, 29331826, 29331830, 264510, 264511, 264910, 264593, 264594, 264556, 264559
2182	11126316 (4383, 4384)	Novel Protein sim. GBank gij462600 sp P34400 M110_CAEEL - MIG-10 PROTEIN	Contains protein domain (PF00169) - PH domain		264558
2183	94140073 (4385, 4386)	Novel Protein sim. GBank gij5420388 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181686, 29331825, 29331827, 264508, 264909, 265008, 264592, 60432229, 264288, 264684, 264766, 35695917, 33657023, 60431602, 60431528, 55810764, 55811576, 65274791, 35695855, 60431850, 56182323, 60432113
2184	21418714 (4387, 4388)	Novel Protein sim. GBank gij2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			264592
2185	88083023 (4389, 4390)	Novel Protein sim. GBank gij2832763 emb CAA15685.1 - (AL009191) /prediction=(method:; /prediction=(method:; /match=(desc:; /motif=(desc: [Drosophila melanogaster]		UNCLASSIFIED	22278996, 22278999, 35696052, 265006, 21906754, 265017, 35695917, 265021, 265022, 35695855
2188	85091631 (4391, 4392)	Novel Protein sim. GBank gij5262487 emb CAB45699.1 - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 264259, 29331822, 66714117, 60432289, 29331827, 35696052, 29331828, 264508, 52844045, 56182435, 264510, 265007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264686, 264687, 52644229, 21906765, 21906766, 21906767, 35695917, 265022, 264691, 33657023, 264693, 18108370, 18108376, 35696423, 55811576, 65274791, 35695855, 264636, 56182323, 18108385
2187	95073813 (4393, 4394)	Novel Protein sim. GBank gij4929567 gb AA034044.1 AF15180 - (AF151807) CGI-49 protein [Homo sapiens]			264768, 264769, 21906765, 21906766, 21906767, 29148627, 55811557, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264693, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 264910, 60432229, 56182323, 33657402, 264758, 83373044, 21906754, 265018, 265019, 22279002, 264482, 264448, 264565, 264288, 264369
2188	88060914 (4395, 4396)	Novel Protein sim. GBank gij3548787 (AC005622) - R30953.1 [Homo sapiens]		UNCLASSIFIED	

2199	86054355 (4397, 4398)	Novel Protein sim. GBank gj12739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]			264105, 264110, 264112, 264688, 55811957, 33657023, 264692, 263967, 20281071, 56526486
2200	87405385 (4399, 4400)	Novel Protein sim. GBank gj3043634[dbj[BAA25481] - (AB011127) KIAA0555 protein [Homo sapiens]	struct		29331824, 264763, 264768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gj3913470[spjO57314[DHXB_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	29331824, 35696052, 264905, 264907, 33657402, 55811386, 265017, 265018, 265019, 264288, 21906788, 35695917, 265020, 265022, 33657023, 33657109, 27486261, 18108370, 35696423, 35695855, 264555, 264556, 83373044, 87188518, 60432113
2202	91672385 (4403, 4404)	Novel Protein sim. GBank gj5262665[embj[CAB45767.1] - (AL080186) hypothetical protein [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	264489, 264259, 29331824, 60432289, 35696052, 264905, 264909, 264592, 265017, 265018, 265019, 18108351, 264762, 284448, 264369, 264288, 264766, 21906765, 21906768, 264690, 264691, 264692, 33657109, 264634, 264636, 264555, 264639, 264558, 264559, 83373044, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank gj1172845[spjP46629[RB25_RABIT - RAS-RELATED PROTEIN RAB-25	Contains protein domain (PF00071) - Ras family	glycoprotein	52646365, 56994075, 264259, 29331822, 29331826, 29331827, 29331828, 264910, 265010, 265011, 87168559, 265018, 265019, 264605, 264288, 21906769, 35695917, 33657023, 264692, 33657109, 35695763, 18108376, 264638, 22279000, 264566, 264567
2204	88088871 (4407, 4408)	Novel Protein sim. GBank gj121035[spjP29348[GBT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-3 SUBUNIT (GUSTDUCIN ALPHA-3 CHAIN)	Contains protein domain (PF00503) - G-protein alpha subunit	UNCLASSIFIED	
2205	84147589 (4409, 4410)	Novel Protein sim. GBank gj4589480[dbj[BAA76768.1] - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	18108394, 18108397, 56182575, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 265008, 265009, 60432229, 265010, 265011, 265018, 264683, 264288, 264369, 264686, 21906766, 21906768, 21906769, 264690, 264691, 264693, 18108388, 55811576, 65274791, 264634, 18108381, 18108384, 60432113, 22279002, 264583, 264566
2206	20620008 (4411, 4412)	Novel Protein sim. GBank gj4557753[reljNP_000372.1pMID1 - midline 1 protein	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264591
2207	87787870 (4413, 4414)				29331822, 56182181, 29331827, 35696052, 52644045, 265006, 265019, 56181562, 55811957, 265021, 33657023, 35695763, 35695855, 60170394, 60432113, 264568
2208	86100830 (4415, 4416)	Novel Protein sim. GBank gj3986746 (AF105228) - tuftelin [Bos taurus]			264906, 265019, 18108351, 21906769
2209	87800420 (4417, 4418)		struct		264112, 265009, 264691, 18108365, 18108374, 264634, 20281166

2210	57152407 (4418, 4420)	Novel Protein sim. GBank gij728837[sp]P39194/ALU7_HUMAN - IIIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gij728837[sp]P39194/ALU7_HUMAN - IIIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	264685, 264686, 18108365, 22279002, 264482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gij3776027[emb]CAA09214] - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278999, 264082, 264094, 29331822, 66714117, 29331826, 29331828, 264907, 52644045, 265009, 60170831, 21906754, 87168559, 265017, 265019, 18108351, 264683, 18108354, 264369, 264766, 264687, 52644228, 21906765, 21906766, 21906767, 21906768, 265021, 33657109, 18108370, 18108374, 264638, 56182323, 18108384, 18108387, 87168518, 264565
2213	91219309 (4425, 4426)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			56182575, 22278996, 22278997, 35696052, 264905, 66712502, 264908, 264828, 56182435, 264112, 265008, 60431735, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 18108351, 264765, 21906765, 21906768, 21906769, 265020, 265021, 264693, 264629, 263974, 263976, 18108379, 55811576, 264556, 264637, 264558, 83373044, 22278002, 264482, 264483

2214	95361453 (4427, 4428)	Novel Protein sim. GBank gi14504325[refNP_000173.1]pHADH - hydroxyacyl- Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein). alpha su	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	264488, 52644507, 18108394, 56182575, 22278994, 22278995, 35696286, 56984075, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 52645080, 29331822, 29147620, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 20281100, 264509, 264807, 66712502, 264908, 29331830, 52644045, 56182435, 264510, 285006, 264511, 264512, 265007, 265008, 265009, 60170831, 264593, 60433356, 60433438, 33109954, 33657084, 52644298, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 264288, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 264532, 60170815, 264690, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 33657182, 27486262, 27486264, 27486265, 35695763, 18108370, 264629, 60431528, 18108374, 18108376, 55810764, 35696423, 35695855, 264634, 264636, 52644332, 264638, 264556, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279002, 264482, 264564, 264565, 264566, 264909, 265008, 264555, 264558, 87168518
2215	95418208 (4428, 4430)	Novel Protein sim. GBank gi1947160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]		
2216	87614046 (4431, 4432)	Novel Protein sim. GBank gi1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]		UNCLASSIFIED
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gi15031707[refNP_005503.1]pGARP - glycoprotein A repetitions predominant		264693
2218	85518254 (4435, 4436)	Novel Protein sim. GBank gi13878636[emb]CAA88953] - (Z49128) similar to cAMP-dependant protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492d4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00560) - Leucine Rich Repeat	264288, 33657109, 264556
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gi1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35696423, 264563
			Contains protein domain (PF01963) - TraB family	264682, 264683, 264688, 264689, 264693, 18108370, 18108376

2220	85354165 (4439, 4440)	Novel Protein sim. GBank gi 4507261 ref NP_003145.1 pSTAT - statherin			264488, 18108394, 18108395, 35696286, 264259, 264097, 60432289, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 264593, 264594, 60433356, 264595, 55812038, 264758, 85658542, 265010, 264601, 264603, 265019, 264605, 264760, 264762, 264448, 264768, 264687, 18108358, 18108357, 264768, 264784, 264369, 264766, 264769, 55811957, 264690, 264691, 33657023, 264692, 18108362, 18108368, 264628, 264629, 18108374, 263978, 264634, 264635, 264636, 264637, 264638, 18108385, 264483, 264566, 264486, 264567
2221	88060927 (4441, 4442)	Novel Protein sim. GBank gi 3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425892 (4443, 4444)			UNCLASSIFIED	264908, 265020, 35695855
2223	95091649 (4445, 4446)			UNCLASSIFIED	265010, 264685, 264690, 264693, 264628, 263974, 263976, 55811576, 264555, 264638, 83373044, 264483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gi 3876005 emb CAA84789 - (Z35719) cDNA EST EMBL:D87419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES....	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED	264259, 264509, 56182435, 265005, 265008, 265009, 264757, 21908754, 18108351, 284693, 18108374, 18108385
2225	85749484 (4449, 4450)	Novel Protein sim. GBank gi 1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans]		transport	22278994, 22278995, 22278999, 52644045, 264600, 265019, 21908765, 21908769
2226	86978953 (4451, 4452)	Novel Protein sim. GBank gi 4826524 emb CAB42852.1 - (AL049848) hypothetical protein [Homo sapiens]			264259, 29331822, 29331824, 29331825, 29331827, 264508, 284908, 265007, 264691, 264634, 264486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278999, 265006, 265008, 18108354, 29148628, 29148784, 27486261, 18108374, 264637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gi 606976 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264091, 264092, 264094, 29331822, 29331825, 66714117, 264693, 263972, 264639, 83373044, 264563
2229	88060931 (4457, 4458)	Novel Protein sim. GBank gi 3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342815 (4459, 4460)	Novel Protein sim. GBank gi 226154 pr 1412350A - DNA polymerase [Human adenovirus type 2]	UNCLASSIFIED	264488, 264768, 52644507, 264769, 21908765, 21908766, 21908767, 21908769, 22278995, 35695917, 22278998, 22278997, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21908754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567, 264563
2231	88060937 (4461, 4462)	Novel Protein sim. GBank gi 3549154 (AC005625) - R27328_1 [Homo sapiens]	UNCLASSIFIED	
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gi 5281316 gb AAD41476.1 AF13312 - (AF133124) transcription factor IIC63 [Homo sapiens]	transcript factor	18108394, 56182575, 22278995, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265006, 265007, 265008, 264910, 264758, 55812038, 264603, 265018, 265019, 18108351, 264682, 264784, 264683, 264369, 264288, 264686, 264687, 264689, 21908765, 21908766, 21908767, 21908769, 29148629, 35695917, 264690, 52644150, 264691, 33657023, 264693, 18108370, 18108374, 55811576, 35695855, 264639, 18108385, 264564, 264908, 33657402, 265018, 264288, 264686, 265020, 264635, 18108385
2233	87752822 (4465, 4466)	Novel Protein sim. GBank gi 42487933 gb AAD13780 - (AF109377) IdlBp [Mus musculus]		
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gi 1706559 sp P54352 EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)	kinase	56182435, 264369, 264688, 21908765, 265020, 264693, 264556, 56526486
2235	91012316 (4469, 4470)	Novel Protein sim. GBank gi 4872734 gb AAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	UNCLASSIFIED	22278997, 264563
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gi 1082675 pr B53814 - p20 protein - human	WD domain, G-beta repeat Contains protein domain (PF00011) - eph Hsp20/alpha crystallin family	264569, 264687, 264769, 265022, 264259, 60432049, 264691, 29331828, 60432289, 20281149, 264906, 264907, 264511, 265008, 265009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264761, 264762, 264763, 264764
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gi 4872734 gb AAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	kinase	264488, 264769, 21908765, 21908766, 21908767, 21908768, 21908769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432229, 33657402, 60433356, 60433438, 83373044, 18108385, 21908754, 18108387, 60432113, 22279000, 265019, 22279002, 264482, 18108351, 264288

2238	84998857 (4475, 4476)		Contains protein domain (PF00286) - Viral coat protein		264509, 264907, 264629, 264634, 264564
2239	87798688 (4477, 4478)				29331825, 265009, 264369, 33657109, 18108370, 18108374, 264557, 264559
2240	94121471 (4479, 4480)	Novel Protein sim. GBank gij2882311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 65274572, 56182575, 35696286, 22278997, 22278999, 264259, 29331827, 35696032, 264508, 52644045, 56182435, 264511, 265007, 265008, 265009, 60433356, 60433438, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 18108351, 264683, 264288, 264768, 264687, 264688, 264769, 21908765, 21908768, 21906769, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35696423, 35695855, 87168518, 22279000
2241	80091951 (4481, 4482)			UNCLASSIFIED	264693, 264629
2242	91228075 (4483, 4484)	Novel Protein sim. GBank gij2494312[sp]P70541[E2BG_RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)]		UNCLASSIFIED synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 264509, 265007, 265009, 264596, 21908754, 265010, 265011, 265017, 265018, 265019, 264448, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657109, 27488282, 27486264, 18108374, 35695855, 264634, 264637, 56182323, 83373044, 56526486, 87168518, 264564
2243	78902026 (4485, 4486)			UNCLASSIFIED	265008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gij2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]		UNCLASSIFIED	264604
2245	95318545 (4489, 4490)	Novel Protein sim. GBank gij470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]	Contains protein domain (PF00534) - Glycosyl transferases group 1	UNCLASSIFIED	52645156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 60433438, 264758, 21906754, 265011, 264603, 264764, 264687, 21906767, 21906768, 21906769, 55811957, 265022, 264691, 264629, 35696423, 264638, 18108387, 60432113, 22279000, 22279002, 264566

2246	94846710 (4481, 4492)	Novel Protein sim. GBank gij496096[dbj]BAA78326.1] - (ABD28068) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 35698052, 264106, 264905, 264907, 265006, 265007, 265008, 60433438, 33109954, 87168559, 265018, 265019, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 27486284, 18108370, 18108374, 65274791, 35695855, 60432113
2247	87862542 (4493, 4494)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	52645156, 52646365, 52645080, 35696052, 33656970, 52648317, 33637084, 265017, 21906768, 21906769, 35695917, 33657109, 52645129, 33657182, 27486261, 27486282, 33657349, 27486265, 18108387
2248	95412986 (4495, 4496)	Novel Protein sim. GBank gij4758502[ref]NP_004123.1]pHABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	calhepsin	264488, 264259, 264907, 29331830, 264909, 265007, 265009, 264595, 21906754, 65274444, 264603, 265019, 264762, 264448, 264288, 264688, 21906766, 55811957, 265021, 264691, 18108374, 264634, 264635, 264636, 264555, 264638, 264557, 264558, 264559, 18108383, 83373044, 18108385, 264486
2249	94685682 (4497, 4498)	Novel Protein sim. GBank gij403846] (AF107772) - TcST11 [Trypanosoma cruzi]	Contains protein domain (PF00515) - TPR Domain	eph	264766, 264628, 264636, 264637
2250	78827508 (4499, 4500)	Novel Protein sim. GBank gij3738140[emb]CAA21241] - (AL031852) valyl-trna synthetase, mitochondrial precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	264908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gij3218467[emb]CAA07090.1] - (AJ006529) putative phosphatase [Gallus gallus]		UNCLASSIFIED	264259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264760, 264448, 264684, 264288, 264690, 264628, 55811576, 264555, 264556, 264557, 264558, 264559, 264568
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gij4929325[gb]AAD33953.1]AF14531 - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	Contains protein domain (PF01813) - ATP synthase subunit D	synthase	264092, 264094, 264259, 29331822, 66714117, 29331828, 264102, 264103, 264104, 264105, 264109, 264112, 264511, 265007, 60433356, 265010, 18108351, 21906767, 21906768, 264691, 263974, 263977, 264488, 264567
2253	91010703 (4505, 4506)			UNCLASSIFIED	65274572, 265019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank glj4502847[etNP_001271.1]pCIRB - cold inducible RNA- binding protein	Contains protein domain (PF000076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	284569, 18108394, 18108398, 58182575, 56994075, 35696286, 22278999, 264094, 60432049, 284259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 284106, 264508, 284509, 284908, 284907, 28331830, 66712502, 264908, 284909, 284510, 265006, 284511, 265007, 265008, 265009, 60170831, 60432229, 60433356, 60433438, 284758, 85858542, 265010, 265011, 87168559, 265017, 265018, 265019, 284448, 264764, 284288, 284369, 284768, 284686, 264768, 284769, 21906765, 21906767, 55811957, 264691, 33657023, 264692, 18108362, 65274620, 263969, 284628, 18108370, 60431528, 263972, 264629, 18108372, 18108377, 18108379, 55811576, 35696423, 35695855, 264630, 264634, 264635, 264636, 264558, 263981, 264638, 56182323, 60170394, 264558, 18108381, 18108382, 83373044, 18108385, 87168518, 60432113, 22279002, 284482, 284564, 284565, 284486, 284587, 18108391
2255	81010546 (4509, 4510)	Novel Protein sim. GBank glj5541865[etmbjCAB51072.1] - (AL096858) hypothetical protein [Homo sapiens]	Contains protein domain (PF000076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	struct	65274572, 58182575, 22278997, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264508, 264905, 264906, 264907, 66712502, 264908, 56182435, 284510, 284511, 265008, 264593, 284595, 21906754, 33109954, 87168474, 265011, 265017, 265019, 264682, 264764, 264369, 284288, 284768, 284685, 284686, 284768, 21906765, 21906768, 21906769, 21906769, 265020, 60170615, 52844150, 284690, 264692, 284693, 33657109, 33657349, 264632, 264636, 52644332, 56182323, 22279000, 22279002
2256	87020531 (4511, 4512)	Novel Protein sim. GBank glj3327174[etbjBAA31655] - (AB014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	264768, 264689, 18108374
2257	80088235 (4513, 4514)			UNCLASSIFIED	22278996, 22278998, 264681, 21906765, 21906768, 284587
2258	88090516 (4515, 4516)	Novel Protein sim. GBank glj3025446 (AC004528) - R32184_2 [Homo sapiens]	Contains protein domain (PF000060) - Ligand-gated ion channel	misc_channel	264808, 264592, 264764

2259	85384155 (4517, 4518)	Novel Protein sim. GBank gi 4884140 emb CAB43278.1 - (AL050110) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108398, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331827, 264905, 66712502, 264908, 264909, 56182435, 265007, 265008, 60432229, 33657084, 87168559, 18108351, 264448, 284683, 264288, 264369, 56181562, 265021, 60170615, 264690, 33657109, 60431528, 18108374, 52644332, 56182323, 18108385, 22279000, 22279002, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gi 3080663 (AC004614) - similar to f-spondin proteins AB006086 (PID:g2529225) [Homo sapiens]	Contains protein domain (PF00090) - oxidase Thrombospondin type 1 domain		56182575, 265020, 264905, 264906, 264908, 35686423, 264511, 264635, 55812038, 264758, 265018, 265019, 264605, 264760, 264563
2281	88074157 (4521, 4522)	Novel Protein sim. GBank gi 3334526 emb CAA16138 - (AL021308) predicted using FGENEH [Homo sapiens]		UNCLASSIFIED	
2262	91639282 (4523, 4524)	Novel Protein sim. GBank gi 487759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]			56182575, 22278999, 29331822, 29331825, 60432289, 29331827, 35696052, 264508, 66712502, 52644045, 56182435, 265006, 265008, 265009, 60433356, 55812038, 265010, 265017, 265019, 264288, 264369, 21906765, 21906767, 55811957, 35695917, 52644150, 33657023, 33657109, 55811576, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gi 3341697 (AC003672) - hypothetical protein [Arabidopsis thaliana]			22278994, 22278997, 264907, 264828, 52644150, 18108381, 264893, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gi 657601 (U66220) - unknown [Nannocystis exedens]		UNCLASSIFIED	264686, 264488, 264768, 264769, 264691, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 35695855, 264510, 264511, 264512, 265007, 265009, 264638, 264639, 264757, 264758, 18108385, 265011, 264760, 264564, 264565, 264764, 264566, 264766, 264768
2265	86918663 (4529, 4530)	Novel Protein sim. GBank gi 477072 pir A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264689, 264910, 264764
2266	87773458 (4531, 4532)	Novel Protein sim. GBank gi 3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF01305) - Ribosomal protein L15 amino terminal region	ribosomal prot	22278995, 22278997, 22278999, 264259, 265008, 265007, 265009, 60433438, 21906754, 265010, 265011, 265017, 264448, 264683, 264288, 264689, 21906765, 21906768, 35695917, 265021, 18108374, 264638, 22279000, 22279002, 264566, 264487

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gij3560229[emb]CAA20697.1] - (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 35696052, 29331828, 264905, 264509, 264907, 264908, 264909, 264512, 265009, 264910, 264593, 33657402, 265010, 265018, 264762, 264448, 264288, 264369, 264768, 52644229, 35695917, 264691, 33657023, 18108382, 33657109, 35698423, 264634, 18108381, 87168518, 264566
2268	85693687 (4535, 4536)	Novel Protein sim. GBank gij728632[sp]P39189[ALU2_SB WARNING ENTRY IIII	cadherin		264488, 264259, 264509, 264595, 265010, 265017, 264766, 18108385, 264486
2269	88177977 (4537, 4538)	Novel Protein sim. GBank gij103418[pir]S17885 - Tcd37 protein - fruit fly (Drosophila melanogaster)	UNCLASSIFIED		56182575, 60432049, 265007, 265009, 264591, 87168559, 264605, 18108351, 21908764, 265020, 264629, 60431528, 264638, 18108385, 18108387, 60432113
2270	80410327 (4539, 4540)				264763
2271	91010392 (4541, 4542)		cyto450		264909, 56182435, 265008, 55812038, 55811957, 33657023, 264693, 33657109, 55810784, 55811576, 56182323
2272	84208220 (4543, 4544)		UNCLASSIFIED		264905, 264908
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gij4176370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin		52645156, 22278996, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264909, 265006, 264593, 60433438, 21908754, 265018, 264689, 21908765, 21908766, 21908767, 21908769, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486264, 18108376, 35696423, 35695855, 264630, 52644332, 264558, 56182323, 22279002
2274	91640217 (4547, 4548)	Novel Protein sim. GBank gij1480112[emb]CAA67961] - (X99842) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52645156, 22278997, 22278999, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264591, 21908754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264766, 21908765, 21908766, 21908767, 21908768, 52644150, 264693, 18108384, 35695763, 18108374, 35698423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87168518, 22279002
2275	88082501 (4549, 4550)	Novel Protein sim. GBank gij3165406 (AC004755) - [os37502_2 [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	
2276	11287447 (4551, 4552)		UNCLASSIFIED		264555, 264556

2277	88084123 (4553, 4554)	Novel Protein sim. GBank gii2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D48802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278999, 35696052, 265008, 265019, 264369, 265020, 265022, 55810764, 264404, 22278002
2278	84133079 (4555, 4556)	Novel Protein sim. GBank gii2618702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278997, 29331826, 60433356, 60433438, 21906754, 285018, 33657023, 264639, 83373044, 264565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gii119714 [sp]P13983 [EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)]		UNCLASSIFIED	264766, 264565
2280	84239723 (4559, 4560)				
2281	95293048 (4561, 4562)	Novel Protein sim. GBank gii4240299 [dbj]BAA74928.1] - (AB020712) KIAA0905 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	265008, 33109954, 265010, 265019, 265020, 264092, 264259, 29331822, 29331824, 29331826, 35696052, 264107, 264908, 264909, 52844045, 265006, 33657402, 60433356, 264758, 265011, 285019, 264881, 264683, 264684, 264686, 21908765, 21908767, 21906768, 21906769, 60170615, 264690, 52644150, 18108362, 264692, 18108368, 18108374, 263978, 264631, 18108381, 264559, 18108385, 56528486, 22279000, 264566, 264567
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gii1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	264488, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265019, 18108351, 21906767, 21906768, 55811957, 33657023, 52645129, 33657109, 33657182, 27486282, 263972, 55811576, 87168518, 20281169
2283	95362388 (4565, 4566)	Novel Protein sim. GBank gii2495729 [sp]Q92556 [Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)]		UNCLASSIFIED	60424179, 56182575, 22278994, 35696286, 22278997, 22278999, 29331822, 29331824, 56182181, 29331825, 29331827, 35696052, 29146499, 264905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33109954, 33657084, 55811388, 87168474, 265010, 265011, 265018, 265019, 55811150, 264683, 264369, 264288, 264688, 21906765, 21908767, 21908768, 29148627, 21908769, 55811957, 265020, 265022, 33657182, 27486261, 18108370, 264628, 18108374, 55810764, 18108379, 55811576, 35696423, 35695855, 264630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264567

2284	95414955 (4567, 4568)	Novel Protein sim. GBank gi 2498787 sp Q64311 PNAD_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAAL)			60424179, 52644507, 18108394, 52646842, 22278994, 35696286, 22278996, 22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331830, 52644045, 56182435, 33657402, 60433438, 33109954, 21906754, 85658542, 87168559, 265018, 265019, 55811150, 264682, 264369, 21906765, 21906766, 21908767, 21908768, 21906769, 55811957, 35695917, 285020, 265021, 60170815, 33657023, 33657182, 27486262, 27486264, 27486265, 18108376, 55810764, 35698423, 35695855, 60431850, 87168518, 60432113, 264482, 264584
2285	87781484 (4569, 4570)	Novel Protein sim. GBank gi 3342234 (U83909) - nuclear antigen EBNA-1 [Cercopithecine herpesvirus 15]	collagen		35696052, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264595, 264760, 18108351, 264682, 264763, 264685, 264766, 264686, 264768, 264693, 264629, 35695855, 264631, 264634
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gi 3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]	kinase		35696286, 58182435, 60170831, 264591, 60432229, 264592, 264593, 264594, 264595, 55812038, 264596, 87168474, 35695917, 264692, 55811576, 264555, 264557
2287	82986696 (4573, 4574)	Novel Protein sim. GBank gi 630905 pir S42731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)	UNCLASSIFIED		264682
2288	94133083 (4575, 4576)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!	lm7		22278995, 56994075, 22278997, 22278999, 264259, 60432289, 264508, 264512, 265008, 33657402, 265017, 265018, 265019, 18108351, 264448, 21906765, 21906766, 21906767, 21906768, 33657023, 264557, 22279000, 22279002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]	kinase		
2280	88084137 (4579, 4580)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]	UNCLASSIFIED		264683
2291	84285281 (4581, 4582)	Novel Protein sim. GBank gi 3253120 (AC005175) - R31449_3 [Homo sapiens]	struct		18108394, 264907, 265006, 265009, 33109954, 52646317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2282	94328834 (4583, 4584)	Novel Protein sim. GBank gj14803672[emb]CAB42643.1]- (A133769) nuclear transport receptor (Homo sapiens)		UNCLASSIFIED	56182575, 35696286, 56994075, 29331824, 29331825, 35696052, 56182435, 60433438, 55812038, 33109954, 87168474, 87168559, 265018, 18108351, 264763, 264448, 264369, 264288, 58181562, 264769, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 33657023, 264693, 65274620, 33657109, 27486264, 264629, 55810764, 55811576, 35695855, 58182323, 56526486, 87168518, 22279000, 264567
2283	87759213 (4585, 4586)	Novel Protein sim. GBank gj3252981 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	sinud	264488, 18108397, 35696286, 264092, 264259, 29331822, 29331826, 264906, 264908, 264511, 264512, 265009, 264910, 18108351, 264764, 264369, 264288, 264685, 264766, 265020, 265022, 264534, 35696423, 264631, 264637, 18108381, 58182323, 264639, 18108385, 264404, 264563, 264565
2284	86693580 (4587, 4588)	Novel Protein sim. GBank gj2062680 (U88964) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - Exonuclease	nuclease	22278997, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35696052, 265018, 264684, 264288, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 33657109, 18108376, 35696423, 35695855, 264634, 22279000, 22279002, 264563, 264486
2285	95312200 (4589, 4590)			UNCLASSIFIED	22278996, 60432289, 264682, 264683, 264689, 18108374
2286	80030781 (4591, 4592)				263974, 263978
2287	94321251 (4593, 4594)	Novel Protein sim. GBank gj5689501[dbj]BAA83034.1]- (AB029005) KIAA1082 protein (Homo sapiens)		transcriptfactor	264488, 65274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331824, 29331828, 29331828, 35696052, 264907, 264908, 52644045, 56182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812038, 21906754, 265011, 265018, 265019, 264448, 264764, 264288, 264766, 21906765, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 60170394, 83373044, 18108385, 56526486, 264564, 264486

2298	95312207 (4595, 4596)	Novel Protein sim. GBank gij3875051[emb]CAB02849) - (Z81050) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D85584 comes from this gene; cDNA EST EMBL:D89046 comes from this gene; cDNA EST yk366b12.3 comes from this gene; cDNA EST yk366b12.5 comes from this gene ...		collagen	6042478, 56181686, 22278995, 35686286, 22278996, 22278998, 22278999, 284490, 264259, 29331822, 29331824, 66714117, 60424269, 35686052, 29331828, 66712502, 56182435, 264510, 265006, 60433438, 21906754, 33109854, 55811386, 285010, 265018, 55811150, 264762, 18108351, 264682, 264683, 264288, 264684, 264686, 264688, 56181562, 264689, 21906766, 21906767, 29148629, 55811957, 29148784, 35695917, 265020, 18108362, 33657023, 18108364, 33657109, 60431602, 18108370, 60431528, 18108374, 55810764, 35698423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22278000, 264482, 264567, 264486
2299	80193720 (4597, 4598)			UNCLASSIFIED	264369
2300	84124346 (4599, 4600)	Novel Protein sim. GBank gij2443886 (AC002284) - Unknown protein [Arabidopsis thaliana]			264488, 22278996, 22278999, 264259, 29331824, 66714117, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 265008, 284910, 265009, 264758, 265010, 87168559, 264600, 265018, 264760, 264762, 18108351, 264764, 264766, 264768, 264769, 21906766, 21906767, 35695917, 265021, 264691, 33657023, 35695763, 18108370, 18108374, 35698423, 35695855, 264631, 264636, 264638, 18108385, 22279002, 264553
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gij2143637[pr]84505 - calcium-dependent actin-binding protein - rat		struct	264908, 264758, 265017, 21906765, 83373044, 264563
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gij2887497 (AC004144) - R34001.1 [Homo sapiens]		UNCLASSIFIED	57644045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gij4884194[emb]CAB43220.1) - (AL049946) hypothetical protein [Homo sapiens]	Contains protein domain (PF00047) - struct Immunoglobulin domain		264259, 60432049, 264907, 264909, 264910, 60432229, 33657402, 265011, 265018, 264762, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gij2494162[sp]Q10005[YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR		UNCLASSIFIED	264259, 29331824, 21906767, 33657182, 33657349
2305	90935911 (4609, 4610)	Novel Protein sim. GBank gij4872686[gb]AAD34738.1) - (AF132150) unknown [Drosophila melanogaster]			83274572, 22278996, 264908, 265006, 21906769, 264691, 264488

2308	95334940 (4611, 4612)	Novel Protein sim. GBank gi 4929565 gb AAD34043.1 AF15180 - (AF151806) CGI-48 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	264488, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264907, 29331830, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 33657402, 21906754, 85658542, 265010, 265011, 264601, 265017, 265018, 264604, 265019, 18108351, 264448, 264288, 264766, 264768, 21906765, 21906766, 21906767, 21906768, 29148629, 28148784, 35695917, 265020, 265021, 265022, 33657023, 264692, 18108370, 18108374, 18108376, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 264566, 264486
2307	79415283 (4613, 4614)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		UNCLASSIFIED	264828
2308	87608409 (4615, 4616)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		synthase	35696286, 264259, 29331822, 29331824, 264112, 264512, 264757, 21906754, 264288, 264690, 27486284, 264631, 264634, 264404
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi 3878058 emb CAB17070 - (Z99942) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72944 comes from this gene; cDN...		glycoprotein	18108397, 22278995, 22278997, 22278998, 22278999, 60432049, 29331822, 29331826, 60432289, 68712502, 60432228, 60433356, 60433438, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21906766, 21906768, 265020, 264691, 264692, 264693, 65274620, 65274791
2310	79601668 (4619, 4620)	Novel Protein sim. GBank gi 2137337 pir j 48281 - gene mCBP protein - mouse	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264508
2311	87721189 (4621, 4622)	Novel Protein sim. GBank gi 2137337 pir j 48281 - gene mCBP protein - mouse		transcriptfactor	18108397, 56182575, 22278995, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 264510, 264511, 265006, 264512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 264683, 264288, 264369, 264686, 33657023, 20281149, 20281069, 264628, 263972, 55811576, 35696423, 20281071, 264632, 264636, 18108385, 18108387, 87168518, 22278990, 264563, 264486

2312	87549681 (4623, 4624)	Novel Protein sim. GBank gjl2911264 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56994075, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 52644045, 60432229, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 60170815, 33657023, 27486281, 27486264, 35696423, 35695855, 18108385, 22279000, 22279002 263981
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gjl3043626(dbj BAA25477) - (AB011123) KIAA0551 protein [Homo sapiens]			
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gjl5596714(emb CAB51401.1) - (AL035398) dJ796117.2 (CGI-51) [Homo sapiens]	UNCLASSIFIED		52644507, 52646365, 52646842, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 52644045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906766, 21906768, 35695917, 52644150, 33657023, 33657109, 52645129, 33657349, 35695763, 18108374, 35696423, 35695855, 52644332, 22279000, 22279002, 264553, 264557
2315	80430119 (4629, 4630)		UNCLASSIFIED		264905, 264906, 264767, 264768, 264693, 55811576, 264635, 56182323, 18108385
2316	94312191 (4631, 4632)	Novel Protein sim. GBank gjl5531827(jb AAD44488.1) - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - glycoprotein UBX domain		52644507, 52645158, 52646365, 22278994, 22278995, 22278996, 56994075, 35696288, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264906, 264907, 29331830, 52644045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906754, 52646317, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264681, 264763, 264448, 264683, 264369, 52644229, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 18108362, 52645129, 33657182, 33657349, 35695763, 18108370, 18108376, 35696423, 35695855, 264631, 264556, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113, 22279000, 264566, 264567

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 264910, 60432228, 264686, 264687, 264688, 264689, 264558, 18108385
2318	79959879 (4635, 4636)			UNCLASSIFIED	264488, 264569, 18108396, 52646365, 22278994, 22278995, 22278996, 58994075, 35686286, 22278997, 22278998, 264259, 52645080, 29331825, 29331826, 29331827, 29331828, 29331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21908754, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 264369, 52644229, 21908764, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27486284, 33657349, 35695763, 18108370, 18108376, 18108379, 35698423, 264558, 83373044, 18108385, 56526486, 87168518, 264564, 264565, 264566
2320	91622426 (4638, 4640)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	22278994, 60432049, 60432289, 29331827, 264511, 265008, 52646317, 265017, 265019, 21908765, 18108372, 18108387, 22279002, 264488, 264687, 18108394, 264689, 21908765, 18108397, 18108398, 21908767, 21908768, 65274791, 22278995, 35695855, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170815, 284555, 264636, 264556, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264693, 60433356, 264559, 60433438, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2321	94320377 (4641, 4642)	Novel Protein sim. GBank gi 3873837 emb CAB02700 (Z81029) Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154); cDNA EST EMBL: T00543 comes from this gene; cDNA EST EMBL: T01062 comes from this gene; cDNA EST EMBL: T01321 comes from this gene; cDNA EST EMBL: T02288 com...		UNCLASSIFIED	
2322	87803165 (4643, 4644)	Novel Protein sim. GBank gi 5678957 emb CAB51685.1 (AL109630) BACR7A4.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264768, 264638

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gi 2494162 sp Q10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H8.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00226) - eph DnaJ domain	22278994, 22278995, 22278997, 60432049, 264259, 29331822, 33656970, 264509, 56182435, 264511, 265008, 60433356, 60433438, 55812038, 33109954, 21906754, 85658542, 87188474, 285011, 87168559, 265017, 265019, 264760, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21906765, 21906767, 21906768, 55811957, 35695917, 265021, 33657023, 18108362, 27486262, 55811576, 264631, 264555, 83373044, 87168518, 60432113, 22279002 264592, 264593, 265020
2324	86633607 (4647, 4648)	Novel Protein sim. GBank gi 2494162 sp Q10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H8.1 IN CHROMOSOME II PRECURSOR	ATPase associated	265020
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gi 2494162 sp Q10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H8.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00067) - cyto450 Cytochrome P450	265006, 264759, 35695855, 56182323
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi 231885 sp P29981 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	UNCLASSIFIED	
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gi 231885 sp P29981 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 265007, 264512, 264910, 264756, 265010, 264766, 264768, 264769, 33657023, 264693, 264628, 264631, 264634, 264638, 264639, 264486
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi 231885 sp P29981 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	UNCLASSIFIED	60433438, 264595, 265017, 264766, 264692, 264629, 264635, 264636, 264638, 56182323, 60432113, 264566
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi 1169343 sp P42209 DIF6_MOUSE - DIFF6 PROTEIN	Contains protein domain (PF00735) - Cell division protein	265017, 264685, 60432113, 264088
2330	87335396 (4659, 4660)	Novel Protein sim. GBank gi 5679136 gb AA046874.1 AF16093 - (AF160934) BcDNA LD14189 [Drosophila melanogaster]	transport	265009
2331	86990483 (4661, 4662)	Novel Protein sim. GBank gi 5679136 gb AA046874.1 AF16093 - (AF160934) BcDNA LD14189 [Drosophila melanogaster]	ATPase associated	35696286, 22278998, 29331824, 60424269, 265006, 265008, 265018, 264448, 264764, 21906765, 35695917, 35695855, 264636, 22279000, 264566
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi 2104452 emb CAB08779 - (Z95397) unknown [Schizosaccharomyces pombe]	UNCLASSIFIED	56182575, 56994075, 29331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263976
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gi 3879985 emb CAA92691.1 - (Z68318) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL:C07930 comes from this gene; cDNA EST EMBL:C08493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST...	UNCLASSIFIED	
2334	84319788 (4667, 4668)	Novel Protein sim. GBank gi 4966270 gb AA052261.2 - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E- value=1e-13, N=1 [C...]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	56182575, 29331825, 21906768, 264636, 83373044

2335	80046103 (4669, 4670)	Novel Protein sim. GBank gi 3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00612) - IQ calmodulin-binding motif	struct	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gi 1929056jemb CAA72805j - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	264907, 35695917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gi 4495063jemb CA839181.1j - (Z85986) dJ108K1.1.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]		UNCLASSIFIED	35696286, 22278999, 56182181, 29331825, 60424269, 56182435, 33657402, 55812038, 55811386, 265017, 265018, 265019, 21906768, 35695917, 284691, 33657023, 33657109, 263972, 35696423, 35695855, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gi 2224689jdbj BAA20829j - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	UNCLASSIFIED	18108394, 29331822, 66714117, 60432289, 264906, 56182435, 265009, 60433438, 264596, 265010, 265019, 18108354, 264288, 264368, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85663319 (4677, 4678)	Novel Protein sim. GBank gi 3873550jemb CAA22127j - (AL033534) serine-rich protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264592, 264369, 264691, 264558
2340	90937716 (4678, 4680)				65274572, 22278994, 35696286, 22278997, 22278999, 264259, 29331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109954, 265017, 265018, 264768, 264685, 21906769, 35695917, 284691, 264692, 35696423, 87168518, 22279000
2341	8775281 (4681, 4682)	Novel Protein sim. GBank gi 3874563jemb CAB02797j - (Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264259, 264908, 264809, 264682, 22279000, 264488, 65274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35696052, 264905, 264509, 29331830, 265006, 60170831, 60432229, 60433356, 87168474, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810784, 35696423, 55811576, 264556, 264558, 18108385, 60432113, 284583, 264584, 264585, 264586, 284587, 264807, 264512, 265011, 264683
2343	87775448 (4685, 4686)	Novel Protein sim. GBank gi 4929741jgb AAD34131.1j AF151894 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	
2344	78953198 (4687, 4688)	Novel Protein sim. GBank gi 2506307j sp P13944 CA1C_CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00092) - von Willebrand factor type A domain	UNCLASSIFIED	264758
2345	94318799 (4689, 4690)			collagen	264488, 264259, 66712502, 264759, 83373044, 264568

2346	94131820 (4691, 4692)	Novel Protein sim. GBank gi 1255411 (U53153) - one short region of weak similarity to S. cerevisiae protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to S. cerevisiae glucose repression mediator protein (SP:P14922) [Caenorhabditis elegans]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35696286, 22278998, 264259, 35696052, 29331828, 33657402, 60433356, 33109954, 87188559, 264603, 265019, 18108351, 264681, 264685, 21908768, 265021, 33657109, 55811576, 35695855, 264637, 52644332, 264557, 83373044, 22279000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264683, 264684, 264766, 264687, 264688, 264691, 264692, 55811576
2348	95196133 (4695, 4696)	Novel Protein sim. GBank gi 1929056[emb]CAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	18108394, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264288, 264766, 264768, 264689, 35695917, 264693, 264628, 18108370, 264628, 18108374, 35696423, 264631, 264635, 264636, 264637, 264638, 264639, 83373044, 18108385, 264567, 264486
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gi 4884106[emb]CAB43254.1] - (AL050062) hypothetical protein [Homo sapiens]			35696052, 29146499, 264908, 264369
2350	88260594 (4699, 4700)				22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33109954, 21906754, 265010, 87188559, 265018, 265019, 284761, 264681, 264288, 18108357, 21906766, 21906767, 264691, 264692, 35695855, 87188518, 22279000, 22279002, 264482
2351	86968042 (4701, 4702)	Novel Protein sim. GBank gi 728832[sp]P39189[ALU2_HUMAN - III] ALU SUBFAMILY SB WARNING ENTRY IIII		kinase	56182575, 264809, 265006, 264558
2352	87337186 (4703, 4704)	Novel Protein sim. GBank gi 731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank gi 1346855[sp]P48809[RB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 264692, 264636
2354	87337189 (4707, 4708)	Novel Protein sim. GBank gi 731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264908, 265006, 265008

2355	91638786 (4709, 4710)	Novel Protein sim. GBank gjl4938503[emb]CAB43861.1] - (AL078465) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56894075, 22278996, 35696286, 22278999, 264259, 29331825, 29331826, 29331828, 29146498, 264905, 264908, 265008, 264758, 87169474, 265010, 265017, 264687, 21908765, 21908767, 21908769, 264691, 264692, 263987, 18108370, 67168518, 22279000
2356	95327688 (4711, 4712)	Novel Protein sim. GBank gjl513920[gb]AAD40377.1] - (AF092135) PTD014 [Homo sapiens]			52644507, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 29331828, 264908, 66712502, 264512, 265007, 265008, 60170831, 60432229, 60433356, 60433438, 264758, 52646317, 33109954, 21906754, 55811386, 87169474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264369, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170815, 33857109, 27486264, 35695763, 55810764, 18108379, 35696423, 55811578, 35695855, 60170394, 56182323, 83373044, 18108385, 56526486, 264404, 60432113, 22279000, 264482, 264563, 264566, 264486, 264567
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gjl4929741[gb]AAD34131.1]AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264488, 264769, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264762, 264565, 264566, 264359, 18108354
2358	87777078 (4715, 4716)	Novel Protein sim. GBank gjl4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 22278999, 264509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833986, 18108374, 264556, 18108385, 264482
2359	87755859 (4717, 4718)	Novel Protein sim. GBank gjl1086830 (U41264) - coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g6.5; coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk16g12....		UNCLASSIFIED	35696286, 22278998, 264905, 264511, 265007, 265008, 60433438, 264288, 264686, 21908769, 265020, 264692, 35695855, 264558, 56526486, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gjl3881545[emb]CAA93779] - (Z59804) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 263981, 22279000
2361	94232191 (4721, 4722)	Novel Protein sim. GBank gjl746487 (U23514) - No definition line found [Caenorhabditis elegans]			22278995, 22278999, 264512, 265009, 264757, 21906765, 65274620, 18108370, 60431528, 18108374, 264635, 60170394, 264482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank gij1171093[sp]P19706[MYSB.ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)]		UNCLASSIFIED	22278998, 264259, 29331822, 29331824, 60432289, 264509, 264512, 60432229, 60433356, 264448, 264682, 264683, 264369, 21906765, 21906768, 21906769, 60432113, 22279000, 22279002
2363	95006635 (4725, 4726)	Novel Protein sim. GBank (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264907, 264629, 264635
2364	94827104 (4727, 4728)	Novel Protein sim. GBank gij5639830[gib]AAD45886.1[AF14601 - (AF146018) hydroxypyruvate reductase (Homo sapiens)]	Contains protein domain (PF00338) - D-isomer specific 2-hydroxyacid dehydrogenases	reductase	264488, 18108394, 264887, 18108398, 22278996, 56994075, 3569286, 22278997, 22278998, 264259, 66714117, 29331825, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 265006, 264512, 265007, 265008, 33657402, 264758, 21906754, 87168474, 265010, 87168559, 264603, 265017, 265018, 265019, 264760, 264762, 18108351, 264448, 264764, 264683, 264684, 264288, 18108355, 264766, 18108358, 264689, 18108359, 21906765, 21906766, 21906767, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 18108368, 18108370, 18108374, 35696423, 35695855, 264635, 264556, 264557, 264639, 60170394, 83373044, 18108383, 18108384, 18108385, 18108388, 56526486, 264482, 264564, 264486
2365	94140746 (4729, 4730)	Novel Protein sim. GBank gij11840045 (U49082) - transporter protein [Homo sapiens]		transport	22278998, 22278998, 22278999, 264907, 264909, 264910, 33657402, 264758, 264600, 264766, 264687, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 83373044, 264566
2366	94312388 (4731, 4732)			UNCLASSIFIED	52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264766, 264689, 21906766, 21906769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264564, 264568
2367	94140910 (4733, 4734)	Novel Protein sim. GBank gij11065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35696286, 21906768, 55810764, 65274791, 264567
2368	94322190 (4735, 4736)				264628

2369	94314334 (4737, 4738)	Novel Protein sim. GBank gjl5360901[dbj BAA82158.1] - (AB029343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52644507, 52646842, 35696286, 264092, 264094, 52645080, 35696052, 264107, 29331830, 52644045, 265006, 265007, 265009, 52644296, 52644229, 264689, 21906765, 21906768, 35695917, 265020, 52644150, 263967, 33657109, 27486265, 35695763, 18108370, 263974, 18108374, 18108376, 52644332, 263981, 18108385, 264508, 264909, 264596
2370	79804120 (4739, 4740)			UNCLASSIFIED	264369
2371	57280406 (4741, 4742)			UNCLASSIFIED	263967, 263981
2372	87642413 (4743, 4744)			UNCLASSIFIED	29331826, 265010, 265019, 35695917, 264634, 60432113
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gjl458582[dbj BAA76813.1] - (AB023186) KIAA0969 protein [Homo sapiens]		UNCLASSIFIED	
2374	94123665 (4747, 4748)	Novel Protein sim. GBank gjl5105131[dbj BAA80445.1] - (AF000061) 246aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01138) - 3' exoribonuclease family	UNCLASSIFIED	264766, 35695917, 35695855, 263981, 284557, 264565
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gjl1351115[sp P47758]SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)		UNCLASSIFIED	60432049, 29331824, 264807, 52644045, 264512, 60433356, 21906754, 52644296, 87168559, 264448, 21906765, 21906768, 21906769, 33657023, 18108368, 55811576, 52644332
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gjl2645435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	ATPase-associated	264259, 29331830, 264909, 264910, 265009, 60433438, 21906754, 265017, 265018, 265019, 264682, 264288, 264685, 21906767, 263972, 35695855, 87168518, 60432113
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gjl5257005[gb AAD41239.1] - (AF083249) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	18108394, 65274572, 22278997, 22278999, 264095, 29331822, 29147620, 29331824, 66714117, 29331825, 29331826, 29331828, 33656970, 29146498, 29146499, 264509, 265006, 265007, 265008, 265009, 60170831, 265010, 265011, 265018, 55811150, 18108351, 264764, 264288, 21906767, 21906768, 29148627, 29148629, 265021, 33657023, 33657109, 18108370, 18108374, 18108379, 35696423, 264556, 83373044, 18108385, 18108388, 55526486, 22279000, 22279002, 264563
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gjl1072198 (U40942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 56182435, 264510, 265009, 60433356, 87168474, 265011, 265018, 264288, 21906765, 33657023, 264557, 56182323, 83373044, 18108385, 22279002, 264482
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gjl3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - kinase WD domain, G-beta repeat	kinase	265017, 264288, 21906768

2380	86923062 (4759, 4760)	Novel Protein sim. GBank gij4502839[ref]NP_001845.1pCOL1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	264908, 264910, 265011
2381	87608241 (4761, 4762)	Novel Protein sim. GBank gij445609[emb]CAB36555) - (AL031846) dJ742C19.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR) domain Modifier domain	helicase	56192575, 264091, 264093, 264259, 29331825, 264105, 264906, 60433356, 21906754, 265017, 265019, 264683, 264289, 264685, 264686, 264687, 264691, 264692, 264693, 55811576, 264636, 264567
2382	91225982 (4763, 4764)	Novel Protein sim. GBank gij4325130[gb]AAD17276] - (AF119716) dMi-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	29331824, 60432229, 264905, 264596, 21906754, 264769, 265022, 264693, 263967, 33657109, 264629, 264631, 264556, 83373044, 60432113, 264482
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gij1902982[db]BAA19005) - (D89049) lecln-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	265009, 21906765, 21906766
2384	95354766 (4767, 4768)	Novel Protein sim. GBank gij2462851 (AF016252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	struct	264488, 52644507, 52645156, 52646365, 35696286, 22278999, 52645080, 29331824, 29331826, 35696052, 29331828, 264906, 264828, 52644045, 265006, 265008, 265009, 33109954, 33657084, 52644296, 265011, 265017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 265020, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108374, 35695855, 264634, 264555, 264556, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22279002
2385	95419485 (4769, 4770)		UNCLASSIFIED		264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331826, 35696052, 52644045, 265006, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22279002, 264563, 264565, 264567
2386	94742649 (4771, 4772)	Novel Protein sim. GBank gij4929699[gb]AAD34110.1[AF15187] CGI-115 protein [Homo sapiens]		glycoprotein	264488, 22278995, 22278996, 22278997, 264259, 29148498, 264112, 264511, 60170831, 60432229, 264595, 60433438, 87168474, 87168559, 264682, 21906765, 21906766, 21906767, 21906769, 29148829, 35695917, 265021, 264690, 33657109, 264628, 18108376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14997980 (4773, 4774)			UNCLASSIFIED	264634
2388	11424604 (4775, 4776)			UNCLASSIFIED	264595
2389	95310650 (4777, 4778)	Novel Protein sim. GBank gil4758058[ref]NP_004372.1 pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor		264488, 22278998, 22278999, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264511, 264512, 264910, 264591, 21906754, 264601, 264604, 264761, 18108351, 264764, 264288, 264766, 264768, 264769, 21906765, 21906768, 264692, 264693, 35696423, 264635, 264636, 264555, 83373044, 22279000, 264488
2390	94320912 (4779, 4780)	Novel Protein sim. GBank gil1644239[dbj]BAA122231 - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	52644507, 56182575, 22278995, 35686286, 22278996, 22278997, 22278999, 29331822, 29331825, 29331826, 35696052, 264905, 52644045, 265009, 264758, 264759, 33109954, 52644296, 85658542, 265011, 265017, 265018, 264605, 52644229, 21906765, 21906767, 21906768, 21906769, 35695917, 52644150, 33657023, 33657109, 33657349, 35695763, 18108370, 18108374, 18108376, 35688423, 35695855, 264555, 52644332, 56182233, 60170394, 83373044, 56526488
2391	80036194 (4781, 4782)			UNCLASSIFIED	263976
2392	94245016 (4783, 4784)	Novel Protein sim. GBank gil4240169[dbj]BAA74863.1 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	35696286, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 265009, 264591, 264758, 264600, 264604, 264762, 264448, 264764, 264369, 264766, 264768, 264769, 264689, 35695917, 264629, 18108374, 263978, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 60170394, 264639, 264565, 264486

2383	95302633 (4785, 4786)	Novel Protein sim. GBank gi4506667 ref NP_000983.1 pRPLP - ribosomal protein, large, P0	Contains protein domain (PF00466) - Ribosomal protein L10	ribosomalprot	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 56994075, 35696286, 22278996, 22278997, 22278999, 264093, 60432049, 264259, 29331822, 29147620, 20281099, 29331824, 29331825, 68714117, 60432289, 29331826, 29331827, 29331828, 35696052, 28146499, 264508, 264509, 264905, 264907, 264908, 66712502, 5264045, 264828, 264909, 56182435, 264112, 264113, 264510, 265006, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52646317, 33109954, 21906754, 55811386, 265010, 265011, 265017, 285018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264389, 264288, 18108354, 264766, 264686, 264687, 264688, 264689, 18108359, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148629, 29148784, 35695917, 265021, 265022, 33657023, 264692, 264693, 18108364, 33657109, 18108368, 27486281, 27486262, 33657349, 35695763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810764, 35696423, 35695855, 264634, 60431850, 264555, 264637, 264557, 263981, 264558, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 265006, 264592, 55811386, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21906765, 21906768, 21906769, 55811957, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108376, 55810764, 55811576, 35696423, 60170394, 18108385, 264564, 264566, 264567
2394	94323268 (4787, 4788)	Novel Protein sim. GBank gi4159888 (AC004908) - zinc finger protein from gene of uncertain exon structure; similar to Q99676 (P/D:3025333) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	264259, 29331824, 264910, 264288, 265021, 83373044, 18108387, 264563, 264566
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gi5712756 b AAD47636.1 AF16079 - (AF160798) calcium transporter CaT1 [Rattus norvegicus]		dna_ma_bind	

2398	95096700 (4791, 4792)	Novel Protein sim. GBank gij1053222[pirj]B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	52646365, 18108397, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264106, 264907, 29331830, 66712502, 264110, 60170831, 264591, 33657402, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 264768, 52644229, 21908768, 21906767, 265020, 265021, 60170615, 264692, 33657023, 65274620, 52645129, 33657182, 27486262, 27486264, 27486265, 264629, 18108374, 35696423, 35695855, 264631, 264556, 52644332, 264558, 83373044, 18108388, 87168518, 22278002, 264482
2397	87280854 (4793, 4794)				52644507, 52645156, 56182575, 264259, 29147620, 264905, 264907, 264908, 264809, 264910, 264758, 52644296, 264603, 264604, 264762, 264681, 264764, 18108357, 264769, 21906768, 264693, 264628, 264635, 264638, 264639, 264564
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gij3258609 (AC005178) - H53_GS1 [Homo sapiens]		UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gij786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 60432289, 264906, 29331830, 56182435, 264112, 264910, 33109954, 21906754, 87168474, 264600, 265017, 265018, 265019, 264764, 264765, 21906765, 21906768, 21906767, 21906769, 35695917, 265020, 265022, 60170815, 33657023, 18108370, 18108374, 264556, 60170394, 264558, 87168518, 22279000, 22279002, 264564, 264566, 264487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank gij2352822[gb]AAB69285.1) - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	21906766, 52646842, 56994075, 33657182, 27486262, 52644296, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gij2352822[gb AAB69285.1] - (AF008845) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	52644507, 52645156, 52644229, 264688, 21906764, 21906765, 52646365, 52646842, 21906766, 21906767, 21906768, 22278995, 35695917, 56994075, 35696286, 22278996, 22278997, 265020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 29331824, 33637109, 52645129, 29331826, 33657182, 29331827, 35696052, 27486261, 27486262, 33656970, 33657349, 27486285, 35695763, 264106, 264905, 35696423, 35695855, 265006, 265007, 265008, 265009, 284637, 52644332, 56812038, 52646317, 18108385, 52644296, 87168474, 265010, 87168559, 80432113, 265017, 265018, 265019, 264563, 264288, 264907, 264908, 264909, 264566
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gij4689259[gb AAD27832.1]AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]			
2403	94135432 (4805, 4806)	Novel Protein sim. GBank gij4929575[gb AAD34048.1]AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF000062) - C-type lysozyme/alpha-lactalbumin family		22278999, 35696052, 265018, 264686, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gij2315785 (AF015685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	35696286, 29331826, 35696052, 265008, 265018, 21908769, 264584
2405	94311851 (4809, 4810)	Novel Protein sim. GBank gij464178[dbj BAA03581] - (D14853) polyprotein [Hepatitis C virus]		UNCLASSIFIED	35696286, 29331822, 265007, 21906754, 265017, 265018, 265019, 264763, 264369, 21906765, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	88094501 (4811, 4812)	Novel Protein sim. GBank gij273363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain	struct	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264106, 264906, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 6043438, 33109954, 265010, 265011, 265018, 265019, 264369, 264685, 264686, 21906768, 21906769, 52644150, 264693, 52645129, 264628, 35696423, 264632, 56182323, 264639, 22279000, 22279002, 264563, 264685, 264686
2407	79465005 (4813, 4814)			UNCLASSIFIED	
2408	67391503 (4815, 4816)	Novel Protein sim. GBank gij423442[pir S33513 - gene F1 protein - mouse]		UNCLASSIFIED	264910, 265010, 264448, 264557

2409	94741770 (4817, 4818)	Novel Protein sim. GBank gij1178601 sp P45966 YNZ6_CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T09A5.6 IN CHROMOSOME III		UNCLASSIFIED	22278995, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29148498, 52644045, 60433438, 33657084, 87168474, 264760, 21906767, 29148627, 29148629, 52644150, 33657023, 263967, 20281069, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518 22278998, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gij4966262 gb AAC48052.2 - (UB4849) Contains similarity to Pfam domain: PF00846 (F- box), Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gij3114713 (AF051346) - Edp1 protein [Mus musculus]		Inf	29331824, 29331827, 29331828, 264764, 264369, 33657109, 56182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gij5410336 gb AAD43038.1 - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278998, 29331827, 264907, 265011, 265017, 265018, 265019, 18108351, 21906766, 265020, 33657109, 264559, 18108385
2413	94133820 (4825, 4826)	Novel Protein sim. GBank gij5262705 emb CAB45778.1 - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264488, 264259, 29331826, 264508, 264905, 264509, 264908, 264907, 264908, 264510, 264511, 264512, 265008, 265009, 264910, 265011, 264682, 264764, 264766, 264686, 264768, 264688, 265021, 33657023, 18108370, 264628, 35695855, 264632, 264634, 264635, 264636, 83373044, 264563, 264564, 264565, 264566, 264567, 264486
2414	94312590 (4827, 4828)	Novel Protein sim. GBank gij1082340 pir J52863 - DNA- binding protein R kappa B - human		ubiquitin	52645156, 52646842, 52646365, 18108398, 56182575, 22278994, 22278995, 56994075, 22278998, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29331830, 264909, 60433356, 33657402, 264594, 52646317, 21906754, 33657084, 265010, 87168559, 265017, 265018, 265019, 264369, 264684, 264687, 264688, 56181562, 21906764, 264689, 21906765, 21906766, 21906767, 29148627, 21906769, 265020, 265021, 60170615, 33657023, 264693, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 18108370, 60431528, 264629, 18108374, 18108378, 55810764, 264636, 52644332, 264638, 264558, 56182323, 83373044, 18108385, 87168518, 22279002

2415	88086002 (4829, 4830)	Novel Protein sim. GBank gj423915[pir][A45439 - myosin I heavy chain - rat]	Contains protein domain (PF00063) - struct	Myosin head (motor domain)	264259, 264808, 60433356, 33657402, 21908754, 265018, 264687, 264689, 21908769, 55811957, 265021, 264690, 264691, 33657023, 264693, 35698423, 56182323, 56526488
2416	94118358 (4831, 4832)	Novel Protein sim. GBank gj3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gj1084944[pir][S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)]	Contains protein domain (PF00153) -	Contains protein domain (PF00153) - Mitochondrial carrier proteins	264094, 29331822, 29331824, 29331827, 264369
2418	94234349 (4835, 4836)	Novel Protein sim. GBank gj1176572[spIP45895]YNA4_CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR.4 IN CHROMOSOME III	UNCLASSIFIED	Contains protein domain (PF00411) - Ribosomal protein S11	56994075, 264091, 264259, 29331824, 29331825, 60432289, 29331828, 264905, 264907, 264511, 265009, 60432229, 21908754, 87168559, 265019, 264682, 21908768, 21908769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264568
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gj284006[pir][S18732 - autoantigen, 64K - human]	struct		264569, 264762, 264448, 264691, 264631, 264634, 264555, 264558, 264638, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gj1076211[pir][S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]	UNCLASSIFIED		29331824, 29331825, 29331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264564
2421	87805345 (4841, 4842)	Novel Protein sim. GBank gj2224567[dbj][BAA20772] - (AB002311) KIAA0313 [Homo sapiens]	UNCLASSIFIED		264909, 264768, 264638
2422	88094714 (4843, 4844)	Novel Protein sim. GBank gj2224567[dbj][BAA20772] - (AB002311) KIAA0313 [Homo sapiens]	transport	Contains protein domain (PF00617) - RasGEF domain	18108392, 18108394, 18108398, 264906, 265006, 265010, 18108351, 18108374, 18108385
2423	88058390 (4845, 4846)	Novel Protein sim. GBank gj4505153[ref][NP_002392.1]pMEKK - MAP/ERK kinase kinase 3	kinase	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	264259, 60432049, 29331822, 29331826, 60432289, 29331828, 265008, 265009, 60433356, 21908754, 265017, 265018, 265019, 21908766, 21908768, 21908769, 265020, 265021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gj2988398 (AC004381) - Unknown gene product [Homo sapiens]	UNCLASSIFIED		56182575, 35696286, 22278997, 60432049, 264259, 29331826, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 265019, 264768, 21908768, 55811957, 264692, 33657023, 33657109, 55811576, 56182323, 83373044, 18108385, 18108388, 60432113, 22279000
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gj2077932[dbj][BAA19879] - (D86556) Protein Kinase [Rattus norvegicus]	kinase	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	264634
2426	87613945 (4851, 4852)	Novel Protein sim. GBank gj20939368[gb][AA053003.1] - (U94619) circulating cathodic antigen [Schistosoma mansoni]	UNCLASSIFIED		22278996, 22278998, 264259, 264102, 264512, 265008, 21908767, 18108370, 18108374, 263976

2427	87622683 (4853, 4854)	Novel Protein sim. GBank gi 4680695 gb AAD27737.1 AF13298 - (AF132982) CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	ribosomalprot	264259, 20281099, 35696052, 265008, 264594, 265011, 264760, 18108351, 264682, 264683, 284369, 264684, 264686, 264687, 264689, 21906766, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gi 1537070 (U63840) - nucleoprotein p54 [Rattus norvegicus]			22278996, 22278999, 35696052, 21906754, 264288, 21906765, 21906768, 21906769, 35695917, 265020, 263972, 22279002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gi 601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	UNCLASSIFIED	22278999, 29331824, 264806, 264909, 264511, 265009, 21906754, 265017, 265018, 265019, 264446, 264883, 264288, 21906765, 21906768, 265021, 264693, 18108381
2430	86948827 (4859, 4860)			UNCLASSIFIED	264112, 264691
2431	87649884 (4861, 4862)	Novel Protein sim. GBank gi 3860729 emb CAA14630 - (AJ235270) CELL DIVISION PROTEIN FTSJ (ftsJ) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein		29331826, 29331827, 35696052, 29146499, 284905, 264906, 264681, 264288, 264689, 21906765, 264692, 35696423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank gi 3876367 emb CAA93287 - (Z69360) Weak similarity to Elmeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]		protease	264634, 264558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank gi 2224593 dbj BAA20784 - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264569, 264905, 265018, 264762, 264683, 264691, 284556, 264557, 264639, 264558 264563
2434	18520148 (4867, 4868)			UNCLASSIFIED	264555
2435	20758044 (4869, 4870)	Novel Protein sim. GBank gi 1263289 (U47856) - fibrin-4 [Araneus diadematus]		UNCLASSIFIED	265008, 264758, 265010, 264689, 27486261, 263972, 18108374, 18108381
2436	88044008 (4871, 4872)	Novel Protein sim. GBank gi 3641352 (AF091234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	29331828, 265007, 265009, 265017, 264760, 264685, 264693, 264585
2437	83363424 (4873, 4874)			UNCLASSIFIED	29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 264910, 265009, 264591, 33657402, 21906754, 265011, 264760, 264764, 264685, 264686, 264768, 35695917, 33657023
2438	84143473 (4875, 4876)	Novel Protein sim. GBank gi 3860014 (AF091088) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	UNCLASSIFIED	264693, 264631, 264632, 56182323, 264558, 83373044, 264563, 264564, 264565, 264566, 264567

2439	94850650 (4877, 4878)	Novel Protein sim. GBank gi 4263519 gb AAD15345 - (AC004044) small nuclear riboprotein Sm-D1 (Arabidopsis thaliana)	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	50424179, 18108397, 56182575, 56181686, 56994075, 22278996, 35696286, 22278997, 22278999, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 29146498, 264509, 264905, 264906, 52644045, 60431735, 33109954, 21906754, 33657084, 55811386, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 33657109, 33657182, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 60431528, 263977, 55810764, 35696423, 65274791, 35695855, 60431850, 56182323, 60432113, 22279000, 22279002, 264567
2440	87641733 (4879, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264907, 264510, 265018, 265019, 264448, 264369, 265020, 265021, 56182323, 264639, 22279002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gi 3024889 sp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HAG116)		UNCLASSIFIED	264488, 264629, 18108374, 264564
2442	87273550 (4883, 4884)	Novel Protein sim. GBank gi 4506013 ref NP_002703.1 pPPP1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278996, 22278999, 29331822, 264768, 264693
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gi 170658 sp Q02975 KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264906
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gi 4758824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	264259, 18108382, 18108383, 18108385, 22279000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gi 2135950 pir J S58222 - PQ-rich protein - human			264259, 35696052, 264369, 18108361
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gi 4753887 emb CAA05409.2 - (AJ002424) p65 protein [Rattus norvegicus]	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	proteaseinhib	265011, 264689, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gi 4885613 ref NP_005409.1 pST5 - suppression of tumorigenicity 5		cadherin	56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 265018, 264692, 65274620, 60431528, 65274791, 56182323

2448	87749680 (4895, 4896)			UNCLASSIFIED	22278996, 22278997, 22278999, 29331828, 35896052, 264107, 264110, 87168474, 87168559, 18108351, 21906767, 21906769, 27486202, 263976
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gij28837[sp]P39194[ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		cadherin	264259, 264828, 265007, 264595, 265021, 56526486
2450	86597784 (4899, 4900)			UNCLASSIFIED	264906
2451	91014583 (4901, 4902)	Novel Protein sim. GBank gij1710021[sp]P35290[RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) - Ras family	glycoprotein	264093, 29331822, 29331824, 29331825, 66714117, 29331826, 29331828, 35896052, 264907, 66712502, 29331830, 264910, 265009, 284758, 265017, 265018, 264762, 264448, 264288, 21906767, 265021, 33657023, 264693, 33657109, 263969, 83373044, 18108385
2452	91230508 (4903, 4904)	Novel Protein sim. GBank gij1504034[dbj]BAA13216] - (D86980) KIAA0227 [Homo sapiens]		isomerase	264102, 264112, 264688, 263972, 18108374, 83373044, 264583
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gij2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	ngfirecep	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank gij1076802[pir]S49915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263994, 66714117, 29331827, 264508, 264509, 284905, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264758, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264686, 264768, 264769, 264534, 264691, 264692, 33657023, 264693, 33657109, 264628, 263978, 35695855, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264563, 264564, 264486
2455	95288301 (4909, 4910)	Novel Protein sim. GBank gij543817[sp]P35585[AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00828) - Adaptor complexes medium subunit family	glycoprotein	264488, 22278996, 264259, 35696052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264689, 21906766, 21906767, 21906769, 29148629, 35695917, 265020, 265022, 33657023, 33657109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264563, 264564, 264565, 264567
2456	88166700 (4911, 4912)	Novel Protein sim. GBank gij2588630 (AC003079) - Ankyrin; like. 54% similar to 2022340A (NID:g1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264693

2457	94118375 (4913, 4914)	Novel Protein sim. GBank gij3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	56181686, 264905, 264907, 264511, 264596, 55811386, 264682, 264684, 264685, 264687, 264691, 33657023, 264693, 35695855, 264636, 264555, 56182323, 264558, 56526486, 264563
2458	85675304 (4915, 4918)	Novel Protein sim. GBank gij2384942 (AF022985) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264691, 264693, 264634, 264559
2459	87551913 (4917, 4918)	Novel Protein sim. GBank gij5441942[gib AAD43187.1 AC004997] supported by mouse EST AA538043 (NID:g2284036) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	27466265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank gij4929701[gib AAD34111.1 AF15187 - (AF151874) CGI-116 protein [Homo sapiens]		kinase	65274572, 35696286, 22278996, 22278997, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 29146499, 264102, 264109, 60433438, 265017, 265018, 265019, 264288, 21908765, 21908768, 21908769, 35695917, 265020, 264691, 33657023, 27486261, 18108374, 35695855, 87168518, 60432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank gij4426862[gib AAD20633] - (AF126062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264259, 29331828, 264910, 18108351, 18108370, 18108374
2462	86998002 (4923, 4924)	Novel Protein sim. GBank gij5420387[emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]			264809, 264758, 264684, 18108374, 264637, 18108385
2463	84388543 (4925, 4926)	Novel Protein sim. GBank gij5052516[gib AAD38588.1 AF14561 - (AF145613) BcDNA GH03108 [Drosophila melanogaster]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264566
2464	91219957 (4927, 4928)	Novel Protein sim. GBank gij5410300[gib AAD4302.1 - (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01399) - PCI domain	protease	264489, 52646842, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696032, 29331828, 264509, 52644045, 264510, 264511, 264512, 265008, 60170831, 264593, 52646317, 33109954, 33657084, 265017, 265018, 265019, 264762, 264448, 264764, 264288, 264766, 21908765, 21908768, 21908769, 21908770, 21908771, 21908772, 21908773, 21908774, 21908775, 21908776, 21908777, 21908778, 21908779, 21908780, 21908781, 21908782, 21908783, 21908784, 21908785, 21908786, 21908787, 21908788, 21908789, 21908790, 21908791, 21908792, 21908793, 21908794, 21908795, 21908796, 21908797, 21908798, 21908799, 21908800, 21908801, 21908802, 21908803, 21908804, 21908805, 21908806, 21908807, 21908808, 21908809, 21908810, 21908811, 21908812, 21908813, 21908814, 21908815, 21908816, 21908817, 21908818, 21908819, 21908820, 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2465	85357483 (4929, 4930)	Novel Protein sim. GBank gij4508401[ref]NP_002871.1[prRAF1 - v-raf-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF000069) - Eukaryotic protein kinase domain	oncogene	18108392, 52644507, 52645156, 52646365, 22278994, 22278995, 35696286, 22278996, 22278998, 264259, 29331822, 29331824, 29331825, 60424269, 60432289, 29331827, 35696052, 29331828, 264907, 29331830, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264910, 33657402, 60433438, 55812038, 21906754, 33109954, 265010, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 284369, 264288, 264685, 264767, 21906765, 21906767, 21906768, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 52645129, 33657109, 27486261, 27486264, 35695763, 264628, 263972, 18108374, 35695855, 264636, 264637, 60170394, 56526486, 87168518, 60432113, 264563, 264564, 264566, 264487 264369
2466	85681386 (4931, 4932)	Novel Protein sim. GBank gij4321619[gb]AAD15788.1] - (AF051098) seven transmembrane domain orphan receptor [Mus musculus]			
2467	88059485 (4933, 4934)	Novel Protein sim. GBank gij3513300 (AC005595) - F16601_1, partial CDS [Homo sapiens]		UNCLASSIFIED	56994075, 264908, 21906768, 33657023
2468	87614698 (4935, 4936)	Novel Protein sim. GBank gij2143455[pir]j58106 - gene DMR-N9 protein - mouse (fragment)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	29331824, 52644045, 265008, 264910, 265019, 21906765, 21906769, 265021 264288, 264628
2469	86294397 (4937, 4938)	Novel Protein sim. GBank gij5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264592, 264692, 264555, 264556, 264557, 264558, 264559, 18108385, 264482
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gij5419882[emb]CAB46424.1] - (AL098749) DKFZp434G153 [Homo sapiens]		UNCLASSIFIED	65274572, 35696286, 29331827, 285007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811576, 56182323
2472	95060811 (4943, 4944)	Novel Protein sim. GBank gij4929747[gb]AAD34134.1[AF15189] CGI-139 protein [Homo sapiens]		UNCLASSIFIED	264092, 60432049, 29331825, 60433356, 265010, 265011, 18108351, 264764, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gij4533009[emb]CAB39630.1] - (AL049481) putative protein [Arabidopsis thaliana]			60424179, 65274572, 22278999, 60424269, 29331826, 265008, 60433356, 60433438, 265010, 18108351, 264448, 264288, 264687, 264689, 265021, 264692, 65274620, 60431528, 65274791, 264556, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gij3252827 (AC004382) - Unknown gene product [Homo sapiens]			65274572, 56994075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264683, 264369, 265020, 264693, 264563, 264564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gij1216486 (U48852) - HT protein [Cricetulus griseus]	Contains protein domain EGF-like domain	Ig1	264259, 29331822, 265006, 265007, 265010, 265011, 264448, 264288, 264369, 264685, 264686, 18108357, 264768, 18108362, 264693, 18108370, 18108374, 18108379, 35898423, 83373044, 18108383, 18108385, 264584, 264565, 264567
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gij3252827 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 60424269, 66714117, 264905, 265006, 264511, 265008, 265009, 264758, 265010, 265011, 18108351, 264681, 264369, 264288, 264689, 21906767, 265020, 18108374, 264639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)			UNCLASSIFIED	263978
2478	17659165 (4955, 4956)			UNCLASSIFIED	265017
2479	94314569 (4957, 4958)	Novel Protein sim. GBank gij1644232[dj]BAA110821 - (D67066) N-WASP [Bos taurus]		Im7	56994075, 22278999, 21906754, 264682, 21906765
2480	95295605 (4959, 4960)			UNCLASSIFIED	264905, 264907, 264765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gij5699469[dj]BAA83018.1] - (AB028989) KIAA1068 protein [Homo sapiens]		collagen	65274572, 56182575, 22278997, 264094, 264259, 29331822, 29331824, 66714117, 29331827, 35898052, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 56182435, 265008, 264910, 33657402, 55812038, 264758, 265010, 265011, 265017, 265018, 264760, 264762, 18108351, 264764, 264288, 264766, 264686, 264768, 21908768, 55811957, 265020, 264691, 264692, 264693, 264629, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22279002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gij321249[pj]S28407 - guanine nucleotide-exchange activator CDC25 homolog - mouse		UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 264768, 264693, 264631, 264632, 264636, 264638, 264639, 264563
2483	87731583 (4965, 4966)			UNCLASSIFIED	264488, 22278995, 264093, 264095, 60432049, 60433356, 60433438, 264448, 264288, 263967, 18108370, 18108385, 18108388, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gij728831[sp]P39188[ALU1_HUMAN - III] ALU SUBFAMILY J WARNING ENTRY III!		kinase	264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gij1185397 (U25281) - SH3 domain binding protein [Rattus norvegicus]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 264600, 264603, 264604, 265018, 264448, 264288, 264685, 264686, 264769, 264689, 35895917, 265022, 264692, 264693, 56182323

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gi 2662167 dbj BAA23715 - (AB007903) KIAA0443 [Homo sapiens]			265017, 264555
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gi 464559 sp P35287 RB14_RAT RAS-RELATED PROTEIN RAB-14	Contains protein domain (PF00071) - Ras family	glycoprotein	22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331822, 35696052, 264108, 264905, 264907, 29331830, 264909, 265006, 264511, 265008, 265009, 60433438, 21906754, 33109954, 87168559, 265018, 264681, 264288, 264667, 21906765, 21906768, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 264534, 33657023, 264692, 33657109, 263972, 18108377, 35696423, 35695855, 60170394, 18108385, 56528486, 22278000, 22279002, 264563, 264482, 264565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	264910, 264448, 264288, 264684, 264691, 264634
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gi 4886439 emb CAB43355.1 - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	264686, 264693, 55811576, 22279002
2490	88069609 (4979, 4980)	Novel Protein sim. GBank gi 2588624 (AC003083) - Rap2 interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	264907, 265008, 22279002
2491	81242116 (4981, 4982)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		im7	264259, 29331826, 265008, 264762, 18108370, 18108376, 18108379
2492	95308202 (4983, 4984)	Novel Protein sim. GBank gi 3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21906764, 21906768, 264692, 60431528, 87168518, 60432113, 22279000

2483	95422415 (4985, 4986)	Novel Protein sim. GBank gij4240307[idbj]BAA74932.1] - (AB020716) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - R3H domain	struct	18108394, 264887, 65274572, 56182575, 22278995, 56994075, 80432049, 29331822, 29331824, 29331825, 29331826, 29331827, 29146498, 264508, 264905, 264509, 264906, 264907, 29331830, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 264910, 21908754, 265011, 264600, 265017, 265018, 264604, 264605, 265019, 55811150, 264762, 18108351, 264681, 264448, 264683, 264369, 264288, 18108355, 18108357, 264687, 21908765, 21906766, 21906767, 21906768, 21908769, 265020, 264691, 264692, 33657023, 33657349, 18108370, 18108374, 18108376, 55810764, 18108379, 55274791, 264630, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 264482, 264566, 264486
2494	30783118 (4987, 4988)			UNCLASSIFIED	264907, 264601
2495	94234551 (4989, 4990)	Novel Protein sim. GBank gij5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		collagen	263994, 22278997, 35696052, 264509, 264905, 264908, 264907, 264908, 264909, 265006, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264768, 264769, 264689, 265020, 264692, 65274620, 264629, 55810764, 35696423, 55811576, 264638, 264637, 18108385, 22279000, 264564, 264567, 264486
2496	80018765 (4991, 4992)	Novel Protein sim. GBank gij4808220[emb]CAB42832.1] - (AL022315) dJ117715.1 (PUTATIVE novel protein) [Homo sapiens]		struct	29147620, 264905, 265008, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108388
2497	91723554 (4993, 4994)			UNCLASSIFIED	52644507, 22278996, 22278999, 29331824, 29331828, 33657402, 21908754, 87168474, 265019, 264369, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 33657023, 18108376, 18108387
2498	87724633 (4995, 4998)	Novel Protein sim. GBank gij1200503 (U47924) - B [Homo sapiens]		UNCLASSIFIED	29331827, 264512, 264910, 264288, 18108374, 35695855
2499	94685125 (4997, 4998)	Novel Protein sim. GBank gij3510234 (AC005581) - R31237_1, partial CDS [Homo sapiens]	Contains protein domain (PF000069) - Eukaryotic protein kinase domain	kinase	264909, 55812038, 264631, 264637, 264558

2500	94648324 (4989, 5000)	Novel Protein sim. GBank gij3881275 emb CAA21725 - (AL032655) predicted using GeneFinder, similar to Inositol monophosphatase family; cDNA EST yk255e11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52644507, 52645156, 22278995, 56994075, 35696286, 22278998, 2642599, 52845080, 29331824, 29331825, 68714117, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 264509, 264510, 264512, 33657402, 60433438, 21906754, 52644296, 87168474, 87168559, 264603, 264681, 284448, 284683, 264288, 264369, 52644229, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 33657182, 35695763, 35696423, 35695855, 52644332, 83373044, 18108387, 87168518, 22279002
2501	94303896 (5001, 5002)	Novel Protein sim. GBank gij4929815 gb AAD34088.1 AF15183 - (AF151831) CGI-73 protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_mn_bind	65274572, 56182575, 35696286, 22278998, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264905, 264908, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264910, 264591, 60432229, 33657402, 60433356, 264595, 55812038, 264758, 264598, 87168474, 87168559, 264600, 264601, 264602, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 264369, 264288, 264766, 18108357, 21908765, 21908766, 21906767, 21906769, 29148629, 35695917, 264692, 33657023, 264629, 35696423, 55811576, 35695855, 264630, 264634, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87168518, 60432113, 22279002, 264566
2502	90993716 (5003, 5004)	Novel Protein sim. GBank gij3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308) [Homo sapiens]	Contains protein domain (PF01237) - Oxysterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264780, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264692, 33657109, 263973, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264563, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gij2196874 emb CAA72638 - (Y11896) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87668706 (5007, 5008)	Novel Protein sim. GBank gj 550420 emb CAA48220 - (X88101) trg [Rattus norvegicus]			264488, 52644507, 52645156, 52646842, 22278994, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264906, 264808, 52644045, 265009, 60433356, 33657402, 60433438, 264595, 33109954, 87168474, 265017, 265019, 264448, 264288, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 52644150, 264682, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52644332, 56182323, 18108387, 87168518, 60432113, 22279002, 264564
2505	8760559 (5009, 5010)			UNCLASSIFIED	264605
2506	81232328 (5011, 5012)	Novel Protein sim. GBank gj 2137562 pir I49635 - mouse Dhnm1 protein - mouse		nuclease	284488, 52644507, 52645156, 52646365, 65274572, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331826, 29331828, 264509, 56182435, 264112, 264593, 60433356, 55812038, 21906754, 265011, 265017, 265018, 265019, 264605, 264762, 18108351, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906768, 21908769, 35695917, 265020, 265021, 265022, 60170615, 33657023, 27486264, 18108379, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264565
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gj 5174489 ref NP_006035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 263994, 264592, 264595, 264369, 264886, 264768, 35695917, 35696423, 264563
2508	85315505 (5015, 5016)	Novel Protein sim. GBank gj 4826433 emb CAB42889.1 - (AL031447) dJ126A5.2.1 (novel protein) (isofom 1) [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 60432049, 264259, 29331828, 265006, 265007, 60433438, 33657084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264369, 18108359, 21906765, 21906769, 55811957, 265020, 265022, 27486261, 33657349, 18108377, 35695855, 60432113, 22279002, 264563, 264565
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gj 263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265007, 265008, 18108357, 264556, 264567

2510	85421379 (5019, 5020)	Novel Protein sim. GBank gij3293537[gbjAAC25762.1] - (AF071059) zinc finger RNA binding protein [Mus musculus]			65274572, 22278994, 22278996, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331828, 33656970, 264908, 66712502, 265007, 264910, 60170831, 60432229, 60433356, 60433438, 21906754, 87168474, 265017, 265018, 264448, 264288, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 264691, 33857023, 264693, 65274620, 33657109, 33657182, 27486282, 33657349, 18108370, 35695855, 264555, 56182323, 83373044, 60432113, 22279002, 265017, 21906764, 265020, 264692
2511	87384281 (5021, 5022)	Novel Protein sim. GBank gij4323152[gbjAAD16228.1] - (AF098863) Ets-protein Spl-C [Mus musculus]			
2512	88084771 (5023, 5024)	Novel Protein sim. GBank gij4502075[refjNP_001135.1]pAMFR - autocrine motility factor receptor	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 264259, 29331825, 29331826, 29146498, 264907, 264909, 265006, 265008, 264591, 60432229, 21906754, 264763, 264683, 264766, 18108357, 264689, 21906769, 264693, 18108370, 263972, 18108374, 264558, 22278900
2513	85357843 (5025, 5026)	Novel Protein sim. GBank gij3004657 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED	60424179, 52845156, 18108394, 22278994, 35896286, 56994075, 22278996, 29331822, 29331824, 60424269, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 265017, 264448, 264369, 56181562, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108366, 33657109, 27486261, 27486262, 33657349, 18108374, 55810764, 35696423, 56182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gij2258437 (AF008197) - syncoilin [Rattus norvegicus]		UNCLASSIFIED	264510
2515	87994509 (5029, 5030)	Novel Protein sim. GBank gij3757727[embjCAA18783] - (AL022727) dJ80119.7 (olfactory receptor-like protein (hs6M1-3)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	
2516	87786908 (5031, 5032)			UNCLASSIFIED	264259, 29146498, 264905, 264288, 29148629, 35695917, 27486261, 264634
2517	87784968 (5033, 5034)	Novel Protein sim. GBank gij4220527[embjCAA23000] - (AL035356) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264091, 29331824, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657109, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2518	94147410 (5035, 5038)	Novel Protein sim. GBank gi 492959 gb AAD34056.1 AF15181 - (AF151819) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29331827, 35696052, 29331828, 264907, 264909, 264511, 265007, 60432229, 60433356, 60433438, 55812038, 265010, 265017, 264448, 264288, 264689, 21906768, 21906769, 265022, 52644150, 264693, 18108370, 263972, 264555, 56182323, 83373044, 18108385, 60432113, 264088 264259, 66714117, 29331826, 29331827, 29331828, 264907, 66712502, 265008, 265008, 264594, 265010, 265011, 265018, 264288, 21906769, 265020, 60431528, 55811576, 65274791, 264632, 264555, 264636, 22279002, 264564
2519	94326180 (5037, 5038)	Novel Protein sim. GBank gi 4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4	kinase		264259, 264908, 264910, 264682, 21906769, 265020, 264563
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gi 4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4	transport		264259, 264908, 264910, 264682, 21906769, 265020, 264563
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gi 5174489 ref NP_005035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 264489, 263994, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 264907, 66712502, 264511, 265006, 265007, 264591, 264592, 264593, 264594, 264595, 264596, 264681, 264448, 264763, 264882, 264764, 264684, 264369, 264288, 264685, 264686, 21906768, 55811957, 264692, 264693, 27486261, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264632, 264558, 18108385, 65274727, 60432113, 264563, 264564, 264565, 264566, 264567
2522	87754052 (5043, 5044)	Novel Protein sim. GBank gi 4580011 gb AAD24201.1 U81002 - (U81002) TRAF4 associated factor 1 [Homo sapiens]	transport		264489, 22278997, 20281171, 21906754, 35695917, 263967, 263976, 263981, 20281169
2523	95340467 (5045, 5046)	Novel Protein sim. GBank gi 1809327 U76374 - skm-			263969
2524	95340469 (5047, 5048)	Novel Protein sim. GBank BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 264512, 265008, 60170831, 33657402, 265010, 87168559, 265019, 264288, 21906765, 21906769, 35695917, 265020, 265021, 265022, 52644150, 264691, 33657023, 33657109, 27486281, 35696423, 65274791, 264559, 83373044, 56526486, 87168518, 264567

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gij2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]		kinase	264488, 22278997, 22278999, 60432049, 60432289, 29331828, 264905, 265008, 55812038, 21906754, 265019, 264369, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 33657109, 60431528, 83373044, 60432113, 22278000, 22279002, 264565
2526	95289404 (5051, 5052)	Novel Protein sim. GBank gij4589628[dijBAA78836.1] - (AB023209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	60424178, 284768, 264687, 264769, 264689, 65274572, 21906767, 56182575, 21906768, 21906769, 55811957, 22278994, 22278995, 35696286, 35695917, 22278996, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264690, 264691, 60432049, 264259, 264097, 33657023, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 27486262, 264508, 264509, 264905, 264907, 18108370, 66712502, 60431528, 264828, 264909, 18108372, 18108374, 56182435, 18108376, 55810764, 55811576, 35696423, 35695855, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33657402, 56182323, 60433356, 60433438, 264595, 55812038, 264596, 264758, 83373044, 52646317, 18108385, 33657084, 18108387, 55811386, 65274727, 56526486, 87168518, 60432113, 265017, 22279000, 265018, 265019, 264564, 18108351, 264448, 264566, 264288, 264486, 264567, 264766
2527	88094580 (5053, 5054)	Novel Protein sim. GBank gij2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gij2085786 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1395185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22278002
2529	86670926 (5057, 5058)	Novel Protein sim. GBank gij3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]		synthase	264908, 264769, 265020, 265021, 18108383
2530	80259978 (5059, 5060)				264369, 264556
2531	87768931 (5061, 5062)			UNCLASSIFIED	29331822, 29331824, 60432289, 264508, 264509, 264906, 265011, 264769, 21906768, 33657023, 87168518, 22279000
2532	87419778 (5063, 5064)	Novel Protein sim. GBank gij2664625[emb]CAA16972] - (AL021811) putative protein [Arabidopsis thaliana]			264593
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gij437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264555

2534	87332322 (5087, 5068)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		UNCLASSIFIED	264259, 35696052, 264905, 265017, 21906769, 265020, 265022, 33657109, 22279000
2535	91225056 (5069, 5070)	Novel Protein sim. GBank gij4468311[embjCAB37992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			65274572, 35696286, 60432289, 29331828, 66712502, 265006, 60432229, 265017, 265018, 265019, 264288, 264369, 264689, 21906768, 265020, 265021, 264636, 60170394, 22279002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gij728836[spP39193]ALU8_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII	kinase		18108398, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 28331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 264910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264769, 264689, 21906765, 21906766, 21906767, 265021, 52645129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 60432113, 22279000, 22279002, 264567, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gij4557026[re]NP_003913.1pHERC - guanine nucleotide exchange factor p532	ubiquitin		65274572, 35696286, 29331822, 29331825, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265011, 264760, 264288, 264685, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 18108374, 35696423, 35695855, 264636, 264558, 60170394, 56182323, 83373044
2538	36653454 (5075, 5076)			UNCLASSIFIED	
2539	94144818 (5077, 5078)			UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 29148499, 264908, 264112, 60170831, 87168559, 264604, 265019, 264685, 264768, 87168518, 22279000, 264565, 264566
2540	94218545 (5079, 5080)	Novel Protein sim. GBank gij1362647[pirj]S53876 - sex-regulated protein janus A - fruit fly (Drosophila pseudoobscura)		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264567
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gij1711658[spP54797]T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264691, 264639, 29331824, 264603, 264604, 264905, 264907, 264908, 264766

2542	95298162 (5083, 5084)	Novel Protein sim. GBank gi 5225320 gb AAD40850.1 AF08310 - (AF083107) sirtuin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophysial hormones, N- terminal Domain	UNCLASSIFIED	264488, 18108394, 52646385, 52646942, 65274572, 22278994, 35699286, 22278996, 264259, 52645080, 29331822, 29331824, 29331827, 35696052, 33656970, 264907, 264909, 52644045, 264510, 265008, 264512, 265007, 265008, 265009, 264910, 60431735, 52646317, 52644286, 265010, 265011, 265018, 265019, 18108351, 264683, 264288, 264685, 264687, 52644228, 264769, 21908766, 21908767, 21908769, 52644150, 33657023, 33657109, 52645129, 33657182, 27486261, 27486264, 33657349, 35695763, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264558, 83373044, 18108385, 18108387, 87168518, 264563, 264564
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gi 5419857 emb CAB46374.1 - (AL086723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)		65274572, 56182575, 22278999, 264259, 29331826, 264907, 264510, 264511, 264592, 264595, 264764, 264369, 264288, 264684, 264766, 264689, 21906765, 21908767, 21908769, 60170615, 264682, 264693, 55811576, 85274791, 264636, 264558, 18108381, 60170394, 264639, 18108385, 60432113, 22279000
2544	94218549 (5087, 5088)	Novel Protein sim. GBank gi 2498110 sp Q63191 AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - MAM domain.	glycoprotein	18108397, 52646365, 22278997, 264259, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 264448, 264688, 264687, 264689, 21906765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 56526486, 22279000, 264482, 264563, 264567
2545	87742845 (5089, 5090)	Novel Protein sim. GBank gi 3327046 dbj BAA31591 - (AB014516) KIAA0616 protein [Homo sapiens]			29331825, 264906, 265009, 60170831, 265017, 264369, 21906767, 60170815, 264692, 33657109
2548	88093861 (5091, 5092)	Novel Protein sim. GBank gi 2996032 (AF054586) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 265007, 22279002

2547	94143868 (5093, 5094)	Novel Protein sim. GBank gi 4929607 gb AAD34064.1 AF15182 - (AF151827) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264488, 18108394, 52646842, 18108397, 56182575, 22278995, 56994075, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 35696052, 29331828, 264104, 264508, 264905, 264906, 264908, 66712502, 264909, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 60431735, 264594, 60433438, 21906754, 52646317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264686, 264687, 56181562, 264688, 264689, 21906765, 21906768, 21908767, 21908768, 29148627, 21908769, 55811957, 265020, 265021, 265022, 264690, 264691, 18108382, 264692, 264693, 27486261, 18108370, 18108374, 55810764, 55811576, 35696423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264558, 264559, 83373044, 18108385, 87168518, 22279002, 264564, 264566, 264488
2548	88179079 (5085, 5096)			UNCLASSIFIED	264488, 18108394, 52646365, 22278994, 35696286, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87168559, 264684, 264369, 52644229, 265021, 33657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22279000, 22279002, 264563, 264567
2549	94186893 (5097, 5098)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00412) - LIM domain containing proteins	struct	56182575, 22278996, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265018, 264688, 21906764, 21906765, 21906766, 21906767, 21908769, 265020, 265021, 52644150, 264691, 18108368, 60431602, 18108376, 35696423, 56182323, 18108387, 264567, 56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638
2550	87778584 (5099, 5100)	Novel Protein sim. GBank gi 2143886 pir J152523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	

2551	95308400 (5101, 5102)	Novel Protein sim. GBank gl 4337103 gb AAD18079 - (AF128758) NG28 [Homo sapiens]		Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 264905, 56182435, 265007, 60433438, 55812038, 21908754, 65274444, 265017, 265018, 264605, 265019, 264288, 21908766, 21908768, 21908769, 265020, 60170615, 264693, 33657109, 35698423, 264638, 56182323, 83373044, 22279000
2552	95332620 (5103, 5104)				UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 35696052, 29331828, 264508, 264907, 56182435, 265008, 264591, 33109954, 264760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811576, 35696423, 35695855, 56182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gl 1711658 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION			UNCLASSIFIED	264686, 264488, 263976, 264768, 29331826, 35696052, 35696423, 264601, 264511, 264602, 264910, 264634, 264760, 264555, 264762, 264906, 264592, 264691, 264566, 264908, 264684, 264587, 264909, 264768
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gl 728835 sp P39192 ALU5_HUMAN - III ALU SUBFAMILY SC WARNING ENTRY III			cadherin	22278997, 29331822, 264508, 21908769, 33657023, 33657109, 56182323
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gl 4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]			nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gl 4106984 (AC003038) - R30923_1 [Homo sapiens]		Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264509, 33657402, 264683, 264684, 264766, 264689, 33657023, 33657109, 35695855, 264558, 264567
2557	79437803 (5113, 5114)					264595
2558	87617591 (5115, 5116)	Novel Protein sim. GBank gl 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN			UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 264906, 264511, 265018, 264448
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gl 4538998 emb CAB39619.1 - (AL049481) AIG1-like protein [Arabidopsis thaliana]			UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 264288, 264765, 264766, 264769, 21906765, 21906766, 60432113, 264462
2560	87984530 (5119, 5120)	Novel Protein sim. GBank gl 5051399 emb CAB44995.1 - (AL078630) 573K1.3 (mm17M1-4) (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE protein)) [Mus musculus]		Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gl 5326825 gb AAD42056.1 AF04495 - (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]			UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432229, 87168559, 265017, 265018, 265019, 264689, 21906766, 21906769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 264558, 18108385, 87168518, 22279002

2562	87645539 (5123, 5124)	Novel Protein sim. GBank gij4106984 (AC003038) - R30923_1 [Homo sapiens]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 60432289, 33657402, 60433356, 21906765, 55811957, 60170615, 33657023, 264693, 35695955, 87168518, 264488, 35696286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52644045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21906767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264566, 264486, 29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2563	88095497 (5125, 5126)	Novel Protein sim. GBank gij4886447[emb]CAB43371.1] - (AL050270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gij1352944[sp]P47179]Y9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR		sulfotransferase	
2565	85530908 (5129, 5130)	Novel Protein sim. GBank gij628012[pir]A53933 - myosin I		UNCLASSIFIED	66714117, 264909, 263978, 264632
2566	80224958 (5131, 5132)	Novel Protein sim. GBank gij628012[pir]A53933 - myosin I myr 4 - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	- struct	18108370, 35695855, 264556, 264558, 18108383
2567	86143590 (5133, 5134)	Novel Protein sim. GBank gij466009[sp]P34548]YJ4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		synthase	265020, 60170815
2568	91233098 (5135, 5136)	Novel Protein sim. GBank gij466009[sp]P34548]YJ4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III			60424179, 18108394, 56181686, 56994075, 22278999, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264769, 21906766, 21906767, 35695917, 265021, 33657023, 18108362, 33657109, 33657182, 35695763, 60431528, 55810764, 18108379, 83373044, 18108385, 60432113, 264482

2569	95313764 (5137, 5138)	Novel Protein sim. GBank gi2599560 gb AAB84166.1 - (AF029674) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcript factor	18108394, 56182575, 56181886, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264906, 56182435, 265008, 265009, 264910, 60432229, 264592, 60433356, 60433438, 21908754, 87168559, 265017, 265018, 265019, 264682, 264448, 264288, 21908765, 21906768, 21906787, 21908768, 29148627, 21906769, 35695917, 265021, 265022, 52644150, 264690, 264691, 264692, 264693, 65274620, 263967, 35695763, 20281089, 263974, 18108374, 55810764, 35696423, 35695855, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264566
2570	94136754 (5139, 5140)	Novel Protein sim. GBank gi4758954 ref NP_004567.1 pPP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	phosphatase	22278996, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35696052, 264907, 264510, 265007, 265009, 264758, 33108954, 285019, 264686, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 35695855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gi732218 sp P34609 YO60_CAEEL - HYPOTHETICAL 128.8 KD PROTEIN ZK1098.10 IN CHROMOSOME III		stud	264508, 264905, 264907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627560 (5143, 5144)	Novel Protein sim. GBank gi4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696286, 29331827, 35696052, 264100, 264104, 264110, 264592, 21906754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35695855, 60170394, 264559, 18108385

2573	95313929 (5145, 5146)	Novel Protein sim. GBank gi 399138 sp P02745 C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00336) - C1q domain	complement	264488, 60424179, 65274572, 56182575, 56181686, 22278995, 58994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264906, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432228, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21906754, 87188474, 265010, 265011, 87168559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264389, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148527, 21906768, 21906769, 265020, 265021, 265022, 60170615, 264690, 52644150, 264691, 264692, 33657023, 65274620, 18108365, 18108368, 27486265, 60431602, 264629, 60431528, 263976, 65274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 58182323, 60170394, 83373044, 18108384, 87168518, 60432113, 264482, 264564, 264565, 264566, 264567, 22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 265008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21906765, 21906766, 21906768, 55811857, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 83373044, 18108385, 264482
2574	94746814 (5147, 5148)	Novel Protein sim. GBank gi 33334982 (AC005306) - R27216_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED	
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF151888) CGI-130 protein [Homo sapiens]		UNCLASSIFIED	
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi 4680881 gb AAD27730.1 AF13295 - (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264259, 35696052, 264908, 60433438, 264681, 18108351, 264288, 52644150, 264628, 35696423
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gi 4337103 gb AAD18079 - (AF129756) NG26 [Homo sapiens]		UNCLASSIFIED	29331825, 265018, 265019, 264685
2578	87786941 (5155, 5156)			UNCLASSIFIED	264488, 264906, 264908, 264910, 264596, 264603, 264604, 264605, 264766, 21906769, 264628, 264630, 264634, 264639, 264563
2579	87282879 (5157, 5158)			UNCLASSIFIED	29331822, 29331824, 264767

2580	88166788 (5159, 5160)	Novel Protein sim. GBank gi 2588628 (AC003080) - Similar to KIAA0289; 60% similarity to AB002297 (PID:g2224539) [Homo sapiens]			265007, 265018, 264762
2581	87899048 (5181, 5182)	Novel Protein sim. GBank gi 4406642(gb AAD20049) - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	collagen	56994075, 29331824, 29331826, 29331828, 264905, 60433356, 60433438, 264758, 87188559, 21906769, 265022, 35685855, 263981
2582	87786789 (5163, 5164)	Novel Protein sim. GBank gi 2739367 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]		eph	264488, 264907, 264908, 264910, 264764, 264684, 264766, 264636, 264555, 264565
2583	91220850 (5165, 5166)	Novel Protein sim. GBank gi 4378112(emb CAA16521.1) - (AL021578) dJ453C12.2 (similar to transcription factor RBP. L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcriptfactor	56181686, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430941 (5167, 5168)			UNCLASSIFIED	264908, 264910, 264768, 264693, 18108374, 55811576, 56182323
2585	80436128 (5169, 5170)	Novel Protein sim. GBank gi 2736151 (AF021935) - myotonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]		kinase	264768
2586	91226136 (5171, 5172)				22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264906, 265007, 265009, 264591, 60433356, 33657402, 265018, 264762, 264288, 21906766, 21906767, 21906769, 265022, 264691, 83373044, 56526486, 22279002
2587	80430943 (5173, 5174)				264908, 265018, 264768, 264693, 55811576, 56182323
2588	80074385 (5175, 5176)			UNCLASSIFIED	264564
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gi 3021598(emb CAA71415) - (Y10389) nuclear protein [Xenopus laevis]		UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264769, 35696423, 264636
2590	87054526 (5179, 5180)	Novel Protein sim. GBank gi 2104689 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	glucoamylase	22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192167 (5181, 5182)	Novel Protein sim. GBank gi 5702202(gb AAD47199.1)(AF12916) - (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]		eph	264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22279002

2592	95332648 (5183, 5184)	Novel Protein sim. GBank gi 3024998 sp Q60936 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56994075, 264259, 29331822, 29331824, 29331828, 60432289, 29331827, 29331828, 264906, 264909, 265007, 265008, 264910, 60432229, 264594, 60433356, 60433438, 55812038, 18108348, 21906754, 265011, 87168559, 265017, 265019, 264764, 264369, 264288, 264766, 265021, 60170615, 33657023, 33657109, 264628, 35698423, 35695855, 264557, 264638, 60170394, 56182323, 83373044, 56526486, 87168518, 264563, 264482, 264565
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF15188) CGI-130 protein [Homo sapiens]		tm7	22278999, 29331825, 264758, 21906754, 52646317, 265010, 18108351, 264288, 264369, 21906768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gi 4929587 gb AAD34054.1 AF15181 - (AF15181) CGI-59 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108398, 56182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331826, 264905, 264909, 52644045, 56182435, 264510, 264512, 265007, 264757, 21906754, 87168474, 265017, 264760, 264448, 264764, 264288, 264766, 264689, 21906768, 33657109, 263975, 263977, 264634, 264556, 60170394, 56182323, 56526486, 264482, 264583, 264564, 264566, 264567 264692
2595	79561676 (5189, 5190)	Novel Protein sim. GBank gi 4309681 gb AAD15478 - (AC006930) R33423.1 [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 265018, 264448, 265021, 60431528
2596	87538637 (5191, 5192)			UNCLASSIFIED	264905, 264509, 264908, 264762, 264766, 35695917, 35695855, 264635, 264636, 83373044, 264486
2597	94784089 (5193, 5194)			UNCLASSIFIED	22278998, 264259, 29331824, 87168474, 264683, 21906768, 35695917, 264691, 33657023, 33657109, 18108370, 18108374, 264564, 264565
2598	88094948 (5195, 5196)	Novel Protein sim. GBank gi 1001351 dbj BAA10838 - (D64006) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	264766, 264769, 21906768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526486, 22279000, 264568
2598	87642889 (5197, 5198)	Novel Protein sim. GBank gi 3941737 (AF109719) - BAT2 [Mus musculus]		MHC	35696286, 264093, 264288, 21906769, 35696423, 35695855
2600	87787846 (5199, 5200)	Novel Protein sim. GBank gi 4263521 gb AAD15347 - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	

2601	91243070 (5201, 5202)	Novel Protein sim. GBank gi 728837 sp P39194 ALU2_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	56182575, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 264908, 265007, 265008, 264591, 60433356, 33857402, 60433438, 21906754, 265011, 265018, 265019, 18108351, 264448, 264369, 21906769, 265020, 60170615, 264693, 33857109, 18108370, 18108376, 56182323, 18108381, 18108385, 22279002, 264563, 60433438, 21906754, 87168559, 264601, 264369, 264288, 21906767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank gi 4406632 gb AAD200471 - (AF131801) Unknown [Homo sapiens]		UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35986052, 56182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33657084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264767, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486262, 18108374, 35698423, 85274791, 35695855, 264555, 264636, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000
2604	94676601 (5207, 5208)	Novel Protein sim. GBank gi 5454030 ref NP_006468.1 pRRP2 - RAS-related on chromosome 22		oncogene	264259, 35696052, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108385, 264628, 35698423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2605	94316756 (5209, 5210)	Novel Protein sim. GBank gi 3628745 db BAA33366 - (AB013721) mitsugumin 23 [Oryctolagus cuniculus]		UNCLASSIFIED	22278998, 264490, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264758, 21906754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21906765, 21906766, 21906768, 21906769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636, 22278996, 264510, 264512, 265009, 264768, 22279002, 264566
2606	87746406 (5211, 5212)				

2607	87627742 (5213, 5214)	Novel Protein sim. GBank gij4826626[gb]AAD30202.1] - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264908, 264907, 264908, 66712502, 264828, 56182435, 55812038, 265010, 265017, 265018, 265019, 264768, 264689, 21906765, 55811957, 265020, 265022, 264692, 33657023, 264693, 33657109, 18108370, 264639, 56182323, 264509, 264907, 264908, 264592, 264758, 264631
2608	81734766 (5215, 5216)	Novel Protein sim. GBank gij226005 (U49973) - ORF2: function unknown [Homo sapiens]			
2609	94843791 (5217, 5218)	Novel Protein sim. GBank gij3024889[sp]P56524[Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)]	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55812038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264766, 264689, 21906765, 21906767, 21906769, 265020, 265021, 264691, 264692, 33657109, 27486261, 18108370, 65274791, 264636, 264556, 56182323, 18108385, 56526486
2610	88177664 (5219, 5220)	Novel Protein sim. GBank gij4336855[gb]AAD17989] - (AF108473) leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]		transcript factor	18108394, 22278994, 56994075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265006, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33657023, 263967, 33657182, 27486261, 18108374, 263976, 55811576, 264638, 87168518, 60432113, 22278999, 265017, 264684, 21906768, 22279000
2611	87428890 (5221, 5222)	Novel Protein sim. GBank gij3876761[emb]CAA92994] - (Z68760) predicted using GeneFinder. Similarity to Mouse FKBP-type peptidyl-prolyl cis-trans isomerases	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	
2612	87771199 (5223, 5224)	Novel Protein sim. GBank gij5679136[gb]AAD46874.1[AF16093] - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009, 264910, 264759, 265017, 21906767, 18108365, 18108388, 60432113
2613	79481496 (5225, 5226)			UNCLASSIFIED	264685
2614	87643948 (5227, 5228)	Novel Protein sim. GBank gij5533081[gb]AAD45009.1[AF16118] - (AF161181) P55T protein [Mus musculus]	Contains protein domain (PF00625) - Guanylate kinase		22278998, 29331825, 264508, 264906, 21906754, 264602, 264766, 264769, 52644229, 21906765, 33657109, 27486264, 18108370, 263972, 264555, 60432113
2615	87381886 (5229, 5230)			UNCLASSIFIED	264768, 18108394, 264692, 264693, 264508, 264509, 264907, 264628, 264908, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264685, 264766

2616	87428895 (5231, 5232)	Novel Protein sim. GBank glj3876761[embjCAA02994] - (Z68760) predicted using Genefinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278995, 22278997, 22278998, 60432049, 60432289, 264828, 60433356, 264594, 60433438, 33109954, 87188474, 265011, 265017, 265019, 264288, 264766, 21906765, 21908767, 285020, 265021, 18108376, 18108377, 18108387, 87168518, 264482, 264587
2617	86976888 (5233, 5234)	Novel Protein sim. GBank glj728831[spj39188]ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		kinase	265010, 265019, 264369, 264893, 55811576, 22279002
2618	91231862 (5235, 5236)	Novel Protein sim. GBank glj3319282 (AF049103) - Huntingtin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	264489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264908, 264907, 66712502, 29331830, 265008, 264910, 265009, 60433356, 60433438, 264758, 21906754, 265011, 87168559, 265017, 265018, 264369, 264288, 264766, 264768, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 33657023, 264892, 33657109, 264628, 18108374, 35695855, 18108381, 83373044, 18108385, 18108388, 56526486, 264563
2619	87694000 (5237, 5238)	Novel Protein sim. GBank glj2431772 (U66411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	- dehydrogenase	264259, 60432289, 60433438, 21906754, 264369, 60432113, 264566
2620	95314841 (5239, 5240)	Novel Protein sim. GBank glj4322567[gbjAAD16097] - (AF090436) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	52644507, 52645156, 52646842, 65274572, 22278995, 56994075, 35696286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35696052, 264907, 66712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264369, 264288, 264687, 264768, 52644229, 264688, 264689, 21906765, 21906768, 35695917, 52644150, 264692, 33657109, 35695763, 35696423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002
2621	80253495 (5241, 5242)				264594, 264636
2622	81780380 (5243, 5244)	Novel Protein sim. GBank glj4557341[refjNP_001174.1]pATP6 - ATPase, H ⁺ transporting, lysosomal subunit 1; vacuolar proton pump, H-ATPase subunit			264488, 264908, 264907, 264908, 264512, 265007, 264758, 35695917, 264634, 264636, 264563, 264482
2623	91633306 (5245, 5246)	Novel Protein sim. GBank glj3880355[embjCAB05209] - (Z62285) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148629

2624	91639308 (5247, 5248)	Novel Protein sim. GBank gjl3880355[emb]CAB05299] - (Z82285) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	56181686, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35698052, 29148489, 68712502, 52644045, 265007, 265008, 60433356, 33109954, 21908754, 265010, 265011, 265019, 264448, 264288, 21906765, 21906766, 21906767, 29148629, 35695917, 265021, 265022, 27486285, 18108370, 60431528, 55811576, 35695855, 56182323, 18108385, 87168518, 22279002, 18108391
2625	86452068 (5249, 5250)	Novel Protein sim. GBank gjl2887429[dbj]BAA24857] - (AB007887) KIAA0427 [Homo sapiens]		UNCLASSIFIED	264091, 264511, 263981
2626	16533787 (5251, 5252)	Novel Protein sim. GBank gjl487416 (L20302) - actin filament protein [Gallus gallus]		struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank gjl88462[pir]J27307 - proline-rich phosphoprotein (gene PRH1, Db allele) - human		UNCLASSIFIED	22278996, 265007, 265009, 264448, 21908767, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gjl3123552[emb]CAA18609] - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 284907, 264909, 265008, 264591, 60433356, 60433438, 265010, 265017, 285018, 264389, 264288, 18108357, 21906765, 21908768, 265022, 63274791, 264638, 18108387, 87168518, 22279002
2629	87376490 (5257, 5258)	Novel Protein sim. GBank gjl4929595[gb]AAD34058.1[AF15182] - (AF151821) CGI-63 protein [Homo sapiens]		synthase	29331825, 29331826, 264102, 265006, 264766, 35695917, 264891, 33657023, 263972, 18108374, 22279000
2630	78188364 (5259, 5260)	Novel Protein sim. GBank gjl321605[pir]JQ11161 - Gag protein - Visna virus (strain EV1)	Contains protein domain (PF000098) - Zinc finger, CCHC class	UNCLASSIFIED	264636, 18108385
2631	94845909 (5261, 5262)				52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 265007, 265008, 284910, 52846317, 33657084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 264448, 264288, 264369, 264766, 264768, 52644229, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 35696423, 65274791, 35695855, 264634, 264637, 52844332, 56182323, 60432113, 264566, 264486
2632	38730414 (5263, 5264)				264685

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gij113954[idbj BAA1088g] - (D84009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)		22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264906, 265006, 265007, 265008, 265009, 55812038, 33857084, 55811386, 265010, 265011, 87188559, 265018, 265019, 264683, 264288, 264886, 29148829, 33657023, 264693, 33657182, 35695763, 55811576, 264639, 56182323, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264565
2634	87330921 (5267, 5268)	Novel Protein sim. GBank gij5441611[emb CAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]		UNCLASSIFIED	29331826, 263972, 264089
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gij4680663[gb AAD27721.1] (AF132946) CGI-12 protein [Homo sapiens]			22278997, 264259, 29331824, 66714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264448, 264288, 21906766, 21906767, 21906768, 29148829, 18108376, 55811576, 35695855, 87168518, 22279000
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gij3879146[emb CAB07846] - (Z93386) Similarly to Yeast hypothetical 52.9 kD protein (SW:P43616); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40		264568, 29331822, 29331828, 265006, 60170831, 264681, 264765, 264885, 29148827, 21906769, 29148784, 265022, 60170815, 264635, 18108385, 56526486, 22279002, 264567
2637	95011298 (5273, 5274)	Novel Protein sim. GBank gij4758208[ref NP_004081.1]pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain		264488, 264489, 52644507, 264887, 52646365, 52646842, 22278994, 22278996, 22278999, 20281171, 264259, 29331822, 52645080, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52646317, 21906754, 52644296, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264687, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 65274820, 27486264, 18108370, 264628, 264629, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 52644332, 264639, 264558, 83373044, 60432113, 264564, 264565, 264566, 264486, 264567

2638	94326733 (5275, 5276)	Novel Protein sim. GBank gi 49298899 gb AAD34105.1 AF15186 - (AF15186) CGI-110 protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52644507, 52646842, 18108398, 55182575, 22278995, 22278995, 35696286, 22278997, 22278999, 264259, 60432049, 29331822, 60424269, 29331826, 35696052, 29146498, 284905, 52644045, 56182435, 60433356, 33657402, 55812038, 55811386, 265019, 264288, 264769, 52644229, 56181562, 29148627, 29148629, 55811957, 29148784, 35695917, 265021, 52644150, 33657023, 65274620, 33657109, 35695763, 18108374, 55810784, 35696423, 55811576, 35695855, 60431850, 56182323, 60432113, 264404
2639	85361346 (5277, 5278)	Novel Protein sim. GBank gi 2190007 gb BAA20355 - (AB004109) phosphatidylserine synthase II [Cricketulus griseus]		synthase	264488, 29331825, 35696052, 264508, 264509, 264909, 264512, 33657402, 60433438, 264758, 85658542, 264600, 265020, 265021, 33657109, 264628, 35696423, 264555, 264639, 264563, 264564, 264565, 264566, 264486
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gi 3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm, score: 17.78 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm, score: 67.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	29331822, 29331826, 264906, 33109954, 265017, 265019, 21906788, 35695763, 264636, 264637, 18108387
2641	11669834 (5281, 5282)	Novel Protein sim. GBank gi 2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank gi 4490304 emb CAB38785.1 - (AL036676) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	264259, 29331822, 33657402, 265019, 264369, 264691, 264634, 56526486, 22279002
2643	87643981 (5285, 5286)	Novel Protein sim. GBank gi 3789797 gb AAC67502.1 - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	helicase	22278997, 264259, 29148499, 56182435, 264910, 265010, 18108351, 264682, 264683, 264369, 264684, 264685, 264686, 29148627, 264690, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264558, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gi 3789797 gb AAC67502.1 - (AF059569) actin binding protein MAYVEN [Homo sapiens]		nucf_rept	284107, 264687
2645	17277228 (5289, 5290)	Novel Protein sim. GBank gi 1708722 sp P49749 EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	265007
2646	94148542 (5291, 5292)			UNCLASSIFIED	264908, 264687, 264632, 83373044

2647	91212878 (5283, 5284)			UNCLASSIFIED	56182575, 22278996, 35696286, 22278998, 264259, 29331822, 56182181, 29331825, 60424269, 60432289, 35696052, 66712502, 264908, 265007, 55812038, 33109954, 21906754, 33657084, 285019, 264448, 264288, 56181562, 21906765, 21906766, 21906768, 21906769, 35695917, 285020, 265021, 52644150, 264693, 33657109, 33657349, 60431528, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264584
2648	87600587 (5295, 5296)				29146498, 56182435, 33109954, 265011, 264682, 55811957, 35695917, 264690, 263976, 18108377, 35696423, 60432113
2649	94128783 (5287, 5288)	Novel Protein sim. GBank gl 3041852 (AC004539) - unknown function; similar to Y09105 (P1D:g1666171) [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278998, 29331824, 29331826, 60432289, 66712502, 56182435, 60170831, 60432229, 33657402, 33109954, 21906754, 265017, 264686, 264688, 21906765, 21906768, 60170815, 264693, 263987, 18108370, 263976, 60170394, 60432113, 22279002, 264563
2650	87287533 (5289, 5300)	Novel Protein sim. GBank gl 5360271[dbj][BAA81908.1] - (AB029335) HrPET-3 [Halocynthia roretzi]			264685
2651	88088745 (5301, 5302)	Novel Protein sim. GBank gl 4240225[dbj][BAA74891.1] - (AB020675) KIAA0888 protein [Homo sapiens]	Contains protein domain (PF00054) Laminin G domain	synthase	29331824, 29331826, 29331827, 265007, 55812038, 21906754, 18108368, 18108384, 22279002, 264567
2652	10343125 (5303, 5304)	Novel Protein sim. GBank gl 4493956[emb][CAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c), Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....)		UNCLASSIFIED	264692
2653	87798735 (5305, 5306)	Novel Protein sim. GBank gl 4493956[emb][CAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c), Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....)		UNCLASSIFIED	265018, 18108370, 18108387, 264566
2654	95103240 (5307, 5308)				60424179, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 65274727
2655	91228018 (5309, 5310)	Novel Protein sim. GBank gl 3875272[emb][CAB02861] - (Z81051) predicted using GeneFinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	transcription factor	56182575, 56181888, 264092, 264259, 56182181, 60432288, 264907, 33657402, 55812038, 21906754, 87168559, 265017, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 33657109, 18108370, 264628, 55811576, 264556, 264639, 83373044, 56526486, 264404, 60432113
2656	84562601 (5311, 5312)	Novel Protein sim. GBank gl 3043718[dbj][BAA25523] - (AB011169) KIAA0597 protein [Homo sapiens]			264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank gij5689509[dbj BAA83038.1] - (AB029009) KIAA1086 protein [Homo sapiens]		dna_rna_bind	264693
2658	88062454 (5315, 5316)	Novel Protein sim. GBank gij3688089 (AC005757) - R32611_1 [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331828, 29331828, 265019, 264683, 21906768, 35695917, 264693, 35695855, 264637, 87168518, 264486, 264567
2659	87600755 (5317, 5318)	Novel Protein sim. GBank gij5420387[emb CAB46879.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	264909, 264910, 265018, 264369, 264769, 21906769, 264693, 263972, 18108388
2660	91718472 (5319, 5320)	Novel Protein sim. GBank gij728837[sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII]	Contains protein domain (PF00036) - EF hand	kinase	264488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 35696052, 264908, 56182435, 265008, 265009, 60433356, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264369, 264288, 264687, 21906765, 29148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22279000, 22279002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank gij4758048[ref NP_004739.1 pCPR8 - cell cycle progression 8 protein]		glycoprotein	60432049, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264909, 264593, 33109954, 265010, 265017, 265018, 265019, 264760, 264448, 264369, 264288, 21906765, 21906768, 265022, 264691, 33657023, 27488262, 60431528, 18108374, 35695855, 18108388, 264482, 264555, 264556, 264558, 264486
2662	80228739 (5323, 5324)	Novel Protein sim. GBank gij3874714[emb CAA91263] - (Z66494) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; [Caenorhabditis elegans]		dehydrogenase	264906, 264909, 264757, 264758, 264767, 264691, 33657023, 264638
2663	87780623 (5325, 5326)	Novel Protein sim. GBank gij1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264509, 264595, 264288, 264685, 264686
2664	85518329 (5327, 5328)	Novel Protein sim. GBank gij1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]		UNCLASSIFIED	35696286, 22278999, 29331822, 35696052, 264906, 264907, 264909, 264510, 264511, 264512, 264593, 60433438, 265019, 264681, 21906765, 21906766, 21906767, 21906768, 265020, 265022, 35696423, 35695855, 22279002, 264482, 264488
2665	87770662 (5329, 5330)	Novel Protein sim. GBank gij4884406[emb CAB43311.1] - (AL050190) hypothetical protein [Homo sapiens]		UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264558, 22279002
2666	87828472 (5331, 5332)	Novel Protein sim. GBank gij5108956[gb AAD39908.1 AF113615] FH1/FH2 domain-containing protein FHOS [Homo sapiens]		nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264632, 264556, 264557, 264558, 284559, 264563, 264565, 264567
2667	87422720 (5333, 5334)	Novel Protein sim. GBank gij2500570[sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1]	Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	

2668	91216716 (5335, 5336)	Novel Protein sim. GBank gij5454186[re]NP_006327.1pZYCj - ZYG homolog	UNCLASSIFIED	56181686, 35696288, 22278998, 22278999, 56182181, 29331824, 60424269, 29331825, 35696052, 29331828, 68712502, 56182435, 60433356, 284758, 21908754, 55811386, 265011, 87168559, 265017, 265019, 55811150, 284448, 264369, 264288, 21906765, 21906768, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 264692, 33657109, 35695763, 60431528, 18108374, 35696423, 55811576, 264634, 60431850, 83373044, 18108385, 87168518, 22279000, 264563, 264564
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gij2147012[pi]JC4899 - proline rich protein - rat		264489, 264889, 21906767, 65274572, 56182575, 21906768, 29148827, 21908769, 29148629, 35696286, 35695917, 22278998, 22278998, 265021, 265022, 60170515, 52644150, 60432049, 264259, 264691, 33657023, 264692, 29331822, 29331824, 29331825, 60432289, 33657109, 29331828, 29331827, 35696052, 29331828, 29148498, 29146499, 264905, 264908, 52844045, 284909, 56182435, 35696423, 65274791, 35695855, 265006, 264910, 264635, 60432229, 264592, 264638, 56182323, 60433356, 60170394, 60433438, 264559, 264595, 55812038, 33109954, 87168559, 60432113, 265019, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gij1723523[sp]Q10362[YDBB_SCHPO - HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	18108370, 263974
2671	91214836 (5341, 5342)	Novel Protein sim. GBank gij4768277[gb]AAD29444.1[AF064255] very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]	transport	52646842, 56994075, 284259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21908754, 264682, 264288, 265021, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 18108376, 18108385
2672	87399123 (5343, 5344)	Novel Protein sim. GBank gij4966346[gb]AAD34877.1[AC008341] Contains two PF01344 Kelch motif domains. [Arabidopsis thaliana]	UNCLASSIFIED Kelch motif	264767

2673	87430749 (5345, 5348)	Novel Protein sim. GBank gll5457337[emb]CAB41505.2] - (AJ236876) poly(ADP-ribose) polymerase-2 [Homo sapiens]	Contains protein domain (PF00844) - Poly(ADP-ribose) polymerase catalytic region.	polymerase	22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331828, 35696052, 60433438, 87168474, 87168559, 265017, 265018, 265019, 264448, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 35695763, 60431850, 60170394, 87168518, 264563
2674	94847721 (5347, 5348)	Novel Protein sim. GBank gll4758824[ref]NP_004280.1[pNRF3 - nuclear factor (erythroid-derived 2)-like 3]	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	264488, 22278996, 35696286, 264091, 264259, 29331824, 29331826, 35696052, 264511, 55812038, 85658542, 264766, 21906765, 35695917, 264629, 35696423, 18108383, 87168518
2675	79563835 (5349, 5350)			UNCLASSIFIED	264691
2676	79628393 (5351, 5352)			UNCLASSIFIED	264906, 265008
2677	84329800 (5353, 5354)	Novel Protein sim. GBank gll1079042[pirl]S52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278999, 264490, 264259, 52645080, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 29146489, 29331830, 284908, 52644045, 265006, 265007, 265008, 265009, 60432229, 60433356, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264682, 264448, 264683, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33657023, 263967, 33657109, 27486264, 27486285, 33657349, 35695763, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 83373044, 18108387, 22279000, 22278002, 264564

2678	95001694 (5355, 5356)	Novel Protein sim. GBank gi 86760 pir A0465 - alanine transaminase (EC 2.6.1.2), cytosolic - human		UNCLASSIFIED	264488, 263894, 264489, 18108394, 52646842, 35696286, 22278999, 264259, 29331825, 35698052, 264508, 264805, 264509, 264906, 264907, 264908, 264909, 264510, 284511, 265006, 264512, 285007, 265008, 264910, 265009, 264593, 264594, 264596, 284758, 33109954, 52646317, 21808754, 285010, 285011, 87168559, 264800, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108364, 18108365, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264486, 264567
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gi 1709233 sp P07514 NC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FADNAD-binding Cytochrome reductase	reductase	264488, 22278996, 35696286, 264259, 29331826, 29331827, 29331828, 264909, 56182435, 264113, 264511, 265008, 60433438, 264758, 85658542, 87168474, 265011, 265017, 265019, 264288, 21908766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810764, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264566
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gi 4589604 db BAA76824.1 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struc	264259, 264102, 264905, 264908, 285007, 265008, 33109954, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2681	80933844 (5361, 5362)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264489, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 264512, 264910, 264594, 60433438, 264758, 264803, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21908769, 35695917, 285020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gi 423468 pir JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	35696286, 264908, 55811386, 265017, 55811150, 55811957, 35695917, 60431528, 55810764, 55811576, 35696423, 65274791, 56526486
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gi 5114351 gb AAD40286.1 - (AF156271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00822) - SPRY domain	interleukinrecept	264909, 264769, 264635, 264636

2684	85787151 (5387, 5388)	Novel Protein sim. GBank glj4886469[emb]CAB43385.1] - (AL050284) hypothetical protein [Homo sapiens]			264593
2685	88054209 (5389, 5370)	Novel Protein sim. GBank glj3342729 (AC005331) - R31341_2 [Homo sapiens]		UNCLASSIFIED	
2686	87628690 (5371, 5372)	Novel Protein sim. GBank glj4650844[db]BAA77027.1] - (AB026190) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF01344) - Kelch motif	struct	264259, 29331822, 60432289, 29331827, 29331830, 264909, 264512, 264596, 264769, 264534, 264555, 264556, 264557, 264558, 60170394, 264559, 264486
2687	87898183 (5373, 5374)	Novel Protein sim. GBank glj5281314[gb]AAD41475.1[AF13312] - (AF133123) transcription factor IIC102 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	transcriptfactor	18108394, 18108396, 22278986, 35696286, 22278997, 29331826, 29331828, 66712502, 21906754, 265011, 264760, 264761, 264763, 264689, 21906765, 35696423, 264559, 18108385, 264563
2688	79959594 (5375, 5376)	Novel Protein sim. GBank glj3880023[emb]CAA97339] - (Z73098) Similarity to yeast hypothetical protein (Swiss Prot accession number Q09695); cDNA EST EMBL:D72982 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00560) - Leucine Rich Repeat		264908, 264760
2689	94122440 (5377, 5378)	Novel Protein sim. GBank glj2477513 (AC002398) - F25965_3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct	22278997, 22278998, 22278999, 29331824, 35696052, 264906, 264908, 56182435, 264512, 264910, 265009, 60433438, 21906754, 18108351, 264682, 264683, 264767, 21906765, 21906766, 21906768, 33657023, 33657182, 27486262, 27486264, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002
2690	88003055 (5379, 5380)	Novel Protein sim. GBank glj2477513 (AC002398) - F25965_3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct	
2691	91219241 (5381, 5382)	Novel Protein sim. GBank glj4107276[emb]CAA67130] - (X98506) acetyl-CoA synthetase [Solanum tuberosum]		synthase	65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264596, 33109954, 265017, 264448, 264288, 264369, 264684, 21906769, 60170515, 60431528, 55810764, 264634, 264636, 264556, 264637, 22279002, 264564, 264566
2692	94111914 (5383, 5384)	Novel Protein sim. GBank glj3513303 (AC005594) - R26984_1 [Homo sapiens]	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	
2693	20438807 (5385, 5386)	Novel Protein sim. GBank glj3122400[sp]O35682[MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264592
2694	94111918 (5387, 5388)	Novel Protein sim. GBank glj3122400[sp]O35682[MUG_MOUSE - MYELOID UPREGULATED PROTEIN			264599
2695	95345513 (5389, 5390)	Novel Protein sim. GBank glj4972740[gb]AAD34765.1] - (AF132177) unknown [Drosophila melanogaster]		collagen	35696286, 56994075, 22278999, 264259, 35696052, 29331830, 265011, 264288, 56181562, 264690, 264692, 33657023, 27486262, 263976, 18108376, 35696423, 35695855, 60170394, 83373044, 56526486, 22279000, 22279002, 264566
2696	87874040 (5391, 5392)	Novel Protein sim. GBank glj728831[sp]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		synthase	264594, 21906768, 18108370, 18108372

2697	91638472 (5393, 5394)	Novel Protein sim. GBank gi 5689473 dbj BAA83020.1 - (AB028991) KIAA1068 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 264781, 18108351, 284448, 264288, 264766, 264688, 264689, 21906765, 21906768, 265020, 265021, 60170615, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87168518, 22279002, 264563, 264482
2698	94325691 (5395, 5396)	Novel Protein sim. GBank gi 841318 (U22818) - mutant sterol regulatory element binding protein-2 [Cricetulus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 28331830, 264909, 5264045, 264910, 60433356, 33657402, 33109954, 265017, 265018, 265019, 264288, 21906765, 21906766, 21906767, 21906769, 29148628, 35695917, 265021, 265022, 52844150, 33657023, 33657182, 27486261, 35696423, 65274791, 264638, 60432113, 22279000
2699	87780650 (5397, 5398)	Novel Protein sim. GBank		UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139836 (5399, 5400)	Novel Protein sim. GBank gi 5174395 ref NP_005006.1 pB120 - Brain protein 120		UNCLASSIFIED	60424269, 56182435, 60432228, 60433438, 55811386, 265017, 55811150, 264448, 56181562, 55811957, 264693, 33657109, 60431528, 264629, 55810764, 55811576, 65274791, 60431850, 60432113
2701	94148584 (5401, 5402)	Novel Protein sim. GBank gi 1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108394, 52645156, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29148499, 265008, 60433356, 33657402, 60433438, 264595, 33657084, 18108351, 264288, 264769, 18108359, 21906768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57295366 (5403, 5404)	Novel Protein sim. GBank gi 2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2703	87648514 (5405, 5406)	Novel Protein sim. GBank gi 5689399 dbj BAA82983.1 - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar)		60432289, 265007, 21906765, 21906768, 265021, 264563

2704	87648515 (5407, 5408)	Novel Protein sim. GBank gj4335694[gb AAB63294] - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278998, 29331828, 29146489, 264805, 264906, 264907, 52644045, 264511, 33857402, 264600, 264602, 265017, 264605, 264781, 18108351, 264764, 264687, 264769, 265021, 264691, 264692, 18108362, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5409, 5410)				264489, 264509, 264511, 264512, 264910, 264593, 87168474, 264604, 264288, 264687, 264769, 264638, 264566, 264486
2706	94326788 (5411, 5412)	Novel Protein sim. GBank gj325952[emb CAA16821.1] - (AL021728) /prediction=(method:; /match=(desc: [Drosophila melanogaster])	UNCLASSIFIED		264488, 52646842, 65274572, 22278994, 56994075, 22278997, 264259, 29331824, 29331825, 29331826, 29331828, 33856970, 264907, 264908, 264909, 52644045, 56182435, 265006, 265007, 60433438, 55812038, 21906754, 52644298, 265010, 264601, 265017, 265019, 264681, 264448, 264682, 264288, 264686, 264687, 264688, 21906766, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 264690, 264691, 33657023, 264692, 264693, 65274620, 27486264, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394, 83373044, 65274727, 87168518, 22278900
2707	88089839 (5413, 5414)	Novel Protein sim. GBank gj3417294 (AC004381) - Unknown gene product [Homo sapiens]			22278996, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52645129
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gj545790[bs 147178 - DARPP-32-dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa]	UNCLASSIFIED		65274572, 264259, 29331822, 29331825, 60432289, 29331828, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264369, 264288, 264765, 264693, 264565
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gj3169705 (AC004780) - F17127, 1 [Homo sapiens]	UNCLASSIFIED		29331822, 18108370, 18108374, 83373044
2710	87627979 (5419, 5420)	Novel Protein sim. GBank gj4466311[emb CAB37992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			29331824, 264759, 264693, 18108382, 18108388

2711	94111920 (5421, 5422)	Novel Protein sim. GBank gij3122400[sp]O35682[MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264488, 264687, 52645156, 264769, 21908764, 21908765, 21906767, 21906768, 21908769, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 284690, 284259, 264691, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182; 29331827, 27486262, 33657349, 264508, 264905, 264907, 60431528, 264908, 264909, 55610764, 35696423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 264557, 264558, 55812038, 33109954, 18108385, 21906754, 33657084, 87168518, 87168474, 87168559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264585, 264764, 264568, 264288, 264768
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gij5081315[gb]AAD39343.1[AF076607] prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferase	264488, 35696286, 22278998, 264259, 29331824, 60432289, 35696052, 264508, 284908, 66712502, 52644045, 265008, 60432229, 33657402, 60433358, 265010, 265019, 18108351, 264681, 264288, 264685, 21906765, 21906766, 21906768, 21908769, 55811957, 35695917, 265020, 265021, 60170815, 264691, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35696423, 35695855, 264555, 52644332, 56182323, 87168518, 60432113 66714117, 264906, 264563
2713	98003064 (5425, 5426)	Novel Protein sim. GBank gij2477513 (AC002398) - F25965_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5429, 5430)	Novel Protein sim. GBank gij4321968[gb]AAD15897] - (AF067430) Smarce1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264764, 284288, 264766, 264768, 264636
2716	98003068 (5431, 5432)	Novel Protein sim. GBank gij2477513 (AC002398) - F25965_3 [Homo sapiens]		glycoprotein	264091, 264259, 29331822, 66714117, 264908, 264369, 264693, 264556, 264563 264593, 264558
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gij3327046[db]BAA31591] - (AB014516) KIAA0616 protein [Homo sapiens]			
2718	79504062 (5435, 5436)				264693
2719	88180423 (5437, 5438)	Novel Protein sim. GBank gij746495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87168559, 265019, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gij1335873 (U46680) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108374, 60424179, 264489, 56182435, 21908765, 21908766, 35698423, 22278997, 265020, 265022, 265006, 265008, 264092, 264636, 60432229, 284691, 264692, 33657023, 264693, 33657402, 83373044, 29331824, 18108368, 60424269, 29331826, 18108385, 52645129, 21908754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22279002, 264905, 264482, 264563, 264906, 18108351, 264681, 18108370, 29331830, 264908, 68712502, 52644045, 264909, 264828, 18108354, 22278995, 35698286, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21908768, 265021, 33657109, 263969, 60431528, 264629, 55811576, 66274791, 35695855, 264631, 264637, 60170394, 56182323, 22279000, 35696286, 22278999, 21906754, 265017, 264762, 264288, 21906765, 21906767, 21906768, 35695917, 18108362, 27486262, 35695855, 284558, 264559
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gij4929683jgb/AAD34092.1 AF15185 - (AF151855) CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023		
2722	91638807 (5443, 5444)	Novel Protein sim. GBank gij3212997jgb/AAC23434.1 - (AC004997) match to ESTs AA667999 (NID:g2626700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g712314); similar to various tre-like proteins including: AF040654 (PID:g2746883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00566) - TBC domain	oncogene	
2723	87387732 (5445, 5446)			UNCLASSIFIED	264508, 264509, 264906, 264909, 264910, 55812038, 264766, 264687, 264629, 264636, 264486
2724	87639563 (5447, 5448)	Novel Protein sim. GBank gij4680681jgb/AAD27730.1 AF13295 - (AF132955) CGI-21 protein [Homo sapiens]		ubiquitin	18108396, 22278999, 20281099, 29331824, 29331826, 60432289, 29331828, 60170831, 60432229, 60433438, 18108351, 264682, 21908766, 21906767, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127_1 [Homo sapiens]		UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21906754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35696423, 18108385, 22279000
2726	86880599 (5451, 5452)	Novel Protein sim. GBank gij3342738 (AC005328) - R26660_1, partial CDS [Homo sapiens]		MHC	264488, 264828, 264685

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gi 731267 sp P39219 RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00849) - RNA pseudouridylylate synthase	synthase	65274572, 56182575, 22278984, 56984075, 22278986, 22278987, 22278989, 60432049, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 264509, 66712502, 264910, 33657402, 60433438, 264758, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 264767, 21906765, 21906767, 21906769, 55811957, 35695917, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 55811576, 35696423, 35695955, 264630, 60431850, 264636, 56182323, 87168518, 60432113, 22279000, 264564, 264565
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	18108394, 56182435, 21906767, 55811957, 35695955, 265021, 264690, 264556, 264259, 264557, 29331822, 264559, 264448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gi 2408095 emb CAB16300 - (Z99168) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	65274572, 264259, 60432289, 66712502, 56182435, 264448, 264288, 264369, 55811957, 265021, 264557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264887, 29331824, 29331826, 35696052, 264107, 56182435, 265008, 265009, 264592, 60431735, 265011, 264601, 265017, 18108351, 264288, 29148627, 55811957, 265021, 264690, 18108368, 18108374, 264557, 264558, 264559, 18108387, 56528486, 264566, 264486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gi 1723239 sp Q10166 YAUB_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME 1	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase		264259, 35696052, 265008, 264758, 284762, 264448, 264288, 29148627, 21906769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	264687, 264489, 18108358, 56182435, 264689, 35696423, 55811957, 265021, 265006, 265008, 264910, 265009, 264690, 264555, 264259, 264556, 264557, 264558, 264559, 18108383, 33657109, 87168518, 265010, 264601, 60432113, 265017, 264905, 264448, 263972, 264369, 264567 29331825, 264509, 264909
2733	87363060 (5465, 5466)			UNCLASSIFIED	
2734	94140286 (5467, 5468)	Novel Protein sim. GBank gi 4519621 db BAA75670.1 - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	60424119, 52644507, 56182575, 264259, 29331828, 264907, 264510, 264910, 60433356, 265019, 55811150, 264681, 264763, 264687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712336 (5469, 5470)	Novel Protein sim. GBank gij3850569 (AC005278) - ESTs gb T21276, gb T45403, and gb AA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278996, 60432289, 29331827, 29146498, 284108, 284909, 284112, 33657402, 87168474, 265017, 264762, 264448, 264764, 264684, 21908765, 264693, 33657109, 263976, 264636, 264638, 264557, 22279000, 22279002, 264567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264905, 264628, 264629, 263978, 264632, 264564
2737	87604526 (5473, 5474)				264680
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gij2558501 dbj BAA22886 (D63850) hepatoma-derived growth factor [Mus musculus]			264488, 265009, 264768, 264691
2739	94318834 (5477, 5478)	Novel Protein sim. GBank gij5420387 emb CAB46679.1 - (AJ243459) proteophosphorylcan [Leishmania major]		UNCLASSIFIED	264684, 83373044, 264566
2740	94148762 (5479, 5480)	Novel Protein sim. GBank gij3417386 emb CAA75495 - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264488, 56182575, 22278995, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146498, 29331830, 265006, 265007, 265009, 60432229, 33657402, 55812038, 87168474, 285010, 285011, 265017, 265018, 265019, 264605, 264681, 264288, 264369, 52644229, 21908765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 264691, 264692, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 60431850, 264639, 56182323, 18108382, 18108385, 65274727, 22279002, 264584
2741	88047518 (5481, 5482)	Novel Protein sim. GBank gij3242764 (AC005154) - similar to protein U28928 (PID:g861306) [Homo sapiens]		UNCLASSIFIED	22278996, 52644045, 52644229, 21906768, 21906769, 265020, 60170615, 264691
2742	87648644 (5483, 5484)	Novel Protein sim. GBank gij4758412 ref NP_004472.1 pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyltransferase 2 (GalNAc-T2)	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264905, 264758, 55812038, 264369, 29148627
2743	87627991 (5485, 5486)	Novel Protein sim. GBank gij4468311 emb CAB37992 - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 264906, 264908, 265006, 60433438, 265017, 18108351, 264448, 264764, 264288, 21906765, 21906767, 264690, 264691, 264693, 263969, 263971, 35695855, 264637, 264558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gij3880433 emb CAA91399 - (Z68521) similar to mitochondrial RNA splicing MSR4 like protein: cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35696423, 35695917, 35695855, 265020, 265021, 264511, 285009, 264490, 264558, 264259, 264557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331826, 21908754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 264482, 264448, 264486, 264369, 264288

2745	87740125 (5489, 5490)	Novel Protein sim. GBank gij4405795[gb AAD19826] - (AF038963) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	35696286, 284509, 264905, 264807, 284908, 264510, 264512, 265008, 264758, 264801, 265017, 264604, 264763, 264288, 264886, 264769, 264693, 35696423, 35695855, 264634, 264636, 264563, 264564, 264565
2746	85418601 (5491, 5492)	Novel Protein sim. GBank gij4758738[re NP_004680.1 pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	UNCLASSIFIED	22278996, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 264905, 264806, 264907, 264908, 264909, 52644045, 265006, 60170831, 264596, 55812038, 265018, 264883, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 33657023, 264693, 33657109, 18108368, 18108374, 264558, 18108385, 22279000, 264563
2747	94112677 (5493, 5494)	Novel Protein sim. GBank gij4557803[re NP_000282.1 pNPC1 - Niemann-Pick disease, type C1		glycoprotein	264569, 52644507, 18108394, 22278995, 35696286, 22278997, 22278999, 52645080, 29331824, 56182181, 29331826, 29331827, 35696052, 264907, 264908, 264909, 265009, 33109854, 55811386, 87168474, 265010, 87168559, 264603, 265019, 264760, 264886, 264768, 21908769, 35695917, 60170815, 264692, 33657023, 52645129, 27486264, 60431528, 18108374, 35696423, 35695855, 264556, 56182323, 18108385, 264482
2748	91214983 (5495, 5496)	Novel Protein sim. GBank gij4181272[emb CAA09984] - (AJ012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00846) - F-box domain.		63274572, 29331828, 264112, 264511, 265019, 264760, 264767, 264768, 264769, 21908768, 21908769, 265020, 27486262, 56526486, 87168518, 22279000
2749	87346307 (5497, 5498)				264259, 264908, 264510, 265008, 265009, 264760, 264369, 264768, 264563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gij1872498 (U74297) - PIUS [Oryctolagus cuniculus]		UNCLASSIFIED	264488, 52644507, 18108396, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 264595, 33657084, 265011, 265019, 18108351, 264288, 264686, 264769, 264689, 55811957, 264693, 27486264, 18108370, 18108374, 264558, 18108385, 264482, 264563
2751	87057465 (5501, 5502)			UNCLASSIFIED	29331822, 29331824, 265017, 33657023
2752	88062875 (5503, 5504)	Novel Protein sim. GBank gij3041859 (AC004534) - OG-2 homeodomain protein-like; similar to U65067 (PID:g1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2753	94138972 (5505, 5508)	Novel Protein sim. GBank gj 3851648 (AF088301) - neural F-box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	56182575, 56994075, 22278988, 28331822, 29331824, 29331825, 29331826, 265007, 264593, 55812038, 33109954, 18108351, 264288, 56181582, 21906767, 21906768, 285021, 264693, 18108374, 65274791, 264632, 58182323, 22279002, 264563, 264587
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gj 535428 (U13736) - calmodulin-like protein [Plum salivum]	Contains protein domain (PF00038) - EF hand	struct	22278989, 66714117, 29331827, 35696052, 29331828, 264906, 264908, 264909, 265011, 265017, 265018, 265019, 264288, 21906765, 21906767, 265022, 33657023, 264693, 56182323, 18108382, 22279000
2755	88001472 (5508, 5510)	Novel Protein sim. GBank gj 2996653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465908 (5511, 5512)	Novel Protein sim. GBank gj 1173539 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - eph	UNCLASSIFIED	264594
2757	95361590 (5513, 5514)	Novel Protein sim. GBank gj 3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]	Src homology domain 2		85658542, 264693
2758	79637846 (5515, 5516)	Novel Protein sim. GBank gj 2072200 (U94863) - p40 [Borna disease virus]		struct	264693
2759	91005312 (5517, 5518)	Novel Protein sim. GBank gj 4914573 (emb CAB43685.1) - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	65274572, 35696286, 66714117, 28331828, 264508, 56182435, 21906754, 55811957, 264629, 264636, 56182323, 22279002, 264908
2760	79824798 (5519, 5520)	Novel Protein sim. GBank gj 3138150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	nuclease	22278998, 29331822, 29331830, 265010, 265019, 264288, 21906765, 21906768, 21906769, 265020, 56182323, 22279002, 264563
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gj 2905843 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF01352) - KRAB box	struct	18108394, 22278998, 264906, 264909, 265006, 265007, 264757, 265010, 265011, 265017, 265019, 18108351, 264448, 264683, 264686, 264768, 265020, 265021, 265022, 264691, 18108362, 264693, 18108365, 33657109, 18108368, 18108370, 18108381, 18108382, 18108384, 18108388, 87168518
2762	87592699 (5523, 5524)	Novel Protein sim. GBank gj 3511122 (AF060503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	transcriptfactor	264369, 35696423
2763	87539968 (5525, 5526)	Novel Protein sim. GBank gj 2905843 (AF045244) - ribitol kinase [Klebsiella pneumoniae]			52646842, 264259, 29331822, 29331825, 29331826, 29331828, 33656970, 264905, 264907, 29331830, 265006, 265009, 21906754, 265019, 264448, 21906769, 27466262, 56182323, 56526486, 87168518, 264487
2764	94305140 (5527, 5528)	Novel Protein sim. GBank gj 2905843 (AF045244) - ribitol kinase [Klebsiella pneumoniae]			

2765	94315105 (5528, 5530)	Novel Protein sim. GBank gij4688672[emb CAA17688.2] - (AL0202018) /prediction=(method:; /prediction=(method:; /match=(desc: [Drosophila melanogaster])			264488, 65274572, 22278995, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264509, 284905, 264908, 264907, 264908, 264909, 264512, 264910, 265009, 264592, 284595, 264758, 55812038, 33109954, 285010, 87168559, 264600, 285018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264766, 264767, 264768, 56181562, 21908764, 21906765, 21906768, 35695917, 265021, 264691, 264692, 33657023, 33657109, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87168518, 22279000, 22279002, 264563, 264482
2768	94315109 (5531, 5532)	Novel Protein sim. GBank gij5441611[emb CAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	- dna_ma_bind	264488, 65274572, 60432289, 264907, 264909, 264511, 264512, 60433358, 264288, 264685, 264689, 35695917, 265022, 264693, 264628, 65274791, 264635, 264555, 264556, 264557, 264638, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gij1079451[pr j A55463] - tropomodulin, skeletal muscle - chicken		struct	264112, 263974, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gij5441322[emb CAB46721.1] - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]		UNCLASSIFIED	264488, 263994, 264489, 35696286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35696052, 264508, 264509, 264905, 264908, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33857402, 264594, 264595, 264757, 264596, 265011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 264686, 264768, 18108357, 264768, 264689, 21908766, 21906768, 21906769, 35695917, 265021, 265022, 33657023, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264486, 264567

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gj[5419859]emb[CAB46375.1] - (AL098725) hypothetical protein [Homo sapiens]		tubulin	264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 264908, 29331830, 56182435, 264592, 33657402, 264448, 264369, 264288, 60170615, 264691, 33657023, 264692, 33657109, 18108374, 55811576, 264634, 264636, 56182323, 83373044, 60432113, 18108398, 22278995, 22278996, 22278999, 264105, 265006, 265019, 18108351, 264687, 21906765, 18108364, 264629, 18108374, 264631, 18108385, 18108388
2770	87730182 (5539, 5540)	Novel Protein sim. GBank gj[5701955]emb[CAB52157.1] - (AL109736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331830, 56182435, 264592, 33657402, 264448, 264369, 264288, 60170615, 264691, 33657023, 264692, 33657109, 18108374, 55811576, 264634, 264636, 56182323, 83373044, 60432113, 18108398, 22278995, 22278996, 22278999, 264105, 265006, 265019, 18108351, 264687, 21906765, 18108364, 264629, 18108374, 264631, 18108385, 18108388
2771	88084071 (5541, 5542)	Novel Protein sim. GBank gj[3083433] (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 264369
2772	95357308 (5543, 5544)	Novel Protein sim. GBank gj[4885531]ref[NP_005465.1]pVY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	264259, 29331822, 29331824, 66714117, 60432289, 29331827, 264905, 265009, 264592, 55812038, 65274444, 264766, 21906769, 33657109, 263978, 264555, 264638, 264557, 83373044, 264563, 264584, 264486
2773	94138994 (5545, 5546)	Novel Protein sim. GBank gj[3288888] (AC005253) - R28445_1 [Homo sapiens]		UNCLASSIFIED	18108374, 264686, 264687, 263976, 56182435, 264689, 55810784, 21906766, 35696423, 55811576, 65274791, 56181686, 55811957, 35695855, 264110, 265021, 264112, 265022, 265006, 265008, 264092, 264094, 60431850, 264637, 264691, 264259, 264692, 263981, 264594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424269, 18108385, 29331826, 29331827, 27486261, 29331828, 35696052, 55811386, 264107, 60432113, 265017, 55811150, 18108351, 264681, 264906, 18108370, 264484, 264682, 20281069, 264448, 66712502, 264683, 264764, 264288, 264684, 264768, 263974, 22278995, 35696286, 22278996, 22278999, 264259, 29331826, 60432289, 35696052, 264112, 33657402, 21906754, 87168559, 265017, 265018, 264288, 21906766, 21906767, 21906769, 35695917, 285020, 265021, 33657023, 33657109, 18108370, 263976, 35696423, 35695855, 87168518, 22279000, 264482
2774	87818908 (5547, 5548)	Novel Protein sim. GBank gj[465852]spP34388]YLS3_CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S18	ribosomalprot	264259, 29331826, 60432289, 35696052, 264112, 33657402, 21906754, 87168559, 265017, 265018, 264288, 21906766, 21906767, 21906769, 35695917, 285020, 265021, 33657023, 33657109, 18108370, 263976, 35696423, 35695855, 87168518, 22279000, 264482

2775	95307987 (5549, 5550)	Novel Protein sim. GBank gi 4688132 gb AAD27775.1 AF07704 - (AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	Contains protein domain (PF00177) - Ribosomal protein S7p/S5a	ribosomalprot	264488, 22278995, 56994075, 22278998, 35698288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 80432289, 29331827, 29331828, 35696052, 265007, 21906754, 265017, 265019, 264448, 264882, 264369, 264288, 18108354, 52644229, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 35895917, 265021, 265022, 60170615, 264691, 18108370, 35696423, 65274791, 35695855, 264634, 60431850, 60170394, 56182323, 264558, 18108388, 22279000, 284563, 264565, 284488, 264567
2776	87781557 (5551, 5552)				56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21806754, 5581386, 285017, 265019, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 55810764, 55811578, 264555, 56526486, 22279000
2777	79818729 (5553, 5554)			UNCLASSIFIED	264907, 264766
2778	82112411 (5555, 5556)			UNCLASSIFIED	264907, 264593, 264760, 264628
2779	87649729 (5557, 5558)	Novel Protein sim. GBank gi 4680711 gb AAD27745.1 AF13297 - (AF132970) CGI-36 protein [Homo sapiens]		UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 35698052, 265006, 264512, 264448, 264288, 29148827, 18108364, 20281149, 18108370, 264629
2780	94679397 (5559, 5560)	Novel Protein sim. GBank gi 4758524 ref NP_004825.1 pH-GK - HPK/GCK-like kinase	Contains protein domain (PF00780) - CNH domain	kinase	29146499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gi 4469352 gb AAD21222 - (AF069502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	60424179, 29331824, 60424269, 66714117, 29331826, 56182435, 87168474, 265017, 264764, 56181562, 21906765, 21906766, 21906768, 35695917, 265020, 33657023, 35695855, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	65274572, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 264905, 264907, 264908, 264909, 52844045, 265009, 265017, 265018, 264604, 265019, 264760, 264683, 264288, 264766, 264685, 264688, 264768, 52644229, 264689, 21906768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016828 (5565, 5568)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		tm7	264908, 264628, 263978, 263981
2784	87614360 (5567, 5568)				264259, 29331822, 29331824, 29331825, 264482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gi 2134933 pir S58890 - collapsin response mediator protein - human		UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21906765, 21906768, 21906769, 265020, 264584
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gi 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCNZ [Drosophila melanogaster]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264905, 265017
2787	87901266 (5573, 5574)	Novel Protein sim. GBank gi 5174507 ref NP_006020.1 pMA1 - paraneoplastic neuronal antigen		UNCLASSIFIED	264768, 21906765, 21906768, 55811957, 22278999, 264093, 60170815, 264259, 29331822, 18108365, 29331824, 33657109, 29331827, 35696052, 264100, 264105, 264908, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 22279002, 55811150, 264369, 264288
2788	88080844 (5575, 5576)	Novel Protein sim. GBank gi 3252826 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gi 2495729 sp Q92556 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	264103, 21906769, 264693
2790	87602784 (5579, 5580)	Novel Protein sim. GBank gi 5101772 emb CAB45135.1 - (AJ242878) p821 [Homo sapiens]		strut	264488, 264768, 264910, 264631, 264636, 264690, 264691, 264259, 264638, 29331824, 264508, 264509, 264905, 264563, 264908, 264628, 18108370, 264907, 264764, 264908, 264288, 264909
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gi 2911266 (AC002550) - Unknown gene product [Homo sapiens]			21906764, 18108368
2792	85083783 (5583, 5584)	Novel Protein sim. GBank gi 2854163 gb AAC02581.1 - (AF045642) No definition line found [Caenorhabditis elegans]			22278996, 22278997, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35696052, 264908, 66712502, 29331830, 264909, 60432229, 60433356, 60433438, 33109954, 265010, 265011, 265017, 265018, 265019, 264682, 264448, 264288, 264369, 264766, 52644229, 21906765, 21906768, 265020, 265021, 33657023, 263974, 18108374, 65274781, 35695855, 264636, 264556, 264558, 56182323, 83373044, 18108385, 56526486, 60432113, 22279000, 264587
2793	87425476 (5585, 5586)			UNCLASSIFIED	264259, 60432289, 66712502, 265009, 264636
2794	85794830 (5587, 5588)			UNCLASSIFIED	264689, 265022, 264691, 18108388, 264567

2785	95334888 (5589, 5590)	Novel Protein sim. GBank gij5454146jrefjNP_006348.1 pUBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBCA15)	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35698286, 22278988, 22278999, 60432049, 264259, 29331822, 29331825, 66714117, 60432289, 29331826, 29331827, 35698052, 29331828, 264907, 66712502, 56182435, 264511, 265007, 264512, 264910, 60432229, 60433356, 60433438, 33109954, 85658542, 265018, 265019, 264288, 264686, 21906764, 21906765, 21906768, 21906769, 21906769, 55811957, 265020, 265021, 265022, 52644150, 33657023, 264693, 65274620, 33657109, 35696423, 55811576, 65274791, 56182323, 56526486, 60432113, 22279002, 264482, 264563, 264484, 264567 18108394, 65274572, 56182575, 56994075, 22278999, 264490, 60432049, 264259 29331822, 29331824, 29331826, 35698052, 264509, 264906, 264907, 264908, 66712502, 56182435, 264510, 265006, 264512, 265007, 265008, 264910, 265009, 264591, 264592, 60433356, 264594, 264595, 55812038 264596, 21906754, 60174639, 87168474, 265010, 265011, 265017, 265018, 265019, 55811150, 264762, 18108351, 264448, 264682, 264389, 264288, 264685, 264766, 264687, 56181562, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 52844150, 264692, 33657023, 18108362, 264693, 65274620, 33657109, 33657182, 27486265, 33657349, 18108374, 35696423, 65274791, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87168518, 22278900, 264563, 264564, 264585, 264566, 264567
2786	94848857 (5591, 5592)	Novel Protein sim. GBank gij4680851 gb AAD27715.1 AF13284 - (AF132940) CGI-06 protein [Homo sapiens]		UNCLASSIFIED	
2787	95110780 (5593, 5594)	Novel Protein sim. GBank gij4838557 gb AAD31040.1 - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278995, 22278996, 22278997, 29331827, 29146499, 264509, 264906, 56182435, 264757, 21906754, 265010, 265017, 265018, 264681, 264682, 264683, 264686, 21906765, 21906767, 21906768, 21906769, 29148629, 265020, 52844150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264563
2788	86198005 (5595, 5596)	Novel Protein sim. GBank gij2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264488, 264490, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264483, 264486, 264567

2799	86090651 (5597, 5598)	Novel Protein sim. GBank gij3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331826, 35696052, 29331828, 264909, 60433356, 33657402, 33109954, 87168474, 264448, 52644229, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 52644150, 35695855, 264634, 60432113, 22279000
2800	88316481 (5599, 5600)	Novel Protein sim. GBank gij4240301[d]BAA74928.1] - (AB020713) KIAA0906 protein [Homo sapiens]		glycoprotein	264488, 56994075, 264259, 20281099, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 264288, 264766, 264686, 60170815, 264691, 264692, 27486265, 264628, 264629, 264636, 264557, 264558, 264559, 87168518, 264594, 264586, 264567
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		265007, 264687
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gij2337865 (AC002464) - organic cation transporter; 50% similarity to JC4884 (PID:g2143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter	transport	264448, 35695855
2803	79577446 (5605, 5606)	Novel Protein sim. GBank		UNCLASSIFIED	264639
2804	57111131 (5607, 5608)	gij4559368[g]b AAD23029.1 AC006585 - (AC006585) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain	peptidase	264566
2805	87398486 (5609, 5610)				264092, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 265009, 21906754, 264369, 264288, 264632, 60170394, 264563, 264482
2806	87898951 (5611, 5612)	Novel Protein sim. GBank gij1168973[sp]P44403 CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278995, 22278996, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29146498, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21906765, 21906767, 21906769, 29148629, 265022, 52644150, 56182323

2807	91720702 (5613, 5614)	Novel Protein sim. GBank gi 4468310 emb CAB37991 - (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]		UNCLASSIFIED	52644507, 52645156, 52646842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 35696052, 29331828, 33656970, 264100, 264105, 264907, 52644045, 60433356, 264594, 60433438, 52646317, 21906754, 33109954, 33657084, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264763, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 27486265, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35696423, 35695855, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gi 5541863 emb CAB51071.1 - (AL096857) hypothetical protein [Homo sapiens]		MHC	60432289, 264510, 265010, 265017, 265018, 264681, 264686, 265021, 264690, 22279000, 264566
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gi 27272561 (AC004002) - similar to ciliary dynein beta heavy chain, 78% Similarity to P23098 (PID:gi118965) [Homo sapiens]		ATPase_associated	18108351
2810	87258032 (5619, 5620)			UNCLASSIFIED	264569, 22278996, 264091, 264259, 29331828, 29146499, 29146629, 29146784, 264693
2811	91235845 (5621, 5622)	Novel Protein sim. GBank gi 3264583 (AC005189) - match to ESTs H97758 (NID:gi1118643) and AA085546 (NID:gi1628773) [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 66712502, 264693
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gi 4240273 dbj BAA74915.1 - (AB020699) KIAA0892 protein [Homo sapiens]		UNCLASSIFIED	264106
2813	91218765 (5625, 5626)	Novel Protein sim. GBank gi 3548791 (AC005620) - R33590_1 [Homo sapiens]		UNCLASSIFIED	56182575, 29331828, 264906, 66712502, 55811368, 265017, 265018, 265019, 264689, 265020, 87168518, 60432113
2814	90880906 (5627, 5628)	Novel Protein sim. GBank gi 3548791 (AC005620) - R33590_1 [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	55274572
2815	79774521 (5629, 5630)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264907, 264909
2816	95358229 (5631, 5632)			UNCLASSIFIED	264488, 35696286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264760, 264681, 264766, 264769, 264689, 21906765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gij1293846 (U56966) - coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 [Caenorhabditis elegans]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 56182435, 264510, 265006, 264511, 264512, 264593, 264758, 265010, 264760, 264781, 264784, 264288, 264687, 264769, 55811957, 35695917, 33657109, 263978, 264634, 264636, 264639, 264584, 264565, 264566, 264488, 264567
2818	88073579 (5635, 5636)	Novel Protein sim. GBank gij549986 (U13149) - possible asposory-associated protein [Pennisetum ciliare]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	66712502
2819	87793527 (5637, 5638)	Novel Protein sim. GBank	Contains protein domain (PF00919) - Uncharacterized protein family	UNCLASSIFIED	264909, 264511
2820	87765744 (5639, 5640)	gij4929773jgb/AAD34147.1(AF15209) CGI-05 protein [Homo sapiens]	UPF0004	UNCLASSIFIED	18108394, 52646365, 52644045, 264112, 265009, 21908754, 265017, 18108351, 264683, 264369, 264686, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gij399144jspiP02747C10C_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264638
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gij2224671jdbj(BAA20820) - (AB002363) KIAA0365 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433356, 33657402, 265011, 264760, 21908765, 60170815, 264638
2823	85320513 (5645, 5646)	Novel Protein sim. GBank gij399144jspiP02747C10C_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gij399144jspiP02747C10C_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)	Novel Protein sim. GBank gij3859683jemb(CAA22020) - (AL033503) conserved hypothetical protein [Candida albicans]			264760
2826	94311905 (5651, 5652)				52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656970, 52644045, 52646317, 33657084, 52644296, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 35696423, 35695855, 52644332, 18108385, 87168518, 264484

2827	95320519 (5653, 5654)	Novel Protein sim. GBank gi 398144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 263994, 264489, 65274572, 29331822, 66714117, 29331827, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264591, 60432229, 264592, 264593, 264595, 264596, 21908754, 265011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 264690, 264691, 264692, 264693, 263972, 264629, 35695855, 264631, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264558, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264567, 264486, 18108391
2828	91228615 (5655, 5656)	Novel Protein sim. GBank gi 3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	phosphatase	29331822, 35696052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264768, 264686, 55811957, 18108370, 18108374, 55810764, 35696423, 55811576, 56182323, 83373044, 87168518 22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 66712502, 264510, 264511, 264593, 60433438, 21906754, 265011, 264603, 18108351, 264288, 21906765, 21906768, 21906769, 29148629, 52644150, 264693, 33657109, 18108374, 264634, 18108385, 60432113, 22279000, 264565, 264486 265008, 265019, 264639, 22279002
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi 4680689 gb AAD27734.1 AF13295 - (AF13295) CGI-25 protein [Homo sapiens]			
2830	88087109 (5659, 5660)	Novel Protein sim. GBank gi 2498667 sp Q61200 NPH1_MOUSE - NEUREXOPHILIN 1			
2831	87614717 (5661, 5662)			UNCLASSIFIED	265017
2832	87631809 (5663, 5664)			UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264688, 21906767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi 2224567 dbj BAA20772 - (AB002311) KIAA0313 [Homo sapiens]			263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi 4589532 dbj BAA76788.1 - (AB023161) KIAA0944 protein [Homo sapiens]		ATPase associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi 2351568 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	264259, 264112, 265010, 264762, 264764, 263974, 264555, 264558, 264559

2837	87766482 (5673, 5674)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108394, 22278997, 22278998, 29331822, 264907, 264909, 265006, 265007, 265018, 265019, 264682, 264288, 21906766, 21906767, 55811957, 35685917, 18108374, 56182323, 22278000, 22279002
2838	87775392 (5675, 5676)	Novel Protein sim. GBank gi 973378 (U31263) - core protein [Hepatitis C virus]		UNCLASSIFIED	18108394, 18108397, 264259, 29331828, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2839	85799317 (5677, 5678)	Novel Protein sim. GBank gi 1575515 (U64899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]		UNCLASSIFIED	264555
2840	87774665 (5678, 5680)	Novel Protein sim. GBank gi 1575515 (U64899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]			264509, 264511, 265011, 264288, 264769, 265020, 264634, 264636, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gi 2224605 db BAA20790 - (AB002330) KIAA0332 [Homo sapiens]	Contains protein domain (PF000076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	56182575, 35696052, 264907, 264808, 264909, 264910, 264593, 264595, 264766, 265022, 264691, 33657182, 35695763, 18108370, 35695855, 264631, 264559, 264563, 264567
2842	80080086 (5683, 5684)	Novel Protein sim. GBank gi 5578957 emb CAB51350.1 - (AL050306) dJ47587.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	264600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gi 5578957 emb CAB51350.1 - (AL050306) dJ47587.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	264906, 264907, 264908, 264909, 264910, 264784, 35695855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gi 585123 p Q08878 FBLC_MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)	Contains protein domain (PF00008) - EGF-like domain		264685
2845	84321719 (5689, 5690)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		homeobox	29146498, 87168474, 264686, 35698423, 83373044, 264564
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gi 5306263 gb AAD41995.1 AC006233 (AC006233) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	29331830, 264909, 265008, 265011, 87168559, 264629, 264556
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gi 3399676 (AC005390) - R31180.1 [Homo sapiens]		UNCLASSIFIED	264908, 264766, 264769, 264629, 264637, 264566
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264490, 264259, 264508, 264905, 264907, 264510, 265007, 265008, 264591, 264592, 264593, 264594, 264595, 55812038, 265010, 265011, 264604, 264763, 264764, 264765, 264766, 264686, 264628, 264629, 264555, 264636, 264556, 264557, 264638, 264558, 264559, 264563, 264566, 264567
2849	88084283 (5697, 5698)	Novel Protein sim. GBank gi 3342218 (AC004131) - Unknown gene product [Homo sapiens]			29331822, 35696052, 264509, 264906, 265007, 264594, 265018, 264288, 263972, 35696423, 18108384, 55526486, 18108390, 35696286, 265008, 265009, 265016, 264286, 35695917, 264693, 18108374, 35695855, 22279000
2850	87623836 (5699, 5700)			UNCLASSIFIED	

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gij4321619[gb AAD15788.1] - (AF051008) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 56182435, 264758, 55611386, 265010, 18108351, 264448, 264369, 21906765, 264691, 264692, 264693, 35695855, 284556, 18108385, 264567, 264591
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gij1825729 (U88308) - similar to drosophila membrane protein PATCHED SP:P18502 (PID:g128645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gij2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF003397) - WW domain	kinase	56182575, 55811150, 264690, 27486262, 27486285, 264632, 56182323, 56528486, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gij2795825 (AC004021) - kelch protein, ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079096) [Homo sapiens]	Contains protein domain (PF01344) - Ketch motif	dna_ma_bind	35696286, 29331824, 29331826, 29331828, 264908, 264768, 264693, 22279002, 264482
2855	94723856 (5709, 5710)	Novel Protein sim. GBank gij1504040[dj BAA13219] - (D86983) similar to D.melanogaster peroxidasin(U11052) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278994, 29331822, 29331824, 29331825, 264908, 264908, 265009, 33109954, 265018, 265019, 264448, 21906765, 265020, 264690, 27486285, 83373044, 22279000, 22279002, 264482
2856	88093359 (5711, 5712)	Novel Protein sim. GBank gij3264583 (AC005189) - match to ESTs H97758 (NID:g1118643) and AA085546 (NID:g1628773) [Homo sapiens]			21906766, 22278997, 265022, 29331822, 29331826, 27486282, 265007, 265009, 265017, 264482, 264563, 18108351
2857	95348286 (5713, 5714)	Novel Protein sim. GBank gij3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	struct	22278995, 35696286, 29331824, 29331825, 35696052, 264103, 264108, 56182435, 21906765, 21906769, 265020, 18108368, 35695763, 22279002, 264563
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gij462585[sp P35227 ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	dna_ma_bind	264369, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264509, 264905, 264906, 29331830, 264908, 52644045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21906754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264764, 264765, 264288, 264369, 264685, 264766, 264768, 18108357, 264769, 21906766, 21906767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264629, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264584, 264566, 264486, 264567
2859	80937675 (5717, 5718)	Novel Protein sim. GBank gij4325320[gb AAD17331.1] - (AF124427) claudin-15 [Mus musculus]		UNCLASSIFIED	60424179, 65274572, 29331828, 264905, 264511, 264758, 265011, 21906767, 21906769, 55811957, 265021, 56182323

2860	87532589 (5719, 5720)	Novel Protein sim. GBank gi 4469185 emb CAB38414.1 - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial RNA (5-Methylaminomethyl-2-thiouridylyl)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284510, 284511, 33109954, 18108351, 284683, 284765, 284369, 284686, 21906765, 284691, 284692, 284693, 18108388, 22278002, 284482
2861	86698507 (5721, 5722)	Novel Protein sim. GBank gi 3941730 (AF108083) - BS4 [Homo sapiens]			284369, 284692
2862	87569585 (5723, 5724)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN - leucine-rich neuronal protein		UNCLASSIFIED	284691, 284638
2863	91220421 (5725, 5726)	Novel Protein sim. GBank gi 3249088 (AC004473) - Contains similarity to goliath protein gb M97204 from D. melanogaster [Arabidopsis thaliana]	Contains protein domain (PF000036) - struct Zinc finger, C2H2 type		55994075, 35685286, 22278998, 29331822, 29331824, 35686052, 29331828, 284106, 284511, 55812038, 33657084, 55811386, 285018, 265019, 21906765, 21906766, 21906769, 35655917, 265020, 265022, 33657023, 33657109, 33657349, 284629, 18108376, 60431850, 56182323, 18108385, 18108387, 87168518, 22279002
2864	87420030 (5727, 5728)	Novel Protein sim. GBank gi 1079451 pir JA55463 - tropomodulin, skeletal muscle - chicken	struct		284259, 284910
2865	95312191 (5729, 5730)	Novel Protein sim. GBank gi 438840 (L19048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 284482
2866	95105480 (5731, 5732)	Novel Protein sim. GBank gi 585703 sp Q07066 PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN	glycoprotein		65274572, 22278996, 22278998, 22278999, 284259, 29331824, 29331827, 29331828, 60433438, 21906754, 265018, 284448, 284764, 52844150, 83373044
2867	86908001 (5733, 5734)	Novel Protein sim. GBank gi 4580997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED		284488, 284768, 21906768, 22278998, 285022, 284259, 284508, 284905, 284907, 284511, 284910, 284635, 284636, 284637, 285011, 265017, 285018, 285019, 284583, 284088, 284566, 284764, 284369, 284567, 284488, 284288, 284766

2868	95303283 (5735, 5736)	Novel Protein sim. GBank gij1202868[emb]CAA63923] - (X94232) t-Cell activation protein [Homo sapiens]		18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 52644045, 264828, 265006, 265007, 265008, 265009, 264591, 60432229, 264593, 60433358, 264595, 21906754, 265017, 265019, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 264691, 33657182, 18108388, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35696423, 35695855, 264632, 56182323, 87168518, 264404, 22278000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88094412 (5737, 5738)		UNCLASSIFIED	264369
2870	84404574 (5739, 5740)		UNCLASSIFIED	264905, 264908, 264764, 21906769, 264634
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gij5306263[gb]AAD41995.1[AC006233] unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567
2872	95312187 (5743, 5744)	Novel Protein sim. GBank gij112205[pir]B39066 - proline-rich protein 15 - rat	kinase	263981
2873	88094252 (5745, 5746)		UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35696423, 35696288, 35695917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264558, 60433438, 60432289, 35696052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264908, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264567, 264909, 264488, 264766, 18108391

2874	94313548 (5747, 5748)	Novel Protein sim. GBank glj3212854 (AC004005) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	52644507, 52645156, 52646355, 56182575, 22278994, 22278995, 56994075, 35696286, 60432049, 264259, 52645080, 28331822, 56182181, 29331824, 60424269, 29331825, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 66712502, 52644045, 285007, 265009, 60433356, 264758, 55812038, 18108348, 52646317, 33109954, 33657084, 265017, 264604, 285018, 285019, 264682, 264369, 264288, 264688, 52644229, 21906766, 21908767, 21908768, 55811957, 265020, 265021, 265022, 52644150, 33657023, 52845129, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22279000, 22279002, 264563, 264565
2875	88083728 (5749, 5750)	Novel Protein sim. GBank glj2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	glycoprotein	22278996, 22278997, 22278999, 29331826, 29331828, 29146489, 66712502, 265008, 265017, 18108351, 264683, 264689, 21908767, 18108376, 18108377, 55811576, 60170394, 22279000, 264487
2876	88080854 (5751, 5752)	Novel Protein sim. GBank glj2979530 (AC004449) - R33683_2 [Homo sapiens]	Contains protein domain (PF00167) - fgl	
2877	94747029 (5753, 5754)	Novel Protein sim. GBank glj4704208 [emb] (CAB41646.1) - (AL035419) d11100H13.1 (putative novel protein) [Homo sapiens]		52646365, 65274572, 56182575, 22278997, 22278998, 22278999, 60432049, 52645080, 60424269, 60432289, 29331827, 35696052, 29331828, 66712502, 52644045, 56182435, 60433356, 33657402, 33657084, 265018, 55811150, 264448, 264388, 21908766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264558, 83373044, 18108385, 56526486, 60432113, 22279000, 22279002, 264563
2878	88095309 (5755, 5756)	Novel Protein sim. GBank glj387677 [emb] (CAB03067) - (Z81077) predicted using GeneFinder; Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264259, 29331822, 29331826, 264805, 264509, 264907, 264909, 264510, 265005, 264511, 264512, 33657402, 264758, 21908754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21908769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264486, 264567

2878	87859122 (5757, 5758)	Novel Protein sim. GBank gi 4895145 gb AAD32752.1 - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - Uracil-DNA glycosylase	UNCLASSIFIED	18108359, 264259, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265008, 264910, 264637, 60170394, 264559, 265017, 264564, 264565, 264567, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gi 4680703 gb AAD27741.1 AF13296 - (AF132966) CGI-32 protein [Homo sapiens]			264488, 52646365, 52646842, 22278994, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 265007, 264512, 265009, 264910, 264594, 21908754, 52646317, 52644298, 87168559, 264600, 264604, 264605, 264760, 264764, 264288, 264766, 264768, 264687, 264769, 21908766, 21908769, 35695917, 265021, 264690, 264692, 33657023, 52645129, 33657109, 33657182, 27486262, 33657349, 264629, 18108374, 35695855, 264634, 264635, 264636, 264637, 264638, 264557, 52644332, 264558, 264559, 83373044, 264404, 22279000, 264563, 264483, 264567, 264486
2881	87650539 (5761, 5762)	Novel Protein sim. GBank gi 733571 (U23452) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 29331822, 52644045, 21906765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gi 118112 (U41559) - No definition line found [Caenorhabditis elegans]			264488, 22278998, 22278999, 29331822, 29331826, 264908, 60170831, 60433356, 55812038, 264681, 264682, 264686, 264687, 264688, 21908768, 21908769, 264693, 263987, 18108374, 55811578, 56182323, 22279002, 264566
2883	95362875 (5765, 5766)	Novel Protein sim. GBank gi 4686008 gb AAD31087.1 AF10693 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264112, 264682
2884	87784643 (5767, 5768)	Novel Protein sim. GBank gi 2224697 dbj BAA20832 - (AB002376) KIAA0378 [Homo sapiens]		UNCLASSIFIED	265018, 264634
2885	83006308 (5769, 5770)	Novel Protein sim. GBank gi 1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264686, 264693
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gi 3882323 dbj BAA34521.1 - (AB018344) KIAA0801 protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	60432049, 264259, 29331828, 264908, 264511, 264595, 60433438, 264596, 265017, 264605, 263969, 263972, 264555, 83373044, 87168518, 264566
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gi 3882323 dbj BAA34521.1 - (AB018344) KIAA0801 protein [Homo sapiens]		UNCLASSIFIED	18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gi 4508015 ref NP_003447.1 pZNF2 - zinc finger protein 205	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264488, 264259, 29331828, 264508, 264906, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486

2889	87606562 (5777, 5778)			UNCLASSIFIED	56994075, 29331824, 265009, 264760, 18108354, 264288
2890	78703853 (5779, 5780)	Novel Protein sim. GBank gjl054085[emb CAA58337] - [X83413] U89 [Human herpesvirus 6]		UNCLASSIFIED	264591, 264766
2891	88094428 (5781, 5782)	Novel Protein sim. GBank gjl3877750[emb CAB01508] - (Z78084) predicted using GeneFINDER; similar to collagen; cDNA EST EMBL:D65865 comes from this gene; cDNA EST EMBL:D69451 comes from this gene; cDNA EST EMBL:D66028 comes from this gene; cDNA EST EMBL:D69658 comes from this gene...		UNCLASSIFIED	264591, 264595, 264369, 264685, 264693, 264628, 264563, 264566
2892	95419745 (5783, 5784)	Novel Protein sim. GBank gjl4929759[gb AAD34140.1]AF15190 - (AF151903) CGI-145 protein [Homo sapiens]		UNCLASSIFIED	65274572, 35696286, 29331828, 264110, 265009, 60433438, 265018, 265019, 18108351, 264288, 21906765, 21906766, 21906769, 55811957, 264690, 65274620, 263967, 35695855
2893	87798014 (5785, 5786)			UNCLASSIFIED	264259, 265010, 264682, 18108370, 264555, 264556
2894	87755985 (5787, 5788)	Novel Protein sim. GBank gjl5668015[gb AAD46135.1] - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	264259, 265006, 60433438, 52644286, 265011, 264369, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gjl3924708[emb CAA84646] - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...	Contains protein domain (PF01437) - Plexin repeat		29331824, 265007, 264762, 264636, 264563
2896	87752122 (5791, 5792)	Novel Protein sim. GBank gjl4885549[ref NP_005456.1]pKRG - protein kinase B gamma	Contains protein domain (PF00089) - Eukaryotic protein kinase domain	kinase	18108392, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29146499, 264906, 264908, 265007, 265009, 265018, 265019, 264369, 264685, 264689, 21906766, 265021, 264693, 33657182, 264639, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gjl4502877[ref NP_001296.1]pCLDN - Clostridium perfringens enterotoxin receptor 1		UNCLASSIFIED	60424179, 56182575, 22278996, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35696052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433356, 60433438, 65274444, 55811388, 265018, 18108351, 264448, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 55811857, 35695917, 264534, 33657023, 33657109, 35695763, 264628, 264629, 60431528, 18108374, 55810764, 55811576, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264566
2898	87750340 (5795, 5796)			UNCLASSIFIED	22278995, 264604, 18108385, 264566

2899	80357670 (5787, 5788)				UNCLASSIFIED	264764, 21906764, 264692
2900	94233538 (5789, 5800)	Novel Protein sim. GBank gi 4581470 emb CAB40137.1 - (Y18483) SLC7A8 protein [Homo sapiens]			glycoprotein	85274572, 56182575, 35696286, 60432049, 264259, 29331824, 66714117, 29331826, 35696052, 29331828, 68712502, 56182435, 265006, 265007, 265008, 265009, 60433356, 264758, 265018, 264764, 264765, 264288, 264768, 21906764, 21906768, 21906769, 265020, 264692, 264693, 32833986, 264631, 83373044, 60432113
2901	87444731 (5801, 5802)	Novel Protein sim. GBank gi 4759272 ref NP_004614.1 pTTC4 - tetrairicopeptide repeat domain 4			phosphatase	22278995, 22278997, 22278999, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 264910, 265009, 21908754, 33657084, 87168474, 265010, 265018, 21906764, 21906765, 21906766, 21906767, 21906768, 33657023, 264693, 33657109, 33657349, 35696423, 35695855, 263981, 56182323, 22279002
2902	85745271 (5803, 5804)	Novel Protein sim. GBank gi 2414615 emb CAB16364 - (Z89259) hypothetical protein [Schizosaccharomyces pombe]				264683, 264691
2903	87606733 (5805, 5806)	Novel Protein sim. GBank gi 1079318 pir JSS2241 - XLCL2 protein - African clawed frog				264887, 22278994, 264259, 29331826, 29331828, 264905, 52644045, 56182435, 264511, 265017, 265018, 18108351, 264448, 264683, 264769, 264689, 35695917, 52644150, 87168518, 60432113, 22279002
2904	86458072 (5807, 5808)	Novel Protein sim. GBank gi 5639823 gb AAD45885.1 AF14367 - (AF143676) multispinning nuclear envelope membrane protein nurim [Homo sapiens]			UNCLASSIFIED	52646365, 22278999, 264259, 35696052, 265011, 265017, 264683, 264769, 35695917, 265020, 263967, 18108374, 35695855, 264637, 264952, 18108385, 18108387
2905	84449826 (5809, 5810)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!			oncogene	265009, 264681, 264682
2906	95341051 (5811, 5812)	Novel Protein sim. GBank gi 4689256 gb AAD27831.1 AF12185 - (AF121858) sorting nexin 8 [Homo sapiens]		Contains protein domain (PF00787) - PX domain	UNCLASSIFIED	22278996, 35696286, 22278998, 264259, 60432289, 29331828, 29331830, 66712502, 265009, 60170831, 33109954, 264448, 264683, 264288, 264689, 21906766, 21906767, 21906768, 55811957, 35695917, 265022, 52644150, 264691, 33657023, 264692, 264693, 35695855, 60432113, 264566

2807	91211383 (5813, 5814)	Novel Protein sim. GBank gj1707078 (U80451) - contains strong similarity to a DNAJ-like domain (PS:PS00636) [Caenorhabditis elegans]	Contains protein domain (PF00226) - eph DnaJ domain	52644507, 56182575, 56181686, 22278995, 56994075, 35696286, 60432049, 56182181, 35696052, 60431735, 264595, 55812038, 21906754, 55811386, 265019, 264682, 264369, 56181562, 21906766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2808	80414246 (5815, 5816)	Novel Protein sim. GBank gj12673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]	helicase	265009, 33109954, 18108351, 264766, 265021, 264691, 264692, 18108374, 264556, 264638, 264557, 264558
2809	87420225 (5817, 5818)		eph	264259, 87168474, 265018, 18108365, 264628
2910	86601075 (5819, 5820)	Novel Protein sim. GBank gj14539335 [emb] [CAB37483.1] - (AL035539) putative protein [Arabidopsis thaliana]		22278995, 264509, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2911	94216615 (5821, 5822)	Novel Protein sim. GBank gj14469187 [emb] [CAB38415.1] - (AL031588) dJ1163J1.3 (novel protein similar to mouse B99) [Homo sapiens]	glucoamylase	52646365, 18108397, 22278995, 22278997, 22278998, 22278999, 29331824, 29331825, 52644045, 265006, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2912	87731803 (5823, 5824)	Novel Protein sim. GBank gj14929637 [gb] [AAD34079.1] [AF15184] - (AF151842) CGI-84 protein [Homo sapiens]	Contains protein domain (PF00904) - Involucrin repeat	52645136, 264092, 60432049, 264259, 52645080, 29331824, 29331825, 66712502, 33109954, 264760, 264683, 264288, 264686, 265021, 264693, 18108368, 263978, 264404
2913	87713823 (5825, 5826)	Novel Protein sim. GBank gj1854065 [emb] [CAA58337] - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED Zinc finger, C2H2 type	52644507, 52645156, 52646842, 56182575, 35696286, 22278997, 264259, 52645080, 29331827, 35696052, 29331828, 264828, 52644045, 56182435, 55812038, 52646317, 21906754, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264682, 264686, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264563
2914	87797300 (5827, 5828)			264557

2915	88081072 (5829, 5830)	Novel Protein sim. GBank gil5174485[ref]NP_008030.1[PKIAA - endocytic receptor (macrophage mannose receptor family)]	Contains protein domain (PF00059) - eph Lectin C-type domain	264569, 264488, 264687, 264768, 21906768, 52646842, 21906787, 21906788, 56182575, 29148629, 35695917, 22278996, 22278997, 22278998, 265021, 22278999, 52644150, 264691, 264259, 60432049, 264692, 52645129, 33657109, 33657182, 29331827, 27486261, 35696052, 29331828, 27486262, 27486264, 27486265, 33657349, 29146498, 29146499, 264906, 264907, 18108370, 264908, 18108372, 52644045, 18108374, 56192435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433356, 56192323, 18108382, 55812038, 18108385, 33109954, 21906754, 33657084, 87168510, 265010, 265011, 60432113, 265017, 265018, 22278000, 265019, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264389, 264288, 264766
2916	95337790 (5831, 5832)	Novel Protein sim. GBank gil5104851[db][BAA80165.1] - (AP000061) 305aa long hypothetical dTDP-4- dehydrohamnose reductase [Aeropyrum pernix]	dehydrogenase	52645156, 65274572, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432288, 29331826, 29331827, 29331828, 33656970, 264509, 264906, 29331830, 52644045, 264909, 56192435, 60170831, 264592, 264593, 33657402, 60433356, 52646317, 21906754, 33109954, 33657084, 52644296, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486264, 35695763, 18108376, 55811576, 35696423, 85274791, 35695855, 52644332, 264557, 264638, 56192323, 18108387, 87168518, 22278002, 264482
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gil3169065[emb][CAA19260.1] - (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264602, 264682, 87168518, 60432113
2918	85690529 (5835, 5836)	Novel Protein sim. GBank gil539218[pil][S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)]		264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gil2564855 (AF030001) - unknown [Mus musculus]		66714117, 66712502, 263981

2920	87769523 (5839, 5840)				35686286, 22278987, 264259, 52645080, 29331824, 29331826, 29331827, 264828, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486284, 27488265, 35696423, 35695855, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 87168518, 60432113
2921	91639982 (5841, 5842)	Novel Protein sim. GBank gij4580013jgb/AAD24202.1 U83194_ - (U83194) TRAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		35686286, 22278987, 264091, 264092, 264094, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29146498, 264104, 264105, 264107, 264509, 264110, 264112, 264512, 60433356, 21906754, 87168474, 265017, 18108351, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108376, 264555, 263981, 56526486, 87168518, 22279000, 22279002
2922	87749762 (5843, 5844)	Novel Protein sim. GBank gij4589514 dbj BAA76779.1 - (AB023152) KIAA0935 protein [Homo sapiens]	Contains protein domain (PF01074) - Glycosyl hydrolases family 38	kinase	264908, 264909, 264511, 265008, 265008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 29146627, 35695917, 264692, 264629, 263978, 55811576, 35695855, 264555, 264558, 56182323, 60170394, 22279000, 264486
2923	95337789 (5845, 5846)	Novel Protein sim. GBank gij4835268 emb CAB42898.2 - (Z83844) dJ37E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00159) - PH domain	struct	264488, 18108397, 22278985, 22278986, 22278987, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 265009, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52644150, 264691, 264692, 33657109, 263974, 18108376, 264631, 264636, 18108385, 18108387, 22279000, 264563, 264566
2924	87781967 (5847, 5848)	Novel Protein sim. GBank gij2133095 pir S72254 - ribosomal protein L36, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - Ribosomal protein L36	ribosomalprot	265017, 264628, 20281152, 264556
2925	95090120 (5849, 5850)	Novel Protein sim. GBank gij2388986 emb CAB11718 - (Z88980) actin associated protein [Schizosaccharomyces pombe]	UNCLASSIFIED		56182575, 35686286, 264259, 60432289, 29331827, 264508, 52644045, 264910, 264591, 60432229, 55812038, 21906754, 264681, 264448, 264683, 264288, 264685, 52644229, 264689, 21906765, 21906768, 21906769, 265021, 265022, 60170615, 264692, 33657023, 264693, 33657109, 35686423, 65274791, 56182323

2926	85343003 (5851, 5852)	Novel Protein sim. GBank gi 283032 pir S22456 - hydroxyproline-rich glycoprotein - perennial teasie			29331828, 265011, 264768, 264689, 264764, 264288, 264630, 264637
2927	80408018 (5853, 5854)				
2928	20452179 (5855, 5856)	Novel Protein sim. GBank gi 3413320 emb CAA069151 - (AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	284559
2929	81622020 (5857, 5858)			UNCLASSIFIED	264569, 264489, 22278994, 35696286, 22278996, 22278998, 22278999, 264094, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 33656970, 264109, 29331830, 52644045, 285009, 33109954, 52644296, 87168559, 264760, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906768, 21906769, 35695917, 264691, 33657023, 264693, 33657109, 18108374, 263976, 35696423, 35695855, 263981, 22279000, 22279002, 264567, 264486
2930	95302755 (5859, 5860)			UNCLASSIFIED	56182575, 56181686, 35696286, 22278996, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52644045, 56182435, 285009, 60170831, 264592, 60432229, 60433356, 87168474, 285010, 265011, 265017, 265018, 265019, 264762, 264448, 264683, 264288, 264768, 21906765, 21906769, 35695917, 60170615, 33657023, 33657109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264567
2931	94312693 (5861, 5862)	Novel Protein sim. GBank gi 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52645156, 22278997, 22278998, 29331822, 52645080, 29331824, 60432289, 33656970, 60433356, 60433438, 33109954, 21906765, 21906766, 21906767, 21906768, 265020, 52644150, 33657023, 33657109, 33657182, 27488265, 35696423, 35695855, 264555, 87168518, 60432113, 264566
2932	79632623 (5863, 5864)				264906, 264907
2933	91720776 (5865, 5866)	Novel Protein sim. GBank gi 3378056 (AF017777) - helicase [Drosophila melanogaster]	helicase		264488, 18108392, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52644045, 56182435, 265007, 265009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52644229, 21906765, 21906766, 21906768, 21906769, 265022, 52644150, 33657023, 33657109, 27488265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264566, 264567

2934	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 264691, 27486282, 264628, 87168518, 22278000
2935	86410579 (5869, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109954, 21908754, 265018, 265019, 264448, 264769, 21906764, 21906765, 265021, 284692, 33657023, 33657109, 33657349, 55810764, 22279000
2936	87605863 (5871, 5872)	Novel Protein sim. GBank gi 4153862 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:942735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811576, 18108387, 60432113, 264563
2937	94853096 (5873, 5874)	Novel Protein sim. GBank gi 5174409[ref NP_006101.1 pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	56994075, 22278999, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 264906, 264908, 264909, 56182435, 265006, 264512, 264910, 60170831, 60433356, 265011, 265018, 18108351, 264448, 264288, 264766, 52644229, 21906765, 29148784, 65274791, 264556, 56182323, 60170394, 264558, 60432113, 264565, 264486, 264587
2938	95419773 (5875, 5876)	Novel Protein sim. GBank gi 3319990[emb CAA76720] - (Y17287) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 56182575, 22278996, 35696286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264905, 66712502, 52644045, 56182435, 264511, 265008, 265009, 60432229, 33657402, 60433438, 55812038, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 264288, 264689, 21906765, 21906767, 21906768, 55811957, 35695917, 265020, 60170615, 264690, 264691, 264692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263976, 35696423, 35695855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56526486, 60432113, 22278002
2939	87786622 (5877, 5878)	Novel Protein sim. GBank gi 3979900[emb CAA89909] - (Z75547) similar to WD domain, G-beta repeat; cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292f8....	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	264907, 265018, 264681, 264685, 264686

2940	95011103 (5879, 5880)				UNCLASSIFIED	22278996, 29331822, 29331824, 66714117, 29331826, 29331828, 264905, 264908, 66712502, 29331830, 265011, 265017, 264764, 264369, 21906766, 21906767, 33657023, 33657109, 32833986, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264566
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gi 3413872 dbj BAA32300 - (AB007924) KIAA0455 protein [Homo sapiens]			UNCLASSIFIED	264557
2942	87430203 (5883, 5884)	Novel Protein sim. GBank gi 1172845 sp P46629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25			glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gi 4929653 gb AAD34087.1 AF15185 - (AF151850) CGI-82 protein [Homo sapiens]			collagen	60432049, 264259, 60432289, 29331827, 29146498, 265008, 264593, 60433356, 60433438, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 264567
2944	95081063 (5887, 5888)	Novel Protein sim. GBank gi 4678282 emb CAB41190.1 - (AL049860) 1-acylcerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensaiton (RCC1)		ATPase_associated	56994075, 22278998, 60432049, 264259, 29331822, 29331824, 60424269, 60432289, 29331826, 29331828, 264905, 264907, 52644045, 264909, 264511, 265008, 265009, 264594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21908765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 56526488, 87168518, 60432113, 22279002, 264482, 264563, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!	Contains protein domain (PF000096) - Zinc finger, C2H2 type		UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 35696052, 264908, 265008, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264389, 264288, 264687, 56181562, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264693, 60431528, 55810784, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264566, 264567

2946	94317315 (5891, 5892)	Novel Protein sim. GBank gij5441952 gb AAD43195.1 AF072864 peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	264488, 264259, 264508, 264509, 264906, 264907, 264909, 264510, 264511, 265007, 264512, 264910, 264591, 264593, 18108351, 264764, 264288, 264684, 264769, 265021, 264692, 33657109, 264628, 264629, 18108374, 264631, 264634, 264636, 264637, 18108380, 264638, 264639, 83373044, 264565, 264566, 264486, 264567
2947	87362952 (5893, 5894)	Novel Protein sim. GBank gij3540281 gb AAC34383.1 - (AF056116) All-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 29146498, 264508, 29331830, 265007, 265008, 265009, 60432228, 21906754, 265010, 265017, 265019, 264766, 264685, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264628, 18108370, 264629, 264630, 18108387, 60432113
2948	87626527 (5895, 5896)	Novel Protein sim. GBank gij5566614 gb AAB65654.2 - (AF001533) mitogen-induced [Mus musculus]			52646842, 22278995, 264259, 29331824, 29331825, 29331827, 29331830, 264909, 265007, 265009, 265019, 264763, 264684, 264288, 264685, 264688, 21906787, 264691, 264692, 264693, 18108374, 55811576, 18108385, 22279002, 264563, 264567
2949	88175545 (5897, 5898)	Novel Protein sim. GBank gij2132923 pir [S67133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)]		UNCLASSIFIED	22278996, 22278997, 60432289, 29331826, 29331827, 29331828, 35696052, 29146499, 264104, 264107, 264905, 66712502, 264908, 60433356, 60433438, 87168559, 264764, 52644229, 56181562, 21906767, 21906768, 21906769, 265022, 60170615, 33657023, 35696423, 263981, 264558, 60432113, 22279002
2950	95086870 (5899, 5900)	Novel Protein sim. GBank gij466102 sp P34629 YOJ6_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00863) - peptidase Cytosol aminopeptidase family		264488, 35696286, 264259, 35696052, 264907, 265007, 264910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35696423, 65274791, 35695855, 264556, 56526486, 264486
2951	87392357 (5901, 5902)	Novel Protein sim. GBank gij4688902 emb CAB41450.1 - (AJ238248) centaurin beta2 [Homo sapiens]			264693

2952	95329852 (5903, 5904)	Novel Protein sim. GBank gjl5596683[emb]CAB51405.1]- (AL098881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00650) - CRAU/TRIO domain.	transcript factor	264687, 52645156, 21906766, 21906769, 22278996, 265020, 264690, 60432049, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696052, 27486262, 264508, 264905, 20281149, 264906, 264907, 29331830, 264908, 264909, 35695855, 264511, 265008, 265009, 264910, 264635, 264636, 60432229, 264638, 60433356, 264639, 264758, 87168518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288 18108396, 56994075, 22278896, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264908, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264758, 52646317, 21906754, 33657084, 52644296, 87168559, 264600, 264760, 264681, 18108351, 264764, 264369, 264288, 264687, 21906765, 21906766, 21906787, 21906768, 21906769, 35695917, 33657023, 18108384, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565 29331822
2953	88093575 (5905, 5906)	Novel Protein sim. GBank gjl119522[sp]P10658[SERC, RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP)	Contains protein domain (PF00266) - Aminotransferases class-V	UNCLASSIFIED	
2954	88086288 (5907, 5908)	Novel Protein sim. GBank gjl4885261[re]NP_005251.1 pGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Transforming growth factor beta like domain	tgf	
2955	87698426 (5909, 5910)	Novel Protein sim. GBank gjl3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331825, 29331826, 35696052, 264808, 52644045, 264512, 60432229, 265018, 265019, 55811150, 264769, 21906767, 21906768, 21906769, 265021, 60170615, 55810764, 264567
2956	85789743 (5911, 5912)	Novel Protein sim. GBank gjl4689254[gb]AAD27830.1 AF121855 - (AF121857) sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		22278996, 264259, 29331827, 264808, 21906788
2957	80933301 (5913, 5914)	Novel Protein sim. GBank gjl4503023[re]NP_000089.1 pCPT2 - carnitine palmitoyltransferase II precursor		cadherin	22278999, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 264448, 264763, 264683, 264288, 264685, 18108357, 29148629, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 56182323, 18108382, 18108385, 18108388, 56526486, 87168518, 264482, 264487
2958	87440014 (5915, 5916)	Novel Protein sim. GBank gjl4240257[db]BAA74907.1]- (AB020691) KIAA0884 protein [Homo sapiens]			264595, 264596, 264681, 264369, 264629, 264631, 264567

2859	95109420 (5917, 5918)	Novel Protein sim. GBank gij988221 (U33005) - Tbc1 [Mus musculus]	Contains protein domain (PF00566) - TBC domain	oncogene	263994, 22278997, 264259, 60432049, 29331828, 29331828, 35696052, 29331830, 66712502, 56182435, 265008, 264512, 265008, 265009, 60433358, 60433343, 264596, 265017, 265018, 264683, 264288, 264766, 264768, 21906766, 21906767, 21906769, 265020, 60170615, 264692, 27486265, 18108374, 65274791, 35695855, 83373044, 56526486, 60432113
2960	87420091 (5918, 5920)			UNCLASSIFIED	35696286, 56182435, 87168474, 265010, 60170615, 35696423, 56182323, 18108383, 87168518, 264483
2961	95413416 (5921, 5922)	Novel Protein sim. GBank gij5596646[emb]CAB05177.2] - (Z82266) predicted using GeneFinder; similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52644045, 265006, 33657402, 21906754, 87168474, 265011, 87168559, 265017, 21906769, 265020, 60170615, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264564, 264557
2962	87912700 (5923, 5924)			UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52646317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264766, 264686, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264565, 264566, 264567, 264486
2963	95313464 (5925, 5926)	Novel Protein sim. GBank gij4240223[dj]BAA74890.1] - (AB020874) KIAA0867 protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21906754, 265018, 264760, 264687, 29148627, 29148784, 265020, 33657023, 264693, 65274620, 33657182, 27486261, 264629, 55810764, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2964	94324617 (5927, 5928)			UNCLASSIFIED	264259, 29331828, 33657402, 265017, 265018, 264692, 18108368, 35696423, 83373044, 18108388

2865	80384762 (5929, 5930)	Novel Protein sim. GBank gi14885447 rel NP_005452.1 pKRML - Kreisler (mouse) mal- related leucine zipper homolog			Transcript factor	264259, 29331826, 264508, 264509, 264905, 264907, 264908, 264909, 264511, 265008, 264910, 264591, 264593, 264594, 33657402, 265011, 264760, 264762, 264764, 264288, 264685, 264766, 264692, 33657109, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264567, 18108391 60432289, 264682, 264448
2866	91725248 (5931, 5932)	Novel Protein sim. GBank gi15262751 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]				
2867	94658303 (5933, 5934)	Novel Protein sim. GBank gi1524225 (U19181) - Rabin3 [Rattus norvegicus]			UNCLASSIFIED	264488, 264508, 264509, 264908, 264909, 264511, 264910, 264594, 264758, 85658542, 264762, 264764, 265021, 264556, 18108381, 264564, 264486
2868	95302778 (5935, 5936)	Novel Protein sim. GBank gi14929715 gb AAD34118.1 AF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)			264687, 52845156, 21906765, 52846365, 21906767, 18108398, 35696423, 22278996, 35696286, 22278997, 265020, 22278999, 265021, 265022, 264093, 264636, 264690, 52844150, 264259, 33657023, 52845080, 264693, 29331822, 56182181, 29331824, 66714117, 29331825, 33109954, 52645129, 29331826, 21906754, 33657182, 29331827, 29331828, 35696052, 27486262, 87168518, 87168474, 265010, 87168559, 265018, 22278000, 265019, 22279002, 264563, 18108351, 264906, 264907, 264448, 68712502, 264566, 264369, 264288
2869	95310957 (5937, 5938)	Novel Protein sim. GBank gi13024743 sp O24734 THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)		eph		52646842, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331828, 264509, 264909, 52644045, 56182435, 265009, 60433438, 55812038, 21906754, 265011, 87168559, 265018, 265019, 264448, 264288, 264369, 52644229, 21906766, 21906768, 21906769, 29148784, 265020, 265021, 52644150, 264691, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2870	88088071 (5939, 5940)	Novel Protein sim. GBank gi13165407 (AC004755) - fos37502.1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox		

2971	94186830 (5941, 5942)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		lm7	264488, 56182575, 35696286, 56994075, 29331824, 29331826, 29146489, 264508, 264905, 264907, 264112, 264910, 21906754, 87168559, 265018, 265019, 18108351, 264689, 21908765, 21906767, 21906768, 265020, 265021, 60170615, 18108364, 264628, 264629, 18108374, 264638, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264584, 264587
2972	86625943 (5943, 5944)	Novel Protein sim. GBank gi 728838 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		kinase	265017, 35695917, 265021, 33657109, 22279002, 264563
2973	91215301 (5945, 5946)	Novel Protein sim. GBank gi 2746789 (AF040842) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 264692, 33657349, 55811576, 264563
2974	91673002 (5947, 5948)	Novel Protein sim. GBank gi 786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	18108392, 52644507, 56182575, 56181686, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331824, 29331825, 66714117, 60424289, 29331826, 29331827, 29331828, 35696052, 66712502, 284908, 52644045, 265007, 264910, 265009, 60433438, 33109954, 21906754, 55811386, 52644296, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264448, 264369, 264288, 52644229, 18108358, 21906765, 21908767, 21908768, 35695917, 265020, 265021, 52644150, 264691, 264692, 33657023, 27486262, 27486284, 35695763, 18108370, 18108376, 55810764, 55811576, 35698423, 35695855, 264630, 264635, 264557, 52844332, 264558, 83373044, 18108387, 87168518, 60432113, 22278000, 264482, 264487
2975	95325213 (5949, 5950)	Novel Protein sim. GBank gi 3880812 emb CAA19508 - (AL023639) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - HECT-domain (ubiquitin- transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85658542, 265011, 265018, 264448, 264288, 264769, 21906767, 265020, 264691, 264559, 83373044
2976	8771202 (5951, 5952)	Novel Protein sim. GBank gi 5679136 gb AA046874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	22278996, 264906, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385
2977	91725254 (5953, 5954)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2878	87332059 (5955, 5956)	Novel Protein sim. GBank gij746549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 264259, 60432289, 29331827, 29146499, 56182435, 265008, 265007, 265009, 60433356, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 264288, 264685, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22279000, 22279002
2879	91725256 (5957, 5958)	Novel Protein sim. GBank gij5262751 (embjCAB45690.1) - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]	complement		264488, 65274572, 56994075, 22278999, 264093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482, 265009, 21906767, 263981, 22279000
2880	86296600 (5959, 5960)			UNCLASSIFIED	264629, 264564
2881	87376330 (5961, 5962)				
2882	93303675 (5963, 5964)	Novel Protein sim. GBank gij4929767 (gbjAAD34144.1) (AF151907) CGI-149 protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264596, 33657084, 264448, 21906765, 21906766, 21906787, 21906788, 21906789, 265020, 265022, 18108365, 33657182, 33657349, 35696423, 83373044, 22279000, 22279002
2883	91725258 (5965, 5966)	Novel Protein sim. GBank gij5262751 (embjCAB45690.1) - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			60424179, 52646842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52644045, 265006, 60431735, 87168474, 265018, 265019, 18108351, 264448, 21906765, 21906768, 35695917, 33657023, 52645129, 18108370, 35696423, 83373044, 56526486, 60432113, 264404, 22279002
2884	94136467 (5967, 5968)	Novel Protein sim. GBank gij2383734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130819) [Homo sapiens]	ATPase_associated		
2885	87099072 (5969, 5970)	Novel Protein sim. GBank gij103160 (pirjIS22126 - finger protein unkempt - fruit fly (Drosophila melanogaster))	UNCLASSIFIED		264910, 55812038, 56181562, 55811957, 264628, 55810764, 264632, 264635, 60432113
2886	86284861 (5971, 5972)				55811957, 264566
2887	86455934 (5973, 5974)		UNCLASSIFIED		264369

2988	95357753 (5975, 5976)	Novel Protein sim. GBank gii4678028[gb AAD27002.1] - (AF077207) HSPC021 [Homo sapiens]	UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 22278997, 22278999, 264092, 264094, 264259, 60432049, 29331824, 29331828, 60432289, 35696052, 29331828, 264107, 264905, 264907, 264908, 66712502, 264828, 264909, 56182435, 265008, 265007, 265008, 60170831, 60432229, 264593, 60433356, 264757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264682, 264448, 264369, 264288, 264685, 52644229, 21906765, 21906767, 21906769, 35695917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35695855, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 264563, 264564, 264565, 264566, 264567
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gii113671[sp P23964 ALUF_HUMAN - IIII ALU CLASS F WARNING ENTRY IIII]	kinase	22278996, 22278997, 264905, 264511, 60170831, 264593, 265019, 21908765, 21906767, 21906768, 18108374
2990	87330444 (5979, 5980)	Novel Protein sim. GBank gii2829836[sp P97346 RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD]	Contains protein domain (PF00071) - Ras family	265007, 264512, 18108351, 264288, 264689, 265020, 264691, 33657023, 33657109
2991	94325361 (5981, 5982)		UNCLASSIFIED	264563
2992	85425164 (5983, 5984)		UNCLASSIFIED	264259, 265019, 264689, 18108385
2993	94325363 (5985, 5986)		UNCLASSIFIED	264488, 29331822, 265017, 264761, 21906769, 65274791, 263981, 264565
2994	94136634 (5987, 5988)	Novel Protein sim. GBank gii248654[sp Q50658 YU02_MYCTU - HYPOTHETICAL 28.7 KD PROTEIN CY339.02]	transport	22278994, 22278995, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265006, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21906767, 21908768, 21906769, 265021, 265022, 33657023, 264693, 35695855, 83373044, 18108385, 22279000, 264565, 264566, 264905, 264907, 265019, 18108351, 264683
2995	87591070 (5989, 5990)	Novel Protein sim. GBank gii2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		65274572, 35696286, 264259, 29331824, 35696052, 29148499, 264508, 264907, 265007, 265008, 60433438, 18108348, 265017, 264681, 264683, 264288, 264766, 264769, 264689, 35695917, 60170615, 33657023, 264692, 264634, 264555, 18108381, 18108382, 18108388, 264484
2996	91013798 (5991, 5992)	Novel Protein sim. GBank gii2829912 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	

2997	87627440 (5993, 5994)	Novel Protein sim. GBank gij4589652[jb]BAA76848.1] - (AB023221) KIAA1004 protein [Homo sapiens]	homeobox	264488, 56182575, 264259, 66714117, 29331826, 35698052, 264508, 264509, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21908764, 21908766, 21908768, 21908769, 27486261, 18108374, 35698423, 264634, 264635, 264636, 264557, 18108385, 87168518
2998	88095381 (5995, 5996)	Novel Protein sim. GBank gij3947589[emb]CAA22252] - (AL034364) cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	52646365, 22278997, 264508, 264908, 18108351, 21908765, 21908767, 18108370, 18108374, 35698423, 264636, 264639
2999	94847055 (5997, 5998)	Novel Protein sim. GBank gij15408[sp]P18835[CC]19_CAEEL - CUTICLE COLLAGEN 19	UNCLASSIFIED	56182575, 22278996, 29147620, 29331825, 29146498, 29146499, 264905, 66712502, 265006, 265009, 21908754, 85658542, 18108351, 29148627, 29148629, 60170615, 33657109, 27486262, 18108370, 18108374, 264556, 264557, 264558, 60170394, 18108385, 264563
3000	95099370 (5999, 6000)	Novel Protein sim. GBank gij1163174 (U32575) - similar to yeast Sec6p. Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]	UNCLASSIFIED	264887, 22278997, 22278999, 264259, 29331822, 29331824, 35696052, 29146498, 264508, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 265008, 265009, 264910, 33657402, 264757, 264595, 264596, 264758, 21908754, 265011, 264600, 265017, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264682, 264764, 264288, 264685, 264766, 264686, 264768, 264769, 21908765, 21908768, 35695917, 265020, 264691, 264692, 33657023, 264693, 33657109, 33657182, 27486261, 264628, 264629, 18108374, 18108376, 35698423, 35698555, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 60170394, 83373044, 20798451, 22279002, 264563, 264486, 264567
3001	86078454 (6001, 6002)	Novel Protein sim. GBank gij2078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing.; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g644442), AA158721 (NID:g1733515), R59840 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]	cathepsin	18108394, 52646842, 56182575, 29331824, 29331825, 29331827, 264910, 33109954, 52644296, 265017, 265019, 264288, 265020, 265021, 52644150, 264692, 35695763, 55810764, 35698423, 56182323, 18108387, 264563, 264564
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gij3599478 (AF085185) - Myosin-1A [Acanthamoeba castellanii]	UNCLASSIFIED	264488, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264510, 265009, 21908754, 264682, 264688, 33657023, 264565

3003	86648078 (6005, 6006)	Novel Protein sim. GBank gij1754969 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	collagen	264512, 264593, 264564, 264567, 264486
3004	88066876 (6007, 6008)	Novel Protein sim. GBank gij2224629 [BAA20802] - (AB002342) KIAA0344 [Homo sapiens]	Contains protein domain (PF01360) - Monooxygenase	oxygenase	29331830, 21906769, 264691, 33657109, 263972, 18108385
3005	87794843 (6009, 6010)	Novel Protein sim. GBank gij4680659 [AAD27719.1] AF13294 - (AF132944) CGI-10 protein [Homo sapiens]			29331822, 29331824, 29331827, 60433438, 265011, 265019, 21906766, 21908767, 21908768, 265020, 33657023, 33657349, 60170394, 22279002, 264567
3006	87422224 (6011, 6012)	Novel Protein sim. GBank gij3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - MHC	MHC	264259, 29331822, 264512, 21906754, 265018, 264687, 21906765, 264691, 264555, 264556, 264558, 18108385
3007	80936005 (6013, 6014)	Novel Protein sim. GBank gij2565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	52644507, 52645156, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264689, 60170615, 18108374, 20281152, 264636, 52644332
3008	80416249 (6015, 6016)				264905, 264593, 264766, 264636
3009	91213387 (6017, 6018)	Novel Protein sim. GBank gij3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	52646842, 58182575, 22278995, 22278996, 264259, 29331825, 29331826, 29331827, 29331828, 35696052, 264508, 264509, 264907, 56182435, 264511, 265007, 264512, 265008, 264757, 264758, 55812038, 264759, 33109954, 21906754, 265010, 265011, 264600, 265017, 265018, 265019, 264760, 18108351, 264288, 264369, 21906764, 21906765, 21906767, 55811957, 265020, 265021, 264691, 18108368, 27486262, 20281149, 18108370, 55811578, 264637, 264556, 264557, 18108381, 264558, 58182323, 264559, 18108385, 18108388, 22279002, 264486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gij4927370 [gjbAAD33084.1] AF06797 - (AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01923) - Protein of unknown function	UNCLASSIFIED	264686, 264687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 265020, 265021, 60170615, 264692, 33657023, 29331822, 264693, 18108364, 29331824, 33657109, 60432289, 29331827, 27486261, 29331828, 264508, 264909, 55811576, 35695855, 265008, 264556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 265019, 264564, 264682, 264764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gij5052319 [gjbAAD38501.1] AF11883 - (AF118838) citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	35696052, 56182435, 264758, 21906754, 265018, 264760, 264762, 18108351, 264682, 264448, 21906766, 65274620, 18108374, 264482, 264564
3012	87753087 (6023, 6024)			UNCLASSIFIED	263972

3013	81238769 (6025, 6026)	Novel Protein sim. GBank gj3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	264488, 263994, 35696286, 22278997, 264259, 29331824, 60424269, 66714117, 35696052, 264905, 264908, 264907, 264908, 264909, 56182435, 264511, 264512, 264910, 264591, 264592, 264593, 264594, 33657402, 60433438, 264595, 264596, 55812038, 264758, 33109954, 21906754, 265010, 265018, 264604, 264760, 264682, 264683, 264764, 264369, 264288, 264765, 264766, 264686, 264768, 264687, 21906767, 35695917, 265020, 33657023, 264692, 264693, 33657109, 264628, 264629, 55811576, 35696423, 35695855, 264630, 264631, 264832, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 264563, 264565, 264566, 264567, 264760
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gj3878374[emb]CAA930811 - (Z68879) Similarity to Yeast Chl12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27948 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33316 comes from...		ATPase_associated	
3015	86995466 (6029, 6030)				22278995, 22278996, 22278997, 264259, 29331824, 29331828, 264908, 265007, 265008, 264910, 265011, 265017, 265019, 264691, 33657109, 18108370, 35695855, 264556, 264564
3016	87759945 (6031, 6032)	Novel Protein sim. GBank gj1168819[sp]P41733[CC91_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52646842, 56994075, 52645080, 29331822, 29331824, 35696052, 33656970, 52644045, 264596, 33657084, 265017, 265019, 52644229, 21906767, 35695917, 52644150, 33657023, 33657109, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 35695855, 87168518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gj4569658[dbj]BAA76851.11 - (AB023224) KIAA1007 protein [Homo sapiens]			264488, 18108397, 22278996, 35696286, 22278999, 264259, 29331822, 60432289, 264908, 29331830, 264909, 56182435, 265006, 265007, 265008, 265009, 264591, 60433356, 60433438, 52646317, 21906754, 55811386, 265010, 265011, 87168559, 265017, 265018, 265019, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 65274620, 52645129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52644332, 83373044, 18108385, 18108388, 56526466, 87168518, 264404, 60432113, 22279000, 264567

3018	11073891 (6035, 6036)	Novel Protein sim. GBank gjl3219332 (AC004020) - Unknown gene product [Homo sapiens]		oncogene	264558 264559, 52644507, 18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 264908, 56182435, 265007, 265008, 60432229, 264593, 60433356, 55812038, 21908754, 87168474, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264689, 21908766, 21908768, 21908769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657348, 264629, 65274791, 264634, 52644332, 56182323, 18108385, 87168518, 22279000, 22279002, 284563
3020	94318251 (6039, 6040)	Novel Protein sim. GBank gjl3414809 (AF061529) - rjs [Mus musculus]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase-associated	264488, 263994, 35696286, 264259, 264508, 264905, 264508, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264763, 264764, 264288, 264369, 264766, 264687, 264688, 264769, 55811957, 35695917, 33657023, 284628, 35696423, 35695855, 264630, 264632, 264634, 284635, 264636, 264637, 264556, 264557, 264638, 264639, 83373044, 18108385, 264564, 264567, 264486
3021	80478512 (6041, 6042)	Novel Protein sim. GBank gjl3880889 (embjCAB09005) - (Z95559) cDNA EST yk236d4.5 comes from this gene; cDNA EST EMBL:C13455 comes from this gene; cDNA EST yk329g6.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]			264769, 264629, 264482
3022	87718500 (6043, 6044)			UNCLASSIFIED	264259, 29331826, 29331828, 264288, 264566
3023	95305484 (6045, 6046)	Novel Protein sim. GBank gjl416592 (spip3233JAGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00614) - Phospholipase D. Active site motif	UNCLASSIFIED	264498, 22278995, 35696286, 22278997, 29331826, 35696052, 264907, 29331830, 52644045, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21908767, 55811957, 35695917, 265021, 18108376, 263978, 264635, 264558, 22279000
3024	86675305 (6047, 6048)			UNCLASSIFIED	60432049, 264760, 21908769, 55811957, 35695917, 264690, 264555, 264559
3025	65706629 (6049, 6050)	Novel Protein sim. GBank gjl295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]			264593, 55811576

3026	87643662 (6051, 6052)	Novel Protein sim. GBank gi 3024052 sp P97924 KARI_RAT - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87188559, 265019, 21906765, 29148627, 263967, 20281148, 20281069, 263975, 263977, 20281071, 56526486, 22279000
3027	94844563 (6053, 6054)	Novel Protein sim. GBank gi 4929647 gb AAD34084.1 AF15184 - (AF151847) CGI-89 protein [Homo sapiens]	Contains protein domain (PF01529) - DHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60432048, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264910, 33657402, 264596, 21906754, 265010, 265011, 87188559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 35695917, 265020, 265021, 265022, 52644150, 264692, 33657023, 264693, 52645129, 33657109, 27486261, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56526486, 22279000, 22279002
3028	94231997 (6055, 6056)	Novel Protein sim. GBank gi 3080521 emb CAA18650 - (AL022599) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87188559, 265018, 264762, 264683, 264765, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 265021, 265022, 33657109, 27486265, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264564
3029	87619284 (6057, 6058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87168474, 265019, 18108351, 21906768, 264534, 264690, 264693, 263969, 18108370, 264558, 22279000, 22279002, 264482
3030	87544828 (6059, 6060)	Novel Protein sim. GBank gi 3757726 emb CAA18782 - (AL022727) dJ8019.1 (olfactory receptor-like protein [Hs6M1-1]) [Homo sapiens]	Contains protein domain (PF00001) - Im7 7 transmembrane receptor (rhodopsin family)	- Im7	
3031	91677853 (6061, 6062)	Novel Protein sim. GBank gi 4530587 gb AAD22105.1 - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 35696052, 264908, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 263974, 18108374, 264558, 56526486, 22279000, 22279002

3032	94130124 (6083, 6084)	Novel Protein sim. GBank gij101951 (U37429) - similar to M. musculus MER5 and other AHP/CTSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - synthase Glycosyl transferases group 1	22278996, 35696286, 264259, 29331824, 29331828, 264907, 29331830, 264758, 33109954, 87168474, 87168559, 265019, 264288, 21906769, 265021, 264693, 35696423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6085, 6086)	Novel Protein sim. GBank gij5031573[refNP_005712.1]pACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - struct Actin	35698286, 264259, 29331826, 35696032, 264508, 264905, 264908, 264907, 264908, 264909, 265008, 264591, 21906754, 265010, 265019, 264681, 264389, 264768, 21906764, 21906768, 35695917, 33657023, 264628, 35695855, 264632, 264635, 264639, 264482, 264563
3034	80415373 (6087, 6088)		UNCLASSIFIED	264906, 264907, 264510, 264592, 265010, 264762, 264768, 264637, 264638, 264486
3035	91220692 (6089, 6070)	Novel Protein sim. GBank gij3738207[embjCAA21262] - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]	UNCLASSIFIED	264636
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gij728837[spjP39194]ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase	264807, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gij4406590[gbjAAD20040] - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]		265017
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gij5360093[gbjAAD42865.1]AF15509 - (AF155099) NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00627) - UNCLASSIFIED UBA domain	22278996, 22278997, 264259, 264905, 265007, 265009, 60433356, 21906754, 265018, 265019, 18108351, 264687, 21906765, 265020, 265021, 65274620, 27486262, 264636, 56182323, 18108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gij475712[embjCAB42094.1] - (AJ238717) ZRP protein [Rattus norvegicus]	UNCLASSIFIED	35696286, 29331828, 264109, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 264691, 18108370, 263972, 264629, 18108374, 263977, 35696423, 264584, 18108391, 264692, 264558, 18108382, 18108385, 264587
3040	90833317 (6079, 6080)	Novel Protein sim. GBank gij488427[embjCAB43247.1] - (AL050037) hypothetical protein [Homo sapiens]		
3041	88312357 (6081, 6082)	Novel Protein sim. GBank gij387607[embjCAB04122.1] - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...	UNCLASSIFIED	56894075, 22278997, 22278998, 29331827, 33656970, 33109954, 21906754, 87168559, 264600, 264683, 21906765, 21906768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gij750236 (U21156) - sarcolemmal associated protein-2 [Oryctolagus cuniculus]	glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank gij854065[embjCAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	3569286, 60424268, 35696052, 264508, 264905, 66712502, 56182435, 55811386, 52644296, 55811150, 35695917, 60170615, 33657109, 18108374, 264634, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gij4104922 (AF042276) - o251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiE/COQ5 methyltransferase family	glycoprotein	22278996, 22278998, 22278999, 29331824, 56182435, 264511, 265007, 60170831, 60432229, 60433356, 33109954, 18108351, 264288, 35695917, 18108388, 18108370, 60170394
3045	94127598 (6089, 6090)	Novel Protein sim. GBank gij4589680[dbjBAA76859.1] - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	264488, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264909, 264511, 265008, 264591, 264593, 33109954, 264604, 264764, 264683, 264288, 264766, 264768, 21906765, 21906768, 55811957, 35695917, 27486262, 18108370, 264628, 18108374, 35695855, 264630, 264632, 264635, 264563, 264564, 264566
3046	88088247 (6091, 6092)			UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264908, 52646317, 55811957, 60432113, 22279000, 22278002, 264482, 264564
3047	95089824 (6093, 6094)			UNCLASSIFIED	264488, 22278996, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264766, 21906768, 21906769, 35695917, 52644150, 33657349, 65274791, 35695855, 264555, 60432113, 22279000, 264566
3048	87629419 (6095, 6096)	Novel Protein sim. GBank gij4588034[gbjAAD25962.1]AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264102, 29148784
3049	88229955 (6097, 6098)	Novel Protein sim. GBank gij5454158[pejNP_006286.1]pVARS - valyl-IRNA synthetase 1	Contains protein domain (PF01406) - IRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 264907, 264758, 87168559, 265018, 264448, 21908766, 265020, 33657109, 35695855, 60432113, 22279000
3050	87643679 (6099, 6100)	Novel Protein sim. GBank gij4589642[dbjBAA76843.1] - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331825, 264909, 265007, 264512, 265019, 264288, 21908766, 265020, 264693, 18108385, 56526486, 87168518, 22279002, 264566
3051	87750599 (6101, 6102)				22278997, 264595, 265018, 264288, 264693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gij117528[spjP14755]CRYL_RABIT - LAMBDA-CRYSTALLIN	dehydrogenase		264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gi 3947613 emb CAA19465.1 - (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35696286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21908754, 265010, 87188559, 264603, 265018, 265019, 264763, 264764, 264288, 21906765, 21906768, 21906768, 21906769, 35695917, 18108374, 35696423, 264638, 56182323, 22279000, 264563
3054	85843510 (6107, 6108)	Novel Protein sim. GBank gi 1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35696286, 35696052, 29331830, 264908, 264909, 264512, 284910, 265017, 264604, 264766, 265020, 33657109, 264628, 35695855, 264636, 264564, 264566, 264486, 60424179, 65274572, 56182575, 35696286, 22278998, 22278999, 60432049, 264259, 60424269, 60432289, 35696052, 56182435, 265006, 265009, 60170831, 60432229, 60431735, 60433356, 264594, 60433438, 21906754, 55811386, 265011, 87168559, 265019, 18108351, 264683, 264288, 264369, 264689, 21906768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810764, 55811576, 35696423, 65274791, 264638, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 264566
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gi 4680655 gb AAD27717.1 AF13294 - (AF132942) CGI-08 protein [Homo sapiens]		transport	264488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264766, 264687, 18108357, 264768, 264768, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264691, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22279000, 22279002, 264563, 264564, 264565, 264566, 264486, 264567
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		glycoprotein	

3057	95412746 (6113, 6114)	Novel Protein sim. GBank gij3878119[embjCAA88860] - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...			264508, 264905, 264907, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264767, 18108374, 264635, 264555, 264637, 264639, 264563, 264584, 264565, 264486
3058	79646226 (6115, 6116)	Novel Protein sim. GBank		UNCLASSIFIED	264593
3059	87629425 (6117, 6118)	gij4588034[gb AAD25962.1 AF09287] - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264480, 264259, 29331824, 29331825, 29331827, 35696052, 29331828, 285007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906769, 29148629, 29148784, 265022, 52644150, 18108370, 264536, 18108385, 264563, 264567
3060	79346691 (6119, 6120)			UNCLASSIFIED	264567
3061	87740984 (6121, 6122)			UNCLASSIFIED	264112, 52644296, 21906768, 33657023, 263974, 18108385
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gij4454680[gb AAD20963] - (AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	264908, 265008, 18108351, 264566
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gij2248532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108359, 264558
3064	91241526 (6127, 6128)	Novel Protein sim. GBank gij4240315[gb BAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52646365, 52646842, 65274572, 56182575, 58181686, 22278995, 22278996, 22278997, 22278998, 264259, 60432049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60432229, 60433438, 55812038, 52644296, 265018, 264682, 264288, 264686, 284768, 264687, 52644229, 264689, 21906768, 264691, 264692, 264693, 18108370, 18108377, 55811576, 264636, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gij5656743[gb AAD45960.1 AC005067] Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and gencan [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 264093, 264094, 264095, 29331824, 60424269, 66714117, 264100, 264907, 265007, 264591, 60432229, 264593, 265011, 265019, 18108351, 264766, 264767, 21906765, 21906768, 264693, 20281069, 22279000, 22279002, 264482, 264566, 264567

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gi 4884268 emb CAB43245.1 - (AL050028) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108397, 22278995, 56994075, 22278996, 264905, 68712502, 265008, 264512, 264910, 264758, 60174638, 264760, 18108351, 264764, 264683, 18108359, 264692, 18108364, 18108368, 18108370, 18108377, 18108379, 60170394, 264567
3067	85422551 (6133, 6134)	Novel Protein sim. GBank gi 4689258 gb AAD27832.1 AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - struct PX domain		264488, 264489, 35696286, 22278996, 56994075, 264259, 29331822, 29331825, 35696052, 29331828, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265010, 265011, 87168559, 264601, 264602, 264603, 264604, 264605, 265019, 264760, 264762, 264448, 264763, 264764, 264288, 264369, 264766, 264768, 264687, 264769, 264689, 21908765, 21908767, 21908768, 35695917, 265020, 265021, 264534, 52844150, 264691, 33657023, 264693, 264628, 60431528, 263977, 35695855, 264630, 264631, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 56526486, 87168518, 22279000, 22279002, 264563, 264483, 264564, 264565, 264566, 264567, 264486
3068	85360651 (6135, 6136)	Novel Protein sim. GBank gi 3878119 emb CAA88860 - (Z49068) similar to GTP-binding protein; cDNA EST	Contains protein domain (PF01926) - struct GTPase of unknown function		22278996, 56994075, 22278998, 22278999, 264259, 264107, 264905, 29331830, 52844045, 264110, 60170831, 264592, 264594, 33657402, 21908764, 33109954, 87168474, 87168559, 265017, 264448, 264764, 264683, 264766, 52644229, 21908765, 21908766, 21908768, 21908769, 60170615, 33657023, 18108370, 18108376, 264634, 264557, 60170394, 56182323, 18108385, 87168518, 22279000, 264482
3069	85412753 (6137, 6138)	Novel Protein sim. GBank gi 3878119 emb CAA88860 - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...			

3070	94319173 (6139, 6140)	Novel Protein sim. GBank gi 3877788 emb CAB05527 - (Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...		synthase	264488, 22278994, 22278995, 22278996, 56994075, 22278997, 22278999, 264259, 29331822, 29147620, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52644045, 56182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33109954, 21906754, 87168474, 265019, 18108351, 264448, 264683, 264288, 52644229, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811576, 35695855, 264634, 264635, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	94325573 (6141, 6142)	Novel Protein sim. GBank gi 4502425 ref NP_001709.1 pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - Iqf Thioredoxin		264488, 65274572, 18108398, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35696052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432228, 264592, 60433356, 33657402, 60433438, 33109954, 52644298, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170815, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567, 56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 284555, 56182323, 60432113, 264564
3072	95115692 (6143, 6144)	Novel Protein sim. GBank gi 1263289 (U47856) - fibroin-4 [Araneus diadematus]		transcriptfactor	

3073	85147248 (6145, 6146)	Novel Protein sim. GBank gi 134840 sp P22528 CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.8 KD PANCORNULIN)		UNCLASSIFIED	264769
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gi 3419847 (AC004982) - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g588461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906767, 264893, 18108368, 18108370, 18108374, 264567
3075	88089532 (6148, 6150)	Novel Protein sim. GBank gi 4557349 ref NP_000458.1 pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264689, 264893, 56526486
3076	87819219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 264691, 264693
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gi 3023956 sp Q00808 HET1_PODAN - VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 35696052, 264511, 60170831, 87188474, 264389, 35695917, 33657182, 27486264, 33657349, 35695763, 35695855, 264639
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gi 3900850 (AC004994) - similar to KIAA0600; similar to d1026456 (PID:g3043724) [Homo sapiens]			22279002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gi 3875410 emb CAB02876 - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644229, 21906768, 265020, 265021, 264693, 18108376, 264631, 52644332, 22279002
3080	93298274 (6159, 6160)	Novel Protein sim. GBank gi 5257221 gb AAD41265.1 - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278996, 22278998, 264490, 264259, 29331824, 6671417, 29331825, 29331826, 29331827, 29331828, 29146499, 264508, 264905, 264828, 52644045, 56182435, 265006, 264591, 264596, 21906754, 60174639, 265010, 264882, 264448, 264763, 264683, 264764, 264288, 264685, 264769, 264688, 264689, 21906765, 21906767, 21906769, 55811957, 35695917, 265020, 60170615, 52644150, 264692, 33657023, 264693, 65274620, 33657109, 27486261, 35695763, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264565, 264484
3081	88094864 (6161, 6162)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	18108398, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264595, 264758, 265011, 265018, 264760, 264761, 264763, 264764, 18108354, 264685, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264565, 264566
3082	80310121 (6163, 6164)				264764, 55811957, 264555, 264564

3083	88095756 (6165, 6166)	Novel Protein sim. GBank gij868241 (U29488) - C56C10.3 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264259, 29331824, 264106, 265008, 264591, 264592, 21906754, 264288, 264767, 21906768, 21906769, 29148784, 264691, 264632, 22279000
3084	87448568 (6167, 6168)	Novel Protein sim. GBank gij476774iprjA37475 - probable structural component p38 - borna disease virus			22278995, 60432289, 35696032, 264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264593, 264595, 264758, 264369, 264288, 264766, 35695917, 285020, 18108374, 35696423, 264631, 264556, 264555, 264586, 264587, 264488
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gij2565057 (U80741) - CAGH44 [Homo sapiens]		UNCLASSIFIED	265011, 264681
3086	87769942 (6171, 6172)	Novel Protein sim. GBank gij3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 264112, 18108351, 264687, 263987, 263974, 55810764, 263981, 18108385, 264487
3087	87462888 (6173, 6174)				52645365, 56994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109954, 21906754, 52646317, 265017, 264682, 264369, 264684, 21906767, 21906768, 265020, 264691, 33657023, 33657109, 52645129, 33657182, 27486262, 35695855, 87168518
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gij3355304 (AF001549) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264591
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gij4689146jgb/AAD27782.1(AF077049) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - dehydrogenase 3-hydroxyacyl-CoA dehydrogenase		18108397, 65274572, 56182575, 56181686, 56994075, 35696286, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432229, 21906754, 55811386, 265017, 265018, 265019, 264760, 55811150, 264288, 264766, 56181562, 21906765, 21906766, 21906767, 21906768, 265021, 60170615, 27486262, 18108370, 60431528, 35696423, 264558, 264559, 60432113, 264486

3090	95342371 (6179, 6180)	Novel Protein sim. GBank gij1354050 (U47024) - MEM3 [Mus musculus]		UNCLASSIFIED	60424178, 52645156, 65274572, 56182575, 56181686, 22278995, 35698286, 56994075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264908, 264908, 52644045, 264828, 265006, 265007, 265008, 60170831, 60432229, 60433356, 33657402, 55812038, 264758, 21906754, 33109954, 52646317, 55811388, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264369, 18108357, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170615, 264650, 52644150, 264691, 33657023, 18108365, 65274620, 33657109, 18108368, 33657182, 27486261, 27486265, 35695763, 18108374, 18108376, 55810764, 35696423, 55811576, 65274791, 35695855, 264557, 56182323, 63373044, 18108387, 18108388, 87168518, 22278000, 22279002, 264563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank gij3873932[emb]CAB01859] - (Z79598) Similarity to Bovine aspartyl beta hydroxylase (TR:G162694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64881 comes from this gene; cDNA EST EMBL:D68139 comes f...		UNCLASSIFIED	35696286, 29331822, 35696052, 264508, 264509, 264905, 264906, 264908, 264909, 264510, 264758, 265010, 265011, 264683, 264685, 264766, 264768, 264769, 264693, 264628, 35696423, 35695855, 264632, 264635, 264639, 264482, 264563, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gi11710756 sp P15880 RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - Ribosomal protein S5	- ribosomal prot	264488, 60424179, 18108396, 22278995, 56994075, 22278998, 35698286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35686052, 29331828, 29146498, 29146499, 284508, 264509, 264905, 264906, 264907, 29331830, 264808, 264909, 264113, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264591, 264592, 60431735, 264593, 264594, 60433438, 264595, 264758, 21908754, 265010, 265011, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 265019, 264760, 264762, 264681, 18108351, 264763, 264682, 264448, 264764, 264683, 264288, 264369, 264765, 264766, 264686, 264767, 264687, 264768, 264769, 264688, 21906764, 264689, 21906765, 21906766, 21806767, 21906768, 21906769, 29148629, 29148784, 35895917, 265020, 265021, 264534, 60170615, 284690, 264691, 264692, 65274620, 33657109, 27486262, 264628, 264629, 18108374, 263978, 18108377, 35696423, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264557, 264558, 264639, 60170394, 18108385, 264259, 29331824, 35696052, 264905, 285008, 60432229, 60431735, 264684, 264369, 264288, 264766, 21806767, 35696423, 83373044, 18108385
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gi15002587 emb CAB44347.1 - (Y17454) LSR1 protein [Homo sapiens]		UNCLASSIFIED	
3094	94316875 (6187, 6188)	Novel Protein sim. GBank gi1400734 sp P31044 PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	- collagen	18108398, 264259, 60432289, 29331827, 264511, 264763, 264288, 264767, 265022, 264691, 264693, 65274791, 56182323, 264564, 264565

3095	84848182 (6189, 6180)	Novel Protein sim. GBank gij487759jgb/AAD31421.1(AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens])	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35696052, 33656970, 29146499, 264508, 264905, 264509, 29331830, 264909, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264681, 264682, 264683, 264764, 264369, 264288, 264686, 264768, 264769, 264689, 21906765, 21906766, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33657023, 264693, 263972, 18108376, 55811576, 35696423, 264952, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 264482, 264563, 264564, 264566, 264487, 18108391, 22278995, 22278996, 22278997, 22278999, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906766, 21906767, 21906768, 35695917, 265020, 60170615, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264566, 264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002
3096	87756128 (6191, 6182)	Novel Protein sim. GBank gij3882221[dbj BAA34470.1] - (AB018293) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - situd Calponin homology (CH) domain		
3097	88264895 (6193, 6194)	Novel Protein sim. GBank gij4468288[emb CAB37981] - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	
3098	80258024 (6195, 6186)				264634, 264637, 264565
3099	91243325 (6197, 6198)	Novel Protein sim. GBank gij303603[dbj BAA02145.1] - (D12621) cytochrome P-450L TBV [Homo sapiens]		cyto450	264488, 35696286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22279002, 264563
3100	87602421 (6199, 6200)	Novel Protein sim. GBank gij1083764[pir B48013] - proline- rich proteoglycan 2 precursor, parolid - rat		UNCLASSIFIED	29331825, 60432289, 35696052, 264910, 60432229, 264592, 264288, 264693, 263967, 264635
3101	79602134 (6201, 6202)			UNCLASSIFIED	264908, 264693, 264628, 264630, 264632

3102	91220892 (6203, 6204)	Novel Protein sim. GBank gi 5305708 gb AAD41781.1 AF12853 - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	- struct	35696286, 22278996, 22278999, 29331827, 35696052, 264909, 264512, 265008, 601170831, 60433356, 33109954, 18108351, 264684, 264689, 21908767, 60170615, 264692, 33657023, 264630, 22279000, 264482, 264564
3103	80938004 (6205, 6206)	Novel Protein sim. GBank gi 464584 sp P35292 RB17_MOUSE - RAS-RELATED PROTEIN RAB-17		UNCLASSIFIED	35695917, 264565
3104	87340633 (6207, 6208)	Novel Protein sim. GBank gi 5032207 ref NP_005698.1 pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	264259, 264684, 264532, 33657182, 264558
3105	94148603 (6209, 6210)				22278997, 264259, 29331824, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22279002, 264563, 264565, 264566, 264486, 264567
3106	95361416 (6211, 6212)	Novel Protein sim. GBank gi 1838574 (U97190) - B0025.2 gene product [Caenorhabditis elegans]			22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 29331822, 264906, 264907, 264908, 52644045, 56182435, 264112, 265008, 265009, 55812038, 265017, 265018, 264883, 264686, 264687, 264788, 52644229, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gi 3341441 emb CAA76851 - (Y17794) winged-helix transcription factor [Gallus gallus]			22278995, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 265009, 60433356, 60433438, 265011, 265017, 265018, 21906765, 21906766, 21906767, 21906769, 265021, 264691, 33657109, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 56526488, 264482, 264487, 56182435, 264288, 264690, 264564
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gi 5032207 ref NP_005698.1 pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gij5002587[emb]CAB44347.1] - (Y17454) LSFRI protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	264480, 264908, 265007, 264910, 264593, 264683, 264684, 264687, 21906767, 21906768, 264693, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95090716 (6218, 6220)	Novel Protein sim. GBank gij1076211[prj]S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii	UNCLASSIFIED		264488, 65274572, 22278995, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432288, 29331826, 29331827, 29331828, 264908, 264510, 265008, 265007, 265008, 265009, 60432229, 33857402, 60433356, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264288, 284369, 21906766, 21906767, 21906768, 265020, 60170615, 264693, 65274620, 18108370, 264638, 18108384, 22279000, 284563, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gij3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264488, 18108398, 66712502, 265017, 265018, 265019, 264448, 21906767, 265020, 33657023, 18108365, 18108368, 35686423, 52644332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gij3900848 (AC005023) - match to EST AA361117 (NID: g2013436) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	
3113	88207098 (6225, 6226)	Novel Protein sim. GBank gij2459910 (AF005856) - anon2A5 [Drosophila yakuba]	Homeobox domain	lm7	18108397, 22278999, 264259, 29331824, 35686052, 264907, 264757, 60433438, 87168559, 264763, 264448, 18108354, 264288, 21906767, 21906769, 35695917, 264690, 264691, 264692, 264693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22279000, 22279002
3114	79843167 (6227, 6228)	Novel Protein sim. GBank gij4966270[gb]AAB52261.2] - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-18, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1 [C....	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	hydrolase	
3115	94117896 (6229, 6230)	Novel Protein sim. GBank gij5032225[re]NP_005676.1[wp]WBC - Williams-Beuren syndrome chromosome region 11		transcriptfactor	60424179, 56182575, 264259, 29331824, 60424269, 29331826, 66712502, 264510, 265007, 60431735, 60433356, 55812038, 55811386, 265019, 264288, 264689, 21906769, 264691, 33657023, 264693, 60431528, 263974, 60431850, 56182323, 264559, 22279000, 22279002
3116	79842835 (6231, 6232)			UNCLASSIFIED	264905, 264758, 21906764, 264690
3117	87771288 (6233, 6234)			UNCLASSIFIED	264510, 265011, 18108351, 264288, 264689, 264691, 18108368, 18108372, 263981, 264558, 264564

3118	94655848 (6235, 6236)	Novel Protein sim. GBank gi 3880563 emb CAB01444.1 - (Z78018) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00008) - EGF-like domain	Igf	52645156, 52646842, 65274572, 56182575, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 264905, 264908, 29331830, 52644045, 56182435, 264510, 264511, 265007, 265008, 265009, 264757, 52646317, 21906754, 33657084, 52644298, 87168474, 87168559, 265017, 265018, 264605, 265019, 264762, 264448, 264682, 264684, 264288, 264766, 56181562, 21906765, 21906766, 21906769, 265020, 265022, 264690, 52644150, 264691, 33657023, 264693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35698423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264486, 265006, 264288
3119	85728796 (6237, 6238)		Contains protein domain (PF00328) - Histidine acid phosphatase		
3120	87344040 (6238, 6240)	Novel Protein sim. GBank gi 5019819 gb AAD37863.1 AF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264509, 264510, 264511, 264512, 264288, 264486
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gi 4501877 ref NP_001088.1 pACRQ - acrosin			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35696052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52644150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)			UNCLASSIFIED	264638
3123	88033003 (6245, 6246)	Novel Protein sim. GBank gi 2439517 (AC002563) - putative RHO/RAC effector protein; 85% similarity to P49205 (PIDg1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	Kinase	18108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27486265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87766899 (6247, 6248)			UNCLASSIFIED	264905
3125	91216607 (6249, 6250)	Novel Protein sim. GBank gi 4980828 gb AAD35412.1 AE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	56181686, 264259, 66714117, 60432289, 29331826, 29331827, 264907, 264908, 264828, 265009, 60433356, 33657402, 60433438, 264758, 18108351, 264288, 29148627, 29148629, 33657023, 33657109, 18108382, 56526486

3126	85337205 (6251, 6252)				UNCLASSIFIED	22278999, 264490, 264259, 60432049, 29331822, 60432289, 29146498, 52644045, 56182435, 265009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264683, 264369, 264689, 29148629, 33657023, 264693, 33657109, 18108374, 55811578, 18108385, 60432113, 22279002, 35696286, 22278996, 22278999, 28331826, 264808, 60433438, 87168559, 264604, 21906765, 21906769, 33657023, 33657349, 264629, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gi 2828280 emb CAA16694.1 - (AL021687) putative protein [Arabidopsis thaliana]				
3128	87674330 (6255, 6256)	Novel Protein sim. GBank gi 3885828 (AF090133) - lin-7-A [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).		misc_channel	22278998, 264259, 52644045, 265008, 21906754, 265017, 265018, 21908768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gi 3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat		kinase	56182575, 264259, 29331825, 29331828, 52644045, 56182435, 60433356, 264600, 264682, 264763, 264784, 264369, 264288, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264564, 264566, 264636
3130	14993860 (6259, 6260)	Novel Protein sim. GBank gi 3329485 (AF064553) - NSD1 protein [Mus musculus]				
3131	95351469 (6261, 6262)	Novel Protein sim. GBank gi 1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat		UNCLASSIFIED	56182575, 264259, 29331824, 264907, 56182435, 264594, 60433438, 55812038, 33109954, 21906754, 33657084, 87168474, 264448, 264766, 21906769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27486261, 33657349, 65274791, 60170394, 56182323, 83373044, 87168518, 264564

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gi 4680647 gb AAD27713.1 AF13293 - (AF132938) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - ubiquitin UBX domain	52644507, 52646842, 52646365, 85274572, 56182575, 22278994, 22278995, 35586286, 56994075, 22278998, 22278997, 22278998, 22278999, 60432049, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 52644045, 56182435, 264910, 60170831, 60432229, 60433356, 33657402, 55812038, 52646317, 21908754, 52644296, 85658542, 87168559, 265017, 265018, 265019, 264448, 264288, 264389, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33657023, 52845129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 18108374, 18108376, 55811576, 35695855, 18108385, 18108387, 56526486, 87168518, 60432113, 22279002
3133	87379414 (6265, 6266)	Novel Protein sim. GBank gi 4507613 ref NP_003738.1 pTNKS - TANKYRASE	polymerase	22278994, 22278998, 264905, 265006, 265007, 87168559, 264760, 21906767, 18108374, 22279000, 22279002, 264563 264595, 264369, 264685, 264628, 264566
3134	84649816 (6267, 6268)	Novel Protein sim. GBank gi 1729827 sp P54633 ITALA_DICDI - FILOPODIN (ITALIN HOMOLOG)		22278998, 264095, 29331826, 33657402, 18108348, 263974
3135	86389356 (6269, 6270)	Novel Protein sim. GBank gi 3093478 (AF012927) - fibrinogen-binding protein [Streptococcus equi]	struct	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 264288, 264769, 264689, 265020, 27486262, 263972, 65274791, 264557, 264558
3136	94845839 (6271, 6272)	Novel Protein sim. GBank gi 627101 pir IS44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264682, 264769, 21906765, 21906766, 21906767, 21906769, 55811857, 35695917, 265020, 265021, 52844150, 18108370, 18108374, 22279000, 22279002, 264482, 264486
3137	88257947 (6273, 6274)	Novel Protein sim. GBank gi 3342730 (AC005331) - R31341_1 [Homo sapiens]	UNCLASSIFIED	

3138	94130188 (6275, 6276)	Novel Protein sim. GBank gii4406759[gb AAD20070] - (AC006838) hypothetical protein [Arabidopsis thaliana]			264569, 264488, 264907, 264511, 264593, 33109954, 87168559, 264681, 264684, 264685, 264686, 264687, 264768, 264688, 264689, 264691, 264692, 264693, 33657109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108388, 60432113, 22279000, 22279002
3139	87325503 (6277, 6278)	Novel Protein sim. GBank gii228938[prf1]1814452C - Hyp-rich glycoprotein [Zea diploperennis]	UNCLASSIFIED		22278997, 22278998, 22278999, 264905, 265018, 265019, 21906765, 265020, 264636, 264557
3140	91222692 (6278, 6280)	Novel Protein sim. GBank gii932[emb CAA37773] - (X53744) 68kDa subunit of signal recognition particle [Canis familiaris]	struct		22278995, 56994075, 35696286, 264908, 264909, 60433358, 21908754, 52644296, 87168474, 87168559, 264683, 264288, 264685, 264686, 265022, 264693, 27486262, 35695855, 264630, 264555, 264566
3141	87323564 (6281, 6282)	Novel Protein sim. GBank gii3213227 (AF035209) - putative v-SNARE Vti1a [Mus musculus]	UNCLASSIFIED		56182575, 35696286, 29331828, 264909, 265009, 265018, 18108351, 264369, 21906766, 29148627, 265020, 264628, 264629, 264631, 18108385
3142	95419028 (6283, 6284)	Novel Protein sim. GBank gii2498197[sp Q95245 C561_P1G - CYTOCHROME B561 (CYTOCHROME B-561)]	cytochrome		52645158, 52646365, 22278995, 35696286, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331827, 29146489, 56182435, 265007, 60170831, 60432229, 33657402, 264595, 60433438, 264758, 21906754, 264288, 264768, 264687, 52644229, 21906765, 21906767, 21906768, 60170615, 52644150, 65274620, 33657109, 35695763, 18108370, 18108376, 65274791, 35695855, 264631, 264557, 87168518, 60432113, 22279000
3143	95351475 (6285, 6286)	Novel Protein sim. GBank gii5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		264488, 56182575, 22278998, 22278999, 29331822, 29331824, 60432289, 35696052, 29331828, 264508, 264905, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 265008, 264910, 60432229, 33657402, 60433356, 60433438, 55812038, 265011, 265019, 264760, 264763, 264448, 264764, 264684, 264288, 264685, 264686, 264768, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 264690, 33657023, 264693, 263987, 33657109, 264628, 264629, 18108374, 263976, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87168518, 60432113, 22279000, 22279002, 264563, 264566, 264486

3144	95336329 (6287, 6288)	Novel Protein sim. GBank gll488446[emb]CAB43322.1] - (AL050225) hypothetical protein [Homo sapiens]			264488, 18108396, 22278996, 35696286, 22278997, 22278999, 29331828, 29331827, 35696052, 29331828, 264106, 265006, 265007, 265009, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21908765, 21908766, 21908767, 265020, 265021, 52644150, 27486261, 18108370, 18108374, 35696423, 56182323, 83373044, 22279000, 22279002, 264567
3145	86611657 (6289, 6290)	Novel Protein sim. GBank gll387970[emb]CAB03330] - (Z81118) Similarly to Human endosomal protein P162 (TR:Q15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from this gene	UNCLASSIFIED		18108397, 29331824, 29146499, 20281100, 265006, 55812038, 265010, 21908766, 29148627, 21908768, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87168518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gll2135746[pir]S69890 - mitogen inducible gene mig-2 - human	Contains protein domain (PF00169) - PH domain	struct	264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 264448, 264369, 21908766, 265021, 264692, 33657109, 18108374, 35696423, 35695855, 60432113, 264584
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gll387427[emb]CAB07315.1] - (Z92825) predicted using GeneFinder; cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	UNCLASSIFIED	56181686, 35696286, 60432049, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 265008, 264910, 60431735, 60433356, 60433438, 265010, 264448, 264288, 265022, 33657023, 33657109, 60431528, 65274791, 264631, 56182323, 264404, 22279002
3148	95382169 (6295, 6296)	Novel Protein sim. GBank gll5225322[gb]AAD0851.1[AF08310] - (AF083108) sirutin type 3 [Homo sapiens]	UNCLASSIFIED		35696286, 35696052, 264511, 85658542, 87168474, 264764, 35696423, 264555, 264556, 264557, 264558, 83373044, 56526486, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gll4200446 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]	Contains protein domain (PF01363) - FYVE zinc finger	eph	29331822, 35696052, 264109, 29148628, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gll3378454[emb]CAA76893] - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - Glutathione S-transferases	transferase	264259, 29331822, 29331824, 29331825, 29331827, 52646317, 264686, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gll172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	oncogene	29331822, 265008
3152	85698108 (6303, 6304)		UNCLASSIFIED		21906754, 87168559, 264605, 21906768, 52644150, 27486264, 35696423, 22279000

3153	95317299 (6305, 6306)	Novel Protein sim. GBank gi 4895041 gb AAD32705.1 AF143957) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - struct WD domain, G-beta repeat		284488, 52646385, 35696286, 22278996, 22278997, 22278999, 60432049, 264259, 29331826, 60432289, 33656970, 264508, 264908, 33657402, 264595, 60433438, 87168474, 87168559, 264601, 265019, 264448, 264682, 264764, 264288, 264369, 264768, 21906765, 21906768, 21906767, 21908768, 21908769, 29148784, 265021, 265022, 60170615, 52644150, 264690, 264691, 33657023, 65274620, 33657109, 18108370, 35695855, 264638, 60170394, 87168518, 60432113, 22279000, 22279002, 22278998, 264259, 29331824, 66712502, 265008, 265010, 265017, 18108354, 264691, 33657023, 264693, 20281149, 18108374, 29331828, 264509, 264905, 264908, 264510, 264511, 264512, 33657402, 264681, 264683, 33657023, 18108370, 264634, 264639, 18108385, 264563, 264488
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi 488066 gb AAD27720.1 AF132945) CGI-11 protein [Homo sapiens]	ATPase associated		56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109954, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 264288, 264689, 21906768, 21906768, 21906769, 35695917, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3155	87722394 (6309, 6310)	Novel Protein sim. GBank gi 728837 sp P39184 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	UNCLASSIFIED		18108396, 264259, 29331826, 35696052, 29146498, 87168559, 265017, 264448, 264288, 264691, 18108366, 52645129, 35696423, 52644332
3156	87737449 (6311, 6312)	Novel Protein sim. GBank gi 5830078 gb AAD45821.1 AC006017) N-acetylglucosaminyltransferase, similar to Q10473 (PID: g1709559) [Homo sapiens]	transferase		264488, 263974
3157	88259577 (6313, 6314)				
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi 5306064 gb AAD41895.1 AF156778) ASB-3 protein [Homo sapiens]	kinase		
3159	94124114 (6317, 6318)	Novel Protein sim. GBank gi 5531272 emb CAB50897.1 - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]	UNCLASSIFIED		56182575, 22278998, 29331824, 264108, 60433356, 264758, 265011, 87168559, 264448, 18108354, 264768, 21906768, 265020, 264691, 264692, 33657109, 18108374, 35696423, 264555, 60170394, 22279000
3160	80221088 (6319, 6320)	Novel Protein sim. GBank gi 3930525 AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	struct		18108351, 264555, 264556, 264557, 264558, 264559

3161	8807411 (6321, 6322)				264488, 2227895, 2227897, 2227898, 264259, 2933182, 6043289, 2933182, 52644045, 265017, 265018, 264448, 264288, 21908784, 21908787, 265020, 18108374, 264636, 264568
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (U1SMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberos scleros, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis , Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberos scleros, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberos scleros, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH 56.3 (U1SMC)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema, Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia.
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (UuMVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer

22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleenITP)		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft vesus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hemin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	rrQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5: 1:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen I		

Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences

<210> 1
 <211> 312
 <212> DNA
 <213> Homo sapiens

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 180
 tcgctggtgg agcgtctgct cgcgtctgct tcttgctcag ccgtcttgcg ggactggggc
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 312

<210> 2
 <211> 104
 <212> PRT
 <213> Homo sapiens

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 Gly Ser Ser Ala Thr Ser Gly Pro Ala Ser Xaa Asp Pro Ser Ala Ser
 35 40 45
 Pro Pro Pro Ile Ser Ala Ala Arg Leu Ser Arg Met Ser Leu Val Glu
 50 55 60
 Arg Cys Ser Ala Ser Ala Ser Cys Ser Ala Val Leu Arg Asp Trp Ala
 65 70 75 80
 Cys Ser Ser Ala Leu Val Arg Ala Ala Ser Met Ser Ala Lys Ser Asp
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 Ser Ala Phe Gly Ser Glu Thr Arg
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<210> 3
 <211> 987
 <212> DNA
 <213> Homo sapiens

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 240
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 480
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 840
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 987

<210> 4
 <211> 329
 <212> PRT
 <213> Homo sapiens

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 Ala Ala Glu Arg Ala Glu Ala Ile Leu Gly Met Asp Ile Lys Gly His
 35 40 45

Thr Val His Lys Val Met Val Ala Glu Gly Ala Asp Ile Ala Glu Glu
 50 55 60
 Tyr Tyr Phe Ser Ile Leu Leu Asp Arg Gly Glu Arg Arg Tyr Leu Ala
 65 70 75 80
 Met Cys Ser Arg Glu Gly Gly Met Asp Ile Glu Thr Leu Ala Lys Glu
 85 90 95
 Arg Pro Glu Ala Leu Ala Lys Val Pro Val Asp Pro Ile Asp Gly Val
 100 105 110
 Asp Asp Ala Lys Ala Arg Glu Ile Leu Ser Glu Ala Gly Phe Pro Asp
 115 120 125
 Ser Glu Gln Asp Ala Ile Val Pro Ala Val Leu Lys Leu Trp Glu Thr
 130 135 140
 Tyr Arg Asp Glu Asp Ala Thr Leu Val Glu Val Asn Pro Met Ile Lys
 145 150 155 160
 Thr Gly Asp Gly Arg Ile Leu Ala Ile Asp Gly Lys Met Thr Val Asp
 165 170 175
 Asn Asn Ala Ser Phe Arg Gln Pro Asp Arg Ala Gly Leu Val Asp Arg
 180 185 190
 Ala Thr Thr Asp Pro Leu Glu Leu Arg Ala Gly Glu Leu Gly Leu Asn
 195 200 205
 Tyr Val Lys Leu Asp Gly Asn Val Gly Val Ile Gly Asn Gly Ala Gly
 210 215 220
 Leu Val Met Ser Thr Leu Asp Cys Val Ala Tyr Ala Gly Glu Asn Phe
 225 230 235 240
 Pro Gly Ser Pro Ala Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala
 245 250 255
 Ser Ala Glu Ile Met Ala Asn Gly Leu Asp Leu Ile Met Ser Asp Glu
 260 265 270
 Gln Val Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys
 275 280 285
 Asp Gln Val Ala Leu Gly Ile Lys Gly Ala Leu Glu Lys Leu Gly Asp
 290 295 300
 Lys Ala Val Lys Pro Leu Val Val Arg Leu Asp Gly Asn Ala Val Ala
 305 310 315 320
 Glu Gly Arg Lys Ile Leu Glu Glu Phe
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<210> 5

<211> 622

<212> DNA

<213> Homo sapiens

<400> 5

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 180
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 240
 gggtagcagg ggcattgggg taatagcctt ctagcccttt ttgagggaaa cacatgggtg
 300

aggcattttt ggggctggga agtggggggc tgggtgtccc tggatggctg tgctggcctc
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 420
 cagaaattta accagagcct gtccctcctt tcttgctgc ccccaacatc tcacaatccc
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<210> 6
 <211> 121
 <212> PRT
 <213> Homo sapiens

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 His Pro Gly Asp Thr Arg Pro Pro Leu Pro Ser Pro Lys Ile Ala Ser
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 Pro Met Cys Phe Pro Gln Lys Gly Leu Glu Gly Tyr Tyr Pro Asn Ala
 35 40 45
 Pro Ala Thr Pro Ser Leu Gln Lys Val Ile Cys Asp Leu Gln Gly Leu
 50 55 60
 Thr Ala Arg Cys Asp Val Ser Cys Cys Gln Ala Glu Arg Gly Leu Gly
 65 70 75 80
 Glu Pro Cys Arg Asp Val Met Thr Ser Tyr Val Leu Gly Asn Lys Val
 85 90 95
 Thr Cys Cys Arg Pro Leu Glu Leu Trp Pro Val Lys Thr Pro Gly Asn
 100 105 110
 Pro Met Ala Arg Arg Glu Thr Val Leu
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<210> 7
 <211> 480
 <212> DNA
 <213> Homo sapiens

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 240
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 480

<210> 8
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 8
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 20 25 30
 Pro Val Arg Glu Trp Cys Val Lys Gly His Leu His Val Gly Lys Arg
 35 40 45
 Glu Asp Leu Asp Phe Ser Gly Thr Glu Met Gly Pro Pro Ala Cys Gly
 50 55 60
 Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg
 65 70 75 80
 Val Val Leu Pro Asp Leu Ser Ser Glu Gly Phe Ala Cys Pro Ala Arg
 85 90 95
 Ala Ala Arg His Arg Gly Pro Ser Gly Thr Pro Met Ala Thr Leu Gly
 100 105 110
 Lys Thr Gly Leu Leu Thr Arg
 115

<210> 9
 <211> 428
 <212> DNA
 <213> Homo sapiens

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 180
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 240
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 300
 aaacagttaa cgaattacat gatccaatgt accagtatcg agttgatacc ggaaattttc
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 420
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 428

<210> 10
 <211> 138
 <212> PRT

<213> Homo sapiens

<400> 10

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Met Arg Asp Trp Gly Ile Glu Gln Lys Trp Met Ser Val Leu Leu Pro
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 20           25           30
Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
 35           40           45
Leu Cys Ala Leu Leu Leu Phe Trp Leu Cys Val Tyr His Gly Ile Arg
 50           55           60
Val Gln Gly Glu Arg Lys Cys Leu Thr Phe Tyr Leu Pro Lys Phe Phe
 65           70           75           80
Ile Val Gly Leu Leu Trp Leu Ala Ser Val Thr Leu Gly Ile Trp Gln
 85           90           95
Thr Val Asn Glu Leu His Asp Pro Met Tyr Gln Tyr Arg Val Asp Thr
100          105          110
Gly Asn Phe Gln Gly Met Lys Val Phe Phe Met Val Val Ala Ala Val
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Tyr Ile Leu Tyr Leu Leu Phe Leu Ile Val
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<210> 11

<211> 453

<212> DNA

<213> Homo sapiens

<400> 11

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180
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240
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300
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453

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<210> 12

<211> 130

<212> PRT

<213> Homo sapiens

<400> 12

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Ser Ser Ala Asp Leu Pro Gly Ser Thr Ser Thr Leu Leu Gly Ser Ser

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Cys	Phe	Met	Pro	Pro	Ile	Ser	Pro	Cys	Pro	Met	Ala	Ala	Trp	Ser	Ile
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Leu	Pro	Met	Pro	Val	Ala	Val	Ser	Met	Pro	Leu	Ala	Cys	Ile	Leu	Ser
	50					55					60				
Ile	Ser	Phe	Trp	Cys	Ser	Ala	Cys	Ile	Ala	Ala	Ser	Pro	Arg	Leu	Asn
65					70				75					80	
Ser	Cys	Ser	Asn	Trp	Pro	Leu	Leu	Thr	Ser	Thr	Lys	Arg	Thr	Val	Ser
			85					90						95	
Pro	Ala	Phe	Thr	Ser	Arg	Ala	Leu	Gly	Glu	Lys	Glu	Met	Ser	Cys	Arg
			100					105					110		
Val	Thr	Ser	Thr	Val	Arg	Val	Ala	Leu	Ser	Ala	Gly	Ala	Gly	Trp	Pro
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Asn	Ala														
	130														

<210> 13

<211> 2034

<212> DNA

<213> Homo sapiens

<400> 13

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 180
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 420
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 960

gcaaggtgaa gcgggcagtg gtgcaggtga ttagcgccca tggcccacca cggctacctg
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 1920
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<210> 14

<211> 222

<212> PRT

<213> Homo sapiens

<400> 14

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Gly	Pro	Gly	Ser	Lys	Asp	Pro	Lys	Ala	Asp	Ser	Val	Arg	Ala	Ile	Ser
			20					25				30			
Val	Arg	Thr	Leu	Tyr	Leu	Val	Ser	Thr	Thr	Val	Asp	Arg	Met	Ser	His
		35				40					45				
Val	Leu	Trp	Pro	Tyr	Leu	Leu	Gln	Phe	Leu	Thr	Pro	Val	Arg	Phe	Thr
	50					55				60					
Gly	Ala	Leu	Thr	Pro	Leu	Cys	Arg	Ser	Leu	Val	His	Leu	Ala	Gln	Lys
65				70					75					80	
Arg	Gln	Glu	Ala	Gly	Ala	Asp	Ala	Phe	Leu	Ile	Gln	Tyr	Asp	Ala	His

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<210> 15
<211> 363
<212> DNA
<213> Homo sapiens
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180
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240
gcgaagaaat acgatctgta caccaagatc accggcggcc agcggatcga cctgttcggc
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360
ggc
363

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<210> 16
<211> 121
<212> PRT
<213> Homo sapiens
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<400> 16
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 1             5             10             15
Cys Lys Pro Ala Val Gly Ser Ile Leu Ala Ser Cys Trp Asn Gln Pro
 20             25             30
Ile Met Asp Pro Ala Leu Val Pro Leu Gln Asp Thr Asn Asp Thr Phe
 35             40             45
Met Ala Asn Met Gln Lys Asn Gly Thr Tyr Ser Ile Ile Pro Arg Ile
 50             55             60
Ala Gly Gly Glu Ile Thr Pro Asp Lys Leu Ile Ala Leu Gly Ala Val

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65              70              75              80
Ala Lys Lys Tyr Asp Leu Tyr Thr Lys Ile Thr Gly Gly Gln Arg Ile
              85              90              95
Asp Leu Phe Gly Ala Gln Leu His Glu Leu Pro Gln Ile Trp Gly Glu
              100              105              110
Leu Val Asp Ala Gly Phe Glu Thr Gly
              115              120

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<210> 17
 <211> 682
 <212> DNA
 <213> Homo sapiens

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<400> 17
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120
tctagcatcc tccagtatgg aggctgcatt aagactgcat gaaggagagg gagagaaggg
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agaaacagag cagctggaca agaggacagg tataggggaat aagggagaag ccagtaaggc
240
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<210> 18
 <211> 110
 <212> PRT
 <213> Homo sapiens

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<400> 18
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              20              25              30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
              35              40              45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
50              55              60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser

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65					70					75				80
Phe	Pro	Thr	Pro	Glu	Ile	Pro	His	Ser	Leu	Ala	Pro	Gly	Thr	Val Ala
				85					90				95	
Ile	Ser	Lys	Pro	Trp	Phe	Pro	Ala	Val	Ser	Gln	Ile	Ala	Arg	
			100					105					110	

<210> 19

<211> 515

<212> DNA

<213> Homo sapiens

<400> 19

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cttggctggc agacatggga cctgcttccc tcttacaccc cagtcttggc aaggatcatg
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120
cgtctgcagt gcagtcttgg gctataagaa aactggggcc actcaatacc tccccctttt
180
tgcccttctt cctcctctgg tccatgggtg ggggtggggg gagcccagtt tcagcaccag
240
cagctggagc ccataccaca ctcatcttct agttctggct gtgggagccc ctcccacagg
300
tttcagttcc ccaagcccca ggctgagtt tttttattg caaaagctgg ttgttgttgt
360
ggctagctcc caggcgtgtg aggtgcagct tgctaagtaa gagctaggaa agagaatagg
420
gtcctgctgt aggtgtccag tctgaaggaa tgcttgggat acttcctcaa gcagttcctt
480
ctcacagtct cctggctgct ccgcatgtca gatct
515

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<210> 20

<211> 130

<212> PRT

<213> Homo sapiens

<400> 20

Met	Gly	Pro	Ala	Ser	Leu	Leu	His	Pro	Ser	Leu	Gly	Lys	Asp	His	Ala
1				5				10						15	
Pro	Ile	Ser	Thr	Met	Leu	Ala	Ser	Leu	Ala	Val	His	Leu	Val	Thr	Thr
			20					25					30		
Val	Cys	Phe	Ser	Ser	Ala	Val	Gln	Ser	Trp	Ala	Ile	Arg	Asn	Thr	Gly
	35						40					45			
Pro	Leu	Asn	Thr	Ser	Pro	Leu	Leu	Ala	Leu	Leu	Leu	Leu	Trp	Ser	Met
	50					55					60				
Gly	Gly	Val	Gly	Gly	Ser	Pro	Val	Ser	Ala	Pro	Ala	Ala	Gly	Ala	His
65				70					75					80	
Thr	Thr	Leu	Ile	Phe	Gln	Phe	Trp	Leu	Trp	Glu	Pro	Leu	Pro	Gln	Val
			85					90					95		
Ser	Val	Pro	Gln	Ala	Pro	Gly	Leu	Ser	Phe	Phe	Tyr	Cys	Lys	Ser	Trp
			100				105						110		
Leu	Leu	Leu	Trp	Leu	Ala	Pro	Arg	Val	Arg	Cys	Ser	Leu	Leu	Ser	
		115				120					125				
Lys	Ser														

130

<210> 21
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 21
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 tagacgcggt gcctatgggt gcggaggacc atggagtgaa gcgagtaaga ctagatgatg
 120
 caacaaatgt gcctgagggt gaaatggcac gagccagtgc caatgagggc atgacacctg
 180
 ttaaccacga caaataccct tctgtccttt taaatgaagc ggcccaggct tcattactgg
 240
 atacaatgac tgcttgact gatgggttca caattgagca attggagctt acacgatctc
 300
 tatgttatga aagagtatta gcacatcgat cctcatggga tcgttcagcc ctgggtcaag
 360
 aattaaagca agttgtccaa ggcatccatn
 390

<210> 22
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Val Ala Glu Asp His Gly Val Lys Arg Val Arg Leu Asp Asp Ala
 1 5 10 15
 Thr Asn Val Pro Glu Gly Glu Met Ala Arg Ala Ser Ala Asn Glu Gly
 20 25 30
 Met Thr Pro Val Asn His Asp Lys Tyr Pro Ser Val Leu Leu Asn Glu
 35 40 45
 Ala Ala Gln Ala Ser Leu Leu Asp Thr Met Thr Ala Cys Thr Asp Gly
 50 55 60
 Phe Thr Ile Glu Gln Leu Glu Leu Thr Arg Ser Leu Cys Tyr Glu Arg
 65 70 75 80
 Val Leu Ala His Arg Ser Ser Trp Asp Arg Ser Ala Leu Ala Gln Glu
 85 90 95
 Leu Lys Gln Val Val Gln Gly Ile His
 100 105

<210> 23
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 23
 ntctcggagg ccgacagcct ggcgggctgg aagccctcgg tgtaccacgt gctgctcatc
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 ctgggcctgt tcgccgtgct gctgtcctgc tgcgcctcgg ccatgtacac cagcgtggag
 120

ggctgggact acgtggactc gctctacttc tgcctcgtca ccttcagcac catcggttc
 180
 ggggacctgg tgagcagcca gcacgcgcc taccggaacc aggggtctta ccgcctgggc
 240
 aacttcctct tcacctctgt cggcgtgtgc tgcatttact cgctcttcaa cgtcactctc
 300
 atcctcatca agcagggtgt caactggatg ctgcgcaagc tgagctgceg ctgctgcgcg
 360
 cgctgctgcc cggctcctgg cgcgc
 385

<210> 24
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 24
 Xaa Ser Glu Ala Asp Ser Leu Ala Gly Trp Lys Pro Ser Val Tyr His
 1 5 10 15
 Val Leu Leu Ile Leu Gly Leu Phe Ala Val Leu Leu Ser Cys Cys Ala
 20 25 30
 Ser Ala Met Tyr Thr Ser Val Glu Gly Trp Asp Tyr Val Asp Ser Leu
 35 40 45
 Tyr Phe Cys Phe Val Thr Phe Ser Thr Ile Gly Phe Gly Asp Leu Val
 50 55 60
 Ser Ser Gln His Ala Ala Tyr Arg Asn Gln Gly Leu Tyr Arg Leu Gly
 65 70 75 80
 Asn Phe Leu Phe Ile Leu Leu Gly Val Cys Cys Ile Tyr Ser Leu Phe
 85 90 95
 Asn Val Ile Ser Ile Leu Ile Lys Gln Val Leu Asn Trp Met Leu Arg
 100 105 110
 Lys Leu Ser Cys Arg Cys Cys Ala Arg Cys Cys Pro Ala Pro Gly Ala
 115 120 125

<210> 25
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 25
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 aggaggggag ttcccagctc tgtatttttg aagggtcagt cttgttgctt ggaccagtga
 120
 ggagccccgt gggatccaga ctcgagtggg tggagccggg gcaggtggga gcagagacac
 180
 tggaggaaaag ctggtcgaat gcactgtgta tttggaggca gaaccagcag agggtcctct
 240
 ggggttgagt tagggcaaaa gagaaagaag gcaccaagcc tggggctctg gttttctctc
 300
 ttacacttgc tgggtggacg gtggtgccac tgaatga
 337

<210> 26

<211> 111
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu
 1 5 10 15
 Gln Ser Phe Glu Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser
 20 25 30
 Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu
 35 40 45
 Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp
 50 55 60
 Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp
 65 70 75 80
 Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp
 85 90 95
 Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn
 100 105 110

<210> 27
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 27
 ccgacgtcga atatccatgc agccgcgcgcg aggatggaga gagcgatgga gcaactcaac
 60
 cgccctgacgc gctcgcgtgcg ccgcgcgcgc accgtggagt tgcccagga taatgaaact
 120
 gctgtttata cattaatgcc aatggttatg gctgatcaac acaggtctgt ttctgaacta
 180
 ctatcaaatt caaaatttga tgtcaattat gcattcggac gtgtgaaaag aagcttgctt
 240
 cacattgcag caaattgtgg atcgggtggaa tgcttggttt tgctgttaaa gaaaggagca
 300
 aatcctaact atcaagatat ttcaggctgt aca
 333

<210> 28
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 28
 Pro Thr Ser Asn Ile His Ala Ala Ala Pro Arg Met Glu Arg Ala Met
 1 5 10 15
 Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val
 20 25 30
 Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met
 35 40 45
 Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Ser Asn Ser
 50 55 60
 Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

65		70		75		80									
His	Ile	Ala	Ala	Asn	Cys	Gly	Ser	Val	Glu	Cys	Leu	Val	Leu	Leu	Leu
		85		90		95									
Lys	Lys	Gly	Ala	Asn	Pro	Asn	Tyr	Gln	Asp	Ile	Ser	Gly	Cys	Thr	
		100		105		110									

<210> 29
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 29
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 gagagctatt tgagcgccgt gacgccgtg agtcccaaag agattcgtca gctgccccgc
 120
 tacaatatca cgatcaagcg cgtcgtgaac atgacgggca agggccgcac gccgagctgg
 180
 tactcgctcg tcgtggctgg caatggctcg ggcctcgtgg gctatggcga aggcaaagat
 240
 actaacatca gccgcgcgaa caaaaaggcg ttccacgccg cggtgaaaaa catggacttg
 300
 gtatcggtcc accggtcgaa gagtggcgcc aacacgctcg agccccccgt cgagggccgc
 360
 tggggcgcta cgcgt
 375

<210> 30
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 30
Xaa Pro Ser Val Leu Ala Ile Met Thr Ala Gly Ser Asp Gln Gly Glu
1 5 10 15
Glu Val Asn Ser Glu Ser Tyr Leu Ser Ala Val Thr Pro Leu Ser Pro
20 25 30
Lys Glu Ile Arg Gln Leu Pro Arg Tyr Asn Ile Thr Ile Lys Arg Val
35 40 45
Val Asn Met Thr Gly Lys Gly Arg Thr Pro Ser Trp Tyr Ser Leu Val
50 55 60
Val Ala Gly Asn Gly Arg Gly Leu Val Gly Tyr Gly Glu Gly Lys Asp
65 70 75 80
Thr Asn Ile Ser Arg Ala Asn Lys Lys Ala Phe His Ala Ala Val Lys
85 90 95
Asn Met Asp Leu Val Ser Val His Arg Ser Lys Ser Gly Ala Asn Thr
100 105 110
Leu Glu Pro Pro Val Glu Gly Arg Trp Gly Ala Thr Arg
115 120 125

<210> 31
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 31
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 gggagcaggc acttacgagc ctgcgcgtca gggatgcttc ctgggccctt gagagtgcag
 120
 agattcctgg atccagagct gcggctgggc ggctgcagct gcgcctggga gtgcagggtc
 180
 cccgccctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttgccc
 240
 ctgcagagtg cacaaacctt gccgcgcttc ctccactgca gcttacgtct ttgcagcagc
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 cactcccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca
 360
 tggcctgcat tgttt
 375

<210> 32
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 32
 Met Gln Ala Met Ser Leu Lys Leu His Thr Leu Trp Ser His Arg Trp
 1 5 10 15
 Gln Trp Gln Pro Ile Gly Ser Gly Cys Cys Lys Asp Val Ser Cys Ser
 20 25 30
 Gly Gly Ser Ala Ala Arg Phe Val His Ser Ala Gly Pro Thr Gly Ala
 35 40 45
 Arg Asn Arg Gln Glu Pro Pro Phe Pro Phe Glu Leu Ala Gly Arg Glu
 50 55 60
 Pro Cys Thr Pro Arg Arg Ser Cys Ser Arg Pro Ala Ala Ala Leu Asp
 65 70 75 80
 Pro Gly Ile Ser Ala Leu Ser Gly Ala Gln Glu Ala Ser Leu Thr Arg
 85 90 95
 Arg Leu Val Ser Ala Cys Ser Arg Ser Ser Pro Leu Leu Ala Pro Thr
 100 105 110
 Ser Ile Ser Glu Gln Ser
 115

<210> 33
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 33
 ccatgcagcc caaccgttgg cgataaagtc cgtttaggcg ataccaattt atgggcaacc
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 attgaacaag atttattaac caaaggtgat gagtgtaaat ttggtggcgg taaaagtgtg
 120
 cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt
 180
 gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaage cgatattggt
 240

attcgcgatg gtcgtattgt cggatcggga caagcaggta accctgacac catggatgac
 300
 gtcacgccaa acatgattat cgggtgctagc acagaagtac ataacgggtgc a
 351

<210> 34
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 34
 Pro Cys Ser Pro Thr Val Gly Asp Lys Val Arg Leu Gly Asp Thr Asn
 1 5 10 15
 Leu Trp Ala Thr Ile Glu Gln Asp Leu Leu Thr Lys Gly Asp Glu Cys
 20 25 30
 Lys Phe Gly Gly Gly Lys Ser Val Arg Asp Gly Met Ala Gln Ser Gly
 35 40 45
 Thr Ala Thr Arg Asp Asn Pro Asn Val Leu Asp Phe Val Ile Thr Asn
 50 55 60
 Val Met Ile Ile Asp Ala Lys Leu Gly Ile Ile Lys Ala Asp Ile Gly
 65 70 75 80
 Ile Arg Asp Gly Arg Ile Val Gly Ile Gly Gln Ala Gly Asn Pro Asp
 85 90 95
 Thr Met Asp Asp Val Thr Pro Asn Met Ile Ile Gly Ala Ser Thr Glu
 100 105 110
 Val His Asn Gly Ala
 115

<210> 35
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 35
 nngctagctg caccaccacc tgttcatgca ggcagagcgg ccaccctca tggaagaaga
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 ggaatccact gtattgggca caggcttctt gctggacctt ggcaagcagg tgcttggtg
 120
 gtaccaggaa gtccagcgtg tacctcagtg cgtcctcccg ataagtcctc tccaccacct
 180
 ggaacacctg gcccaacagg gtgggggctg ttgcctcaaa gggaggatac agggcggcga
 240
 gagggtcttg cacacagtcc tccactggct caggctccat ggctcggcgc cgggcccgcg
 300
 ccgacgcttg gtcgggaggc cggggccggg cgcgccaccg cctcccttca cgcgt
 355

<210> 36
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 36
 Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

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      1           5           10           15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
      20           25           30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
      35           40           45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Pro Gly Thr Pro Gly
      50           55           60
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
      65           70           75           80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
      85           90           95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
      100           105           110
Thr Ala Ser Leu His Ala
      115

```

<210> 37
 <211> 492
 <212> DNA
 <213> Homo sapiens

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<400> 37
acgcgtggcc ttcgtctgcc accaggaccg actcagcccc accgggtttc cggaccgcgc
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gcaaccatga caaggcgat gttgtgatct ggggtggattc cttctccgac atgctcgagg
120
gatecggatct ctccggcgga gtcacgggtgc ttgccgaggc cggctatcgc ccacgggtcc
180
tcgccgacga cgtctgctgc ggggtgacgt ggatcactac cggtcagctc gacgggtgctc
240
ggcgtcggct gcgcgctggt ctgcagctgc tggcaccct gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcgtga tgacgcactc cgcctcctgc
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca taccgtcgcc gagatgcttg
420
aggcagcaca gtggacccca ccctcgctag caggccacac cctcgctcgt cagccccatt
480
gtcatcccgc gg
492

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<210> 38
 <211> 127
 <212> PRT
 <213> Homo sapiens

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<400> 38
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
      1           5           10           15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
      20           25           30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
      35           40           45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val

```

```

      50              55              60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu
65              70              75              80
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met
      85              90              95
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser
      100             105             110
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala
      115             120             125

```

<210> 39
 <211> 412
 <212> DNA
 <213> Homo sapiens

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<400> 39
aacgaaggtn ccgtacgcgc tctgaaagcc ctgcgtaaaag agcggtccga tcgccgggaa
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gtgatngca ccgcaaaat gcaggtggtc gaagccgcga gttcaggcaa gattgtcttt
120
gaaatggaag acgtttatta cagcattgcc ggaaaacaac tggtagagcaa cttctctgcg
180
caagtcacgc gtggtgataa aattgcgctg attggcccga acggttggtg taaaacgacg
240
ttgctgaaac tgatgttaag taagattcag gcagacagcg gccgtgttca ctgcggtact
300
aaactggaag ttgcgtactt cgaccagcac cgtgctgagc tggatcctga gcgtacggtg
360
atggataacc tggccgaagg taagcaggaa gtgatggtaa atggccgtgt an
412

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<210> 40
 <211> 137
 <212> PRT
 <213> Homo sapiens

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<400> 40
Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
1              5              10              15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
      20              25              30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
      35              40              45
Ile Ala Gly Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
      50              55              60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65              70              75              80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
      85              90              95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
      100             105             110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
      115             120             125
Gln Glu Val Met Val Asn Gly Arg Val

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130

135

<210> 41
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<400> 41
 gaattcaagt ggacacaggc tccacgcccg cgtctcaccg ataagagcta caagcacaac
 60
 tactatgacg agcgggtttc gtcgaagag cgtcttgagc gcactgtggc taaggatttc
 120
 gtcacgacgg aggtcgagcc catgtgggat gcggtgatg tcatgcggat gggttaaggat
 180
 ctcttcatcc agcacggtct gacgacaaat cggaagtcaa tggagtgggt taagcgttac
 240
 taccgccgatt tccgcgttca cgcggtgaat ttccctgggg atccgtaccc gatccatata
 300
 gacgcgacct ttgtgccgct tcgtccgggg ctcatcatca acaacccgaa tcgtccactg
 360
 ccgcaggagc agaggaagat cttcgaggcc aatgactggc agatcggtga tgctgctcag
 420
 ccggcgcacg acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc
 480
 ttggtacttg atccgaagac ggtcatctgc gaggcttcgg aagttcatca gatggagcag
 540
 atggacaagc tgggtatgaa cgtcatcccg gtcgccttcc gtgacgcgta cccattcggg
 600
 ggaggtctcc actgcgccac agctgatgta tatcgccaag gtacctgtga ggactacttc
 660
 ccgaatcagg tcgacgaccc gaccttggtg tgagaaaacc ccgtgggtcat gtcatgactg
 720
 acggatctcg gtggctcggg acggaactta cgttgctcgt taccgggccg ccgggtctga
 780
 tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc
 840
 aacgtcaaac aggaagtcc aggcgtcggg acgatgaacc agaaagtggg attcgtgtcc
 900
 atgcttcttt ctgcaacggg tatggggttg gtgggtactt tcgggcgtct cagcactcct
 960
 gtggatccca cgacgggcag taagtacatc atcgggtgatt ttttggccac tggtaggatg
 1020
 atagtcgggg tcctgggatt tctgcttatt atcgtcatatc ttggaaaatg gtctgagctc
 1080

<210> 42
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 42
 Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser
 1 5 10 15
 Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu


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<210> 43
<211> 358
<212> DNA
<213> Homo sapiens
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<210> 44
<211> 105
<212> PRT
<213> Homo sapiens
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441

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      1             5             10             15
Leu Gly His Arg Gly Cys Leu Pro Ala Ala Pro Gly Arg Ala Val Asp
      20             25             30
Thr Thr Ala Trp Ser Ala Val Pro Gly His Cys His Ala His Arg Cys
      35             40             45
Pro Leu Arg Met Asp Leu Gly Phe Arg Ile Arg Val Ala Tyr Gln Arg
      50             55             60
Glu Ser Gln Ile Leu Lys Glu Val Gln Ser Pro Glu Gly Met Ile Ser
      65             70             75             80
Leu Arg Asp Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln
      85             90             95
Leu Pro Leu Leu Thr Ser Ala Leu His
      100             105

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<210> 45

<211> 905

<212> DNA

<213> Homo sapiens

<400> 45

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gtcgacgata aaggagtatt tgcgcagcag cagtatgatg ctctcggtga ggccgggtttc
60
gcggctcctg gaatcccaga gcagtatggt ggccgacggtg cggatgcatg tgcgtccgca
120
ataatcatgg aagaggtcgc tcgagtcctgt gcgtcgctcgt ccaccgtcat atcgccaat
180
gagcttggtgta ccgtccctct cctcaaatac ggtagcgagg agcagaggaa acgttatctt
240
tctgaagttg cttcgggttaa ggcacttttc ggatatgcgc tctccgaggc tgatgctgga
300
tcagatccag ctgcacttaa gtgtcgagcc gacgaagatg gggacagttt cgtcctgaat
360
ggcgtaagg cttgggtcac ggaggctggc gaggccaagt acctggtgat atttgcggtt
420
actgaccag acgatccgcg ccacagaatc agcgcgttga tggccatgc agatgaccg
480
ggcattagct acggggctcc ggagcacaaa atggggatac gcgggtcagt taccaggga
540
gtggttttca agaatacgcg tatccccaag gaacgagtaa ttggccgtcg agggcacggt
600
ctgagtgttg ctctaggtac gcttgataac tctcgtgtct cgattgctgc tcaagcagt
660
ggaattgccc aaggagcttt agacattgcc acggattacg tccagaagcg caagcagttt
720
ggccagccac tgtccaattt tgagggaatc cagttcatgc tcgcagacat ggcaatgcgt
780
ttggaggcgg cgcgagcgct gacatactct gcagctgacg gtagtgggcg ccagactgac
840
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900
tgcac
905

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<210> 46

<211> 301
 <212> PRT
 <213> Homo sapiens

<400> 46
 Val Asp Asp Lys Gly Val Phe Ala Gln Gln Gln Tyr Asp Ala Leu Val
 1 5 10 15
 Glu Ala Gly Phe Ala Ala Pro Gly Ile Pro Glu Gln Tyr Gly Gly Asp
 20 25 30
 Gly Ala Asp Ala Ile Ala Ser Ala Ile Ile Met Glu Glu Val Ala Arg
 35 40 45
 Val Cys Ala Ser Ser Ser Thr Val Ile Ser Ser Asn Glu Leu Gly Thr
 50 55 60
 Val Pro Leu Leu Lys Tyr Gly Ser Glu Glu Gln Arg Lys Arg Tyr Leu
 65 70 75 80
 Ser Glu Val Ala Ser Gly Lys Ala Leu Phe Gly Tyr Ala Leu Ser Glu
 85 90 95
 Ala Asp Ala Gly Ser Asp Pro Ala Ala Leu Lys Cys Arg Ala Asp Glu
 100 105 110
 Asp Gly Asp Ser Phe Val Leu Asn Gly Val Lys Ala Trp Val Thr Glu
 115 120 125
 Ala Gly Glu Ala Lys Tyr Leu Val Ile Phe Ala Val Thr Asp Pro Asp
 130 135 140
 Asp Pro Arg His Arg Ile Ser Ala Leu Met Val His Ala Asp Asp Pro
 145 150 155 160
 Gly Ile Ser Tyr Gly Ala Pro Glu His Lys Met Gly Ile Arg Gly Ser
 165 170 175
 Val Thr Arg Glu Val Val Phe Lys Asn Thr Arg Ile Pro Lys Glu Arg
 180 185 190
 Val Ile Gly Arg Arg Gly His Gly Leu Ser Val Ala Leu Gly Thr Leu
 195 200 205
 Asp Asn Ser Arg Val Ser Ile Ala Ala Gln Ala Val Gly Ile Ala Gln
 210 215 220
 Gly Ala Leu Asp Ile Ala Thr Asp Tyr Val Gln Lys Arg Lys Gln Phe
 225 230 235 240
 Gly Gln Pro Leu Ser Asn Phe Glu Gly Ile Gln Phe Met Leu Ala Asp
 245 250 255
 Met Ala Met Arg Leu Glu Ala Ala Arg Ala Leu Thr Tyr Ser Ala Ala
 260 265 270
 Asp Arg Ser Gly Arg Gln Thr Asp Asp Val Ser Tyr Phe Gly Ala Ala
 275 280 285
 Ala Lys Cys Phe Ala Ser Asp Thr Ala Met Ala Val Cys
 290 295 300

<210> 47
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 47
 aagctttag agctagtccg aagcggactg tcggtacgcc aagctgctaa aagatgtggg
 60
 atgcatttta ccgctgcgta tgccgtagct acggaagctg ggtgccatat ccggttaagt
 120

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg
 180
 gcgagcctgc ctggtggtga tgctggcgcg gcagtaggaa ttgatcgctg actgcgttta
 240
 gatttcgaaa aaggactcac caaatcccag ggctgcagcag aagagttcat acccgctcggc
 300
 gaagacgcca gcacgtataa cagacttatg aaagcgctgc gccaacgcca tgatgtcatc
 360
 aaatccggaa agcttgccc
 379

<210> 48
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met His Leu Thr Ala Ala Tyr Ala Val Ala Thr Glu Ala Gly Cys His
 1 5 10 15
 Ile Arg Leu Ser Gln Tyr Ala Arg Lys Val Arg Gln Thr Gln Leu Arg
 20 25 30
 Val Glu Tyr Leu Arg Leu Arg Leu Ala Ser Leu Pro Gly Gly Asp Ala
 35 40 45
 Gly Ala Ala Val Gly Ile Asp Arg Arg Leu Arg Leu Asp Phe Glu Lys
 50 55 60
 Gly Leu Thr Lys Ser Gln Gly Arg Arg Glu Glu Phe Ile Pro Val Gly
 65 70 75 80
 Glu Asp Ala Ser Thr Tyr Asn Arg Leu Met Lys Ala Leu Arg Gln Arg
 85 90 95
 His Asp Val Ile Lys Ser Gly Lys Leu Ala
 100 105

<210> 49
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 49
 tgatcatgat gctggcatgg actattctgg tccctgttcc tctctcacct gctgaaggac
 60
 atccctctaa tttttgtgtc tccttctgta tcatcaaatt ttcctctctc actgagtctc
 120
 ttgcatctcc ttggaagcat gctgtactat gtcccatcct taaagaactc cccttgtctg
 180
 cacattaccc tctgccagct ggctcatttt tctgctcccc tttacagggg aactcttcaa
 240
 aaagttatct ccacctcctt ccattctcatg ttctcttgaa cctgcagtac tgggtgctcc
 300
 ctctcttttg
 309

<210> 50
 <211> 101
 <212> PRT

<213> Homo sapiens

<400> 50

```

Met Met Leu Ala Trp Thr Ile Leu Val Pro Val Pro Leu Ser Pro Ala
 1           5           10           15
Glu Gly His Pro Ser Asn Phe Cys Val Ser Phe Cys Ile Ile Lys Phe
      20           25           30
Ser Leu Ser Thr Glu Ser Leu Ala Ser Pro Trp Lys His Ala Val Leu
      35           40           45
Cys Pro Ile Leu Lys Glu Leu Pro Leu Ser Ala His Tyr Pro Leu Pro
      50           55           60
Ala Gly Ser Phe Phe Cys Ser Pro Leu Gln Gly Asn Ser Ser Lys Ser
65           70           75           80
Tyr Leu His Leu Leu Pro Ser His Val Leu Leu Asn Leu Gln Tyr Trp
      85           90           95
Val Leu Pro Pro Phe
      100

```

<210> 51

<211> 512

<212> DNA

<213> Homo sapiens

<400> 51

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agatctttga agaattgcc cactgtcttc ctccctgctt ataatttcct tattccctag
60
gatgtgatcc ttgttcttgg ggcctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgcgtggc attcccactt gcatctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagtctgt cttgtacttc atgtgcccct
300
caaaatcttc tgttgctgag ggagaagagg ccagccggta ttgaggaaca actagcactt
360
tctgcttccg cgteccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgaggacct
420
ctgaggctgg gctggatggg acatcaggtg ggcctctgt ttcatttatg tgacctccca
480
tcagggtcttc tggttggatc ctgctttcta ga
512

```

<210> 52

<211> 125

<212> PRT

<213> Homo sapiens

<400> 52

```

Met Glu Lys Lys Arg Arg Arg Gly Lys Arg Asn Pro Gln Met Leu Leu
 1           5           10           15
Lys Ser Tyr Cys Val Ala Phe Pro Leu Ala Ser His Leu Leu Asp Arg
      20           25           30
Cys His Cys Ala Leu Thr Ser Cys Lys Asp Thr Gly Glu Met Ser Leu

```

```

          35          40          45
Ser Cys Thr Ser Cys Ala Pro Gln Asn Leu Leu Leu Arg Glu Lys
          50          55          60
Arg Pro Ala Gly Ile Glu Gln Leu Ala Leu Ser Ala Ser Ala Ser
65          70          75          80
Gln Gly Asp Val Gly Val Leu Asn Pro His Arg Gly Cys Gly Pro Leu
          85          90          95
Arg Leu Gly Trp Met Gly His Gln Val Gly Pro Leu Phe His Leu Cys
          100          105          110
Asp Leu Pro Ser Gly Leu Leu Val Gly Ser Cys Phe Leu
          115          120          125

```

<210> 53
 <211> 474
 <212> DNA
 <213> Homo sapiens

```

<400> 53
accggtacac ctacgtcacc cgtaaaaacc gacgcaatac ccggatcgcc tcgtcctcaa
60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gaggcccgct aatggccaaa
120
aagtccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
180
cgcgccgaac tcaaggccat catgaagtgc ccaactgcct cattggacga acgcatggag
240
gcacgcgta agctgtctcg cctgccgcgc gattcatccc ccgtgcggtt acgtaaccgt
300
gaccaagtcg acgggcgctcc ccgcggctac gttggcaagg ccggtgtgtc ccgtatccgt
360
ttccgtgaga tggcccaccg cggcgaactc cccggaatcg cgaagtcaag ctggtgaagc
420
catggcagta ccgaagcgaa agaagtcccg ttcgaccacg cgatcataggc gggc
474

```

<210> 54
 <211> 101
 <212> PRT
 <213> Homo sapiens

```

<400> 54
Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
1          5          10          15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
          20          25          30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
          35          40          45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
          50          55          60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
65          70          75          80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
          85          90          95
Ala Lys Ser Ser Trp

```

100

<210> 55
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 55
 ccatggccca ggacagccgg catatcggct acgactacgg tacaccggtg gcgccacagt
 60
 tcggcgcgagc caagcccgca gcgtgctgcc aggcgcaagc gacaaacacc ggcccgtggg
 120
 tgggtgttcga ccatgtgctg tgcacccacg acacctttct gatcgacgtc tttctcaacc
 180
 agcccgatgc caccgcgag caggtcaatg ccgacaaccc gcactacgtc gggcgtttca
 240
 gccgcacgg catggggctg gtggatgaca agggccggtg cattaccag ggcgtatcgc
 300
 gcgcgttgaa tgcggcgcg agcaccaagg cgctgaacct gggaccgagt gacgcggcgc
 360
 agttatcggg gaggcgta
 378

<210> 56
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val
 1 5 10 15
 Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln
 20 25 30
 Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr
 35 40 45
 His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr
 50 55 60
 Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser
 65 70 75 80
 Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln
 85 90 95
 Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn
 100 105 110
 Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg
 115 120 125

<210> 57
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 57
 agaccacccc gacacagatc aggagtcgtc atgtccagaa agaagaaggt cggcatcctc
 60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc gcggatttgg caaggctgcc
 120
 atccgccagc acgacatgga gctcatcggt attcaggacg gctttcttgg attggcgga
 180
 aaccgcacca tctcccttgg cccgcgtgcc ctctcaggca tcttgacggt cggcgggacc
 240
 atcctgggaa ctagccgtga caaggtaaat cacatgatta tcgacggcga ggaacgggat
 300
 atggtcccca ccacgctga gaattacgag aagctggggc ttgacgcttt ggtgactttg
 360
 ggtggcggtg gcaccgcaa gaacgcgt
 388

<210> 58
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 58
 Arg Pro Thr Arg His Arg Ser Gly Val Val Met Ser Arg Lys Lys Lys
 1 5 10 15
 Val Gly Ile Leu Thr Ala Gly Gly Asp Cys Pro Gly Leu Asn Ala Ala
 20 25 30
 Ile Arg Gly Phe Gly Lys Ala Ala Ile Arg Gln His Asp Met Glu Leu
 35 40 45
 Ile Gly Ile Gln Asp Gly Phe Leu Gly Leu Ala Gly Asn Arg Thr Ile
 50 55 60
 Ser Leu Gly Pro Arg Ala Leu Ser Gly Ile Leu Thr Val Gly Gly Thr
 65 70 75 80
 Ile Leu Gly Thr Ser Arg Asp Lys Val Asn His Met Ile Ile Asp Gly
 85 90 95
 Glu Glu Arg Asp Met Val Pro Thr Thr Val Glu Asn Tyr Glu Lys Leu
 100 105 110
 Gly Leu Asp Ala Leu Val Thr Leu Gly Gly Gly Thr Ala Lys Asn
 115 120 125
 Ala

<210> 59
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 59
 ggtaccatcg gagctcgaca agaaatgggtt ggggtgaagtc gtggcttctg ctccaccag
 60
 tgccctcatg ggtcagccca cctgaatatc ttcatgcctg tgcatttctc ctgatgttca
 120
 cgtgtgccct gtgtttttac gcatctgtga tcgtgcaccc acgcgtctca gagaggagcc
 180
 cgtttgggaa tccggagaat gtgcgtggc ggaagagcgt cacacactgg aagcaaacct
 240
 cagaccgcgt ggacaagacc aaggatgaaa tggaacacga ggccttggtg gaaggggaacc
 300

tggcaaccga ggcaagccta gtggttctgg acacactgga gatcatcgtg cagacgggtga
 360
 tgctttcaga agccccgggag agcgtcttgg gggcagtgcct gaaggttctg ctgtaca
 417

<210> 60
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 60
 Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro
 1 5 10 15
 Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp
 20 25 30
 Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys
 35 40 45
 Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala
 50 55 60
 Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln
 65 70 75 80
 Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu
 85 90 95
 Lys Val Val Leu Tyr
 100

<210> 61
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 61
 agatcttcac agccttagac ttttttcatg ggtgccttac agttttggag gtccttatcc
 60
 gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag
 120
 tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga
 180
 ccgctgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagtcc
 240
 tcccctagac cgggccccatg gccaggcctg accacagagc tcccattgcc tttcctgcac
 300
 gcgt
 304

<210> 62
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 62
 Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala
 1 5 10 15

Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr
 20 25 30
 Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe
 35 40 45
 Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala
 50 55 60
 Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly
 65 70 75 80
 Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala
 85 90

<210> 63
 <211> 577
 <212> DNA
 <213> Homo sapiens

<400> 63
 cgcgtcaagg ggggtctacac cgggacgatt aacgcctcgg tgggagtatt catcaccgcg
 60
 ctgacgggtgc tagctgggtg gctcacccta gccgggcgta tcagtgtcgg ggaactcgtc
 120
 accgtgggtcg ggctggccca aaccctcggc cctccgctgc gagcactggg cgtcgacacc
 180
 gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc
 240
 ccggcagcct ggcagatcca ccccgacgac ggtgcccgca ccacaccggg tgatggcccg
 300
 gtggagttgc acatcccggg cagggatttc cagcttgacg tcgccggcgg caccatgtg
 360
 ggtatcatgg cgctcaatc ggtctgtgac gccttgggcg aggcgataga ccacggctcc
 420
 gagaccgtct tgaatggggg tcccgcagc cgctcaacc ctgcccacg gcgtcgtctg
 480
 gtgctgggtg cccccgctc cccggaactg ttcgacgata ctgcccgctg gaacatcgtg
 540
 cttgacagcc agacgactgt cgccaggctg aatgcat
 577

<210> 64
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 64
 Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val
 1 5 10 15
 Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly
 20 25 30
 Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr
 35 40 45
 Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu
 50 55 60
 Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser
 65 70 75 80

```

Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
      85                      90                      95
Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
      100                    105                    110
Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
      115                    120                    125
Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
      130                    135                    140
Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
      145                    150                    155                    160
Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
      165                    170                    175
Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
      180                    185                    190

```

<210> 65

<211> 339

<212> DNA

<213> Homo sapiens

<400> 65

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gtcgaccgcg ccttgggata gctcgaagg ggcagcctgg accaggtagc ggaagaagtc
60
aagaaggccg ctttcaagat caccgcgccc gggcaactag tgggcacccat ggcctccgag
120
cgccctggcg tacccttcgg catcatcgac ctttcgcttg cccctactgc cgaattggga
180
gattcggggg cccacatcct tgagcatatg ggattggacc aagtaggcac gcacggcaca
240
actgctgctt tggctctgct taacgacgcc gtaaagaaag gcggcatgat ggctgcccc
300
cgcgtcgccg gtttgtctgg ctccctcatc ccgggctcc
339

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<210> 66

<211> 113

<212> PRT

<213> Homo sapiens

<400> 66

```

Val Asp Arg Ala Leu Gly Ser Leu Glu Gly Ala Ser Leu Asp Gln Val
1      5      10      15
Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
20     25     30
Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
35     40     45
Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
50     55     60
His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
65     70     75     80
Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys Lys Gly Gly Met
85     90     95
Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
100    105    110

```

```
<210> 67
<211> 446
<212> DNA
<213> Homo sapiens
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```
<210> 68
<211> 133
<212> PRT
<213> Homo sapiens
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<210> 69
<211> 552
<212> DNA

<213> Homo sapiens

<400> 69

nnaagggttaa ggagaaaagc aaggaccttg caaagagagc ctctgtgccg gagaggctgg
 60
 ccctcaagga ggagccaaaa gaagacccca gtggagcagc tgtgcccag atgccaaaaa
 120
 agtccctcaa gattgccagc ttcattccca aaggggggaa gctcaacagt gccagaagg
 180
 agcnccatgg ccccttcctt cagtgggaata ccaaaaccag gaatgaaaag catgcccggg
 240
 aaatccccaa gtgccccagc gccttccaag gaagggggagc ggagccggag tgggaagctg
 300
 agctcaggac tccccagca gaagccccag ctggacggca gacactccag ttcctcttcc
 360
 agcctggcgt cctcagaagg aaaaggccca ggagggacca ccctgaacca cagcatcagc
 420
 agccagactg tcagtgggtc tgtcgggacc acccagacca caggaagcaa tnnaccgtca
 480
 gtgttcagct acctcagccc cagcagcaat acaaccatcc caacactgcc acggttgac
 540
 ctttcctgta ca
 552

<210> 70

<211> 184

<212> PRT

<213> Homo sapiens

<400> 70

Xaa	Arg	Val	Arg	Arg	Lys	Ala	Arg	Thr	Leu	Gln	Arg	Glu	Pro	Leu	Cys
1				5					10					15	
Arg	Arg	Gly	Trp	Pro	Ser	Arg	Arg	Ser	Gln	Lys	Lys	Thr	Pro	Val	Glu
		20						25					30		
Gln	Leu	Cys	Pro	Arg	Cys	Gln	Lys	Ser	Pro	Pro	Arg	Leu	Pro	Ala	Ser
	35					40					45				
Ser	Pro	Lys	Gly	Gly	Ser	Ser	Thr	Val	Pro	Arg	Arg	Ser	Xaa	Met	Ala
	50				55					60					
Pro	Ser	Leu	Ser	Gly	Ile	Pro	Lys	Pro	Gly	Met	Lys	Ser	Met	Pro	Gly
65				70					75				80		
Lys	Ser	Pro	Ser	Ala	Pro	Ala	Pro	Ser	Lys	Glu	Gly	Glu	Arg	Ser	Arg
		85						90					95		
Ser	Gly	Lys	Leu	Ser	Ser	Gly	Leu	Pro	Gln	Gln	Lys	Pro	Gln	Leu	Asp
	100						105					110			
Gly	Arg	His	Ser	Ser	Ser	Ser	Ser	Leu	Ala	Ser	Ser	Glu	Gly	Lys	
	115					120					125				
Gly	Pro	Gly	Gly	Thr	Thr	Leu	Asn	His	Ser	Ile	Ser	Ser	Gln	Thr	Val
	130					135					140				
Ser	Gly	Ser	Val	Gly	Thr	Thr	Gln	Thr	Thr	Gly	Ser	Asn	Xaa	Pro	Ser
145				150					155					160	
Val	Phe	Ser	Tyr	Leu	Ser	Pro	Ser	Ser	Asn	Thr	Thr	Ile	Pro	Thr	Leu
		165						170					175		
Pro	Arg	Leu	His	Leu	Ser	Cys	Thr								
		180													

<210> 71
 <211> 316
 <212> DNA
 <213> Homo sapiens

<400> 71
 cgcgttgaaa tggcgttcga acttaaacgt ttacatattg actccgtgcc attaaacatt
 60
 ttgaatcctg ttaaaggagc tccatttgaa agcaacgaag ctttacgtcc tttaaataac
 120
 ttacgtacct tcgccgtatt ccgtttcatc ttgccaaacg cattgatacg aactgcaggt
 180
 ggccgcgaag taaatctacg agacttacaa gcttatgctc taaaagggtg cctaaacggt
 240
 atcatggttg gtggctactt aactactggc ggtcgttcac ctcaagacga tctccaaatg
 300
 attcaagact tggagt
 316

<210> 72
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 72
 Arg Val Glu Met Ala Phe Glu Leu Lys Arg Leu His Ile Asp Ser Val
 1 5 10 15
 Pro Leu Asn Ile Leu Asn Pro Val Lys Gly Thr Pro Phe Glu Ser Asn
 20 25 30
 Glu Ala Leu Arg Pro Leu Asn Ile Leu Arg Thr Phe Ala Val Phe Arg
 35 40 45
 Phe Ile Leu Pro Asn Ala Leu Ile Arg Thr Ala Gly Gly Arg Glu Val
 50 55 60
 Asn Leu Arg Asp Leu Gln Ala Tyr Ala Leu Lys Gly Gly Leu Asn Gly
 65 70 75 80
 Ile Met Val Gly Gly Tyr Leu Thr Thr Gly Gly Arg Ser Pro Gln Asp
 85 90 95
 Asp Leu Gln Met Ile Gln Asp Leu Glu
 100 105

<210> 73
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 73
 nntaccggca agatcctggc cgaagggtgac gtcgaggttt ctgaggctat cgactttgct
 60
 gcttggtatg tcgaccgagc cgaggagctc gagggcgctc acggtgcccc gtttgtgccg
 120
 ccacgagtga ccgtcgtcac cccgccgtgg aacttcgccc tgtctattac cgccggatcc
 180

acccttgccg ctctggccgc cggatcgta gtactactca agcccgtcc acaggcccg
 240
 cactgtgctg ccgtcatctc tgaatgcctg tgggaggctg ggatcccgcg ggacgttctg
 300
 cagctcgtcg atgttgagga aaatgaggct ggtaaaccac tggtagacca ccccgaggtc
 360
 gatcgggtca tcctcacggg aggt
 384

<210> 74.

<211> 128

<212> PRT

<213> Homo sapiens

<400> 74

Xaa	Thr	Gly	Lys	Ile	Leu	Ala	Glu	Gly	Asp	Val	Glu	Val	Ser	Glu	Ala
1			5					10					15		
Ile	Asp	Phe	Ala	Ala	Trp	Tyr	Val	Asp	Arg	Ala	Glu	Glu	Leu	Glu	Gly
		20					25					30			
Val	Asp	Gly	Ala	Gln	Phe	Val	Pro	Pro	Arg	Val	Thr	Val	Val	Thr	Pro
		35				40					45				
Pro	Trp	Asn	Phe	Ala	Leu	Ser	Ile	Thr	Ala	Gly	Ser	Thr	Leu	Ala	Ala
	50				55					60					
Leu	Ala	Ala	Gly	Ser	Ser	Val	Leu	Leu	Lys	Pro	Ala	Pro	Gln	Ala	Arg
65				70					75					80	
His	Cys	Ala	Ala	Val	Ile	Ser	Glu	Cys	Leu	Trp	Glu	Ala	Gly	Ile	Pro
			85					90					95		
Arg	Asp	Val	Leu	Gln	Leu	Val	Asp	Val	Glu	Glu	Asn	Glu	Ala	Gly	Lys
		100					105					110			
His	Leu	Val	Ser	His	Pro	Glu	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Gly
		115				120						125			

<210> 75

<211> 405

<212> DNA

<213> Homo sapiens

<400> 75

gaattcgtct cggaatacac gctggaaaat tcggccgaga tgtccggggt gcgctcanac
 60
 cgcattgagg cgctggccga gctctatgcc gatcccaaga ccagggtggt gagcttctgg
 120
 accatgggct tcaaccagca caccgcggc gtctggtgca acaatctcgt ctacaacatc
 180
 cacctgctga ccggaataat ctgcagccc ggcaacagcc cggttctcgt gaccgggcag
 240
 ccacggcct gggcacggc gcgcgaggtc ggtaccttct cgcacgcct gccgcggac
 300
 atggtggtca ccagcaaggc gcaccgcgac atcgccgaga agatctggca gctgccggaa
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<210> 76

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 76
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 35 40 45
 Arg Gly Val Trp Cys Asn Asn Leu Val Tyr Asn Ile His Leu Leu Thr
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 Gly Lys Ile Ser Thr Pro Gly Asn Ser Pro Phe Ser Leu Thr Gly Gln
 65 70 75 80
 Pro Ser Ala Cys Gly Thr Ala Arg Glu Val Gly Thr Phe Ser His Arg
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<210> 77
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 <213> Homo sapiens

<400> 77
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<210> 78
 <211> 799
 <212> PRT
 <213> Homo sapiens

<400> 78
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 35 40 45
 Asn Asn Leu Leu Arg Leu Pro Phe Gly Cys Gly Glu Gln Asn Met Ile
 50 55 60
 His Phe Ala Pro Asn Val Phe Val Leu Lys Tyr Leu Gln Lys Thr Gln
 65 70 75 80
 Gln Leu Ser Pro Glu Val Glu Arg Glu Thr Thr Asp Tyr Leu Val Gln
 85 90 95
 Gly Tyr Gln Arg Gln Leu Thr Tyr Lys Arg Gln Asp Gly Ser Tyr Ser
 100 105 110
 Ala Phe Gly Glu Arg Asp Ala Ser Gly Ser Met Trp Leu Thr Ala Phe
 115 120 125
 Val Leu Lys Ser Phe Ala Gln Ala Arg Ser Phe Ile Phe Val Asp Pro
 130 135 140
 Arg Glu Leu Ala Ala Ala Lys Ser Trp Ile Ile Gln Gln Gln Gln Ala
 145 150 155 160
 Asp Gly Ser Phe Leu Ala Val Gly Arg Val Leu Asn Lys Asp Ile Gln
 165 170 175
 Gly Gly Ile His Gly Ile Val Pro Leu Thr Ala Tyr Val Val Val Ala
 180 185 190
 Leu Leu Glu Thr Gly Thr Ala Ser Glu Glu Glu Arg Gly Ser Thr Asp
 195 200 205
 Lys Ala Arg His Phe Leu Glu Ser Ala Ala Pro Leu Ala Met Asp Pro
 210 215 220
 Tyr Ser Cys Ala Leu Thr Thr Tyr Ala Leu Thr Leu Leu Arg Ser Pro
 225 230 235 240
 Ala Ala Pro Glu Ala Leu Arg Lys Leu Arg Ser Leu Ala Ile Met Arg
 245 250 255
 Asp Gly Val Thr His Trp Ser Leu Ser Asn Ser Trp Asp Val Asp Lys
 260 265 270
 Gly Thr Phe Leu Ser Phe Ser Asp Arg Val Ser Gln Ser Val Val Ser
 275 280 285
 Ala Glu Val Glu Met Thr Ala Tyr Ala Leu Leu Thr Tyr Thr Leu Leu
 290 295 300
 Gly Asp Val Ala Ala Ala Leu Pro Val Val Lys Trp Leu Ser Gln Gln

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Arg Asn Ala Leu Gly Gly Phe Ser Ser Thr Gln Asp Thr Cys Val Ala
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Leu Gln Ala Leu Ala Glu Tyr Ala Ile Leu Ser Tyr Ala Gly Gly Ile
          340          345          350
Asn Leu Thr Val Ser Leu Ala Ser Thr Asn Leu Asp Tyr Gln Glu Thr
          355          360          365
Phe Glu Leu His Arg Thr Asn Gln Lys Val Leu Gln Thr Ala Ala Ile
          370          375          380
Pro Ser Leu Pro Thr Gly Leu Phe Val Ser Ala Lys Gly Asp Gly Cys
385          390          395          400
Cys Leu Met Gln Ile Asp Val Thr Tyr Asn Val Pro Asp Pro Val Ala
          405          410          415
Lys Pro Ala Phe Gln Leu Leu Val Ser Leu Gln Glu Pro Glu Ala Gln
          420          425          430
Gly Arg Pro Pro Pro Met Pro Ala Ser Ala Ala Glu Gly Ser Arg Gly
          435          440          445
Asp Trp Pro Pro Ala Asp Asp Asp Pro Ala Ala Asp Gln His His
          450          455          460
Gln Glu Tyr Lys Val Met Leu Glu Val Cys Thr Arg Trp Leu His Ala
465          470          475          480
Gly Ser Ser Asn Met Ala Val Leu Glu Val Pro Leu Leu Ser Gly Phe
          485          490          495
Arg Ala Asp Ile Glu Ser Leu Glu Gln Leu Leu Leu Asp Lys His Met
          500          505          510
Gly Met Lys Arg Tyr Glu Val Ala Gly Arg Arg Val Leu Phe Tyr Phe
          515          520          525
Asp Glu Ile Pro Ser Arg Cys Leu Thr Cys Val Arg Phe Arg Ala Leu
          530          535          540
Arg Glu Cys Val Val Gly Arg Thr Ser Ala Leu Pro Val Ser Val Tyr
545          550          555          560
Asp Tyr Tyr Glu Pro Ala Phe Glu Ala Thr Arg Phe Tyr Asn Val Ser
          565          570          575
Thr His Ser Pro Leu Ala Arg Glu Leu Cys Ala Gly Pro Ala Cys Asn
          580          585          590
Glu Val Glu Arg Ala Pro Ala Arg Gly Pro Gly Trp Phe Pro Gly Glu
          595          600          605
Ser Gly Pro Ala Val Ala Pro Glu Glu Gly Ala Ala Ile Ala Arg Cys
          610          615          620
Gly Cys Asp His Asp Cys Gly Ala Gln Gly Asn Pro Val Cys Gly Ser
625          630          635          640
Asp Gly Val Val Tyr Ala Ser Ala Cys Arg Leu Arg Glu Ala Ala Cys
          645          650          655
Arg Gln Ala Ala Pro Leu Glu Pro Ala Pro Pro Ser Cys Cys Ala Leu
          660          665          670
Glu Gln Arg Leu Pro Ala Ser Ser Ser Thr Tyr Gly Asp Asp Leu
          675          680          685
Ala Ser Val Ala Pro Gly Pro Leu Gln Gln Asp Val Lys Leu Asn Gly
          690          695          700
Ala Gly Leu Glu Val Glu Asp Ser Asp Pro Glu Pro Glu Gly Glu Ala
705          710          715          720
Glu Asp Arg Val Thr Ala Gly Pro Arg Pro Pro Val Ser Ser Gly Asn
          725          730          735
Leu Glu Ser Ser Thr Gln Ser Ala Ser Pro Phe His Arg Trp Gly Gln

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<400> 81

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<210> 82
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 82
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 Cys Leu Cys Val Xaa Val Cys Val Arg Ala Cys Val Cys Thr Cys Val
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 His Val His Val Cys Ala Pro Val Cys Met Ser Val Cys Thr Arg
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<210> 83
 <211> 411
 <212> DNA
 <213> Homo sapiens

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<210> 84
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 84
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 20 25 30
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 35 40 45
 His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp
 50 55 60
 Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe
 65 70 75 80
 Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu
 85 90 95
 Ile Lys Ala Phe Ala Leu Phe Lys Glu Arg Thr Lys Ser Pro His Pro
 100 105 110
 Leu Val Ile Ala Gly Ala Glu Gly Pro Ser Ser Glu Glu Val His
 115 120 125

<210> 85
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 85
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 240
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<210> 86
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 86
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 Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn

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Gly Val Pro Ala Glu Lys Ile Asn Lys Val Leu Glu Gly Arg Pro His
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Ile Val Asp Ala Ile Thr Asn Gly Glu Val Gln Leu Val Phe Asn Thr
65          70          75          80
Thr Glu Gly Pro Gln Ala Leu Ala Asp Ser Arg Ser Leu Arg Arg Ala
      85          90          95
Ala Leu Leu His Lys Val Pro Tyr Tyr Thr Thr Leu Ser Gly Ala
      100          105          110

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<210> 87
 <211> 355
 <212> DNA
 <213> Homo sapiens

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<400> 87
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240
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<210> 88
 <211> 96
 <212> PRT
 <213> Homo sapiens

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<400> 88
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Cys Pro Val Val Leu Leu Ser Asp Val His Ser Val Gly Val Gln Gly
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Asp Gly Arg Thr Tyr Gly Ser Pro Ile Val Leu Arg Pro Val Thr Ser
      35          40          45
Glu Asp Ala Met Thr Ala Asp Trp Ala Arg Ile Pro Tyr Asp Val Leu
      50          55          60
Glu Lys Ile Ser Thr Arg Ile Thr Asn Ala Cys Pro Gln Ile Asn Arg
65          70          75          80
Val Val Leu Asp Ile Thr Ser Lys Pro Pro Ala Thr Ile Glu Trp Glu
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<210> 89
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 89

ATTORNEY DOCKET NO.: 15966-543

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<210> 90

<211> 61

<212> PRT

<213> Homo sapiens

<400> 90

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Leu	Lys	Ser	Met	Pro	Leu	Pro	Leu	Asn	Asp	Val	Thr	Gln	Ala	His	Arg
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<210> 91

<211> 327

<212> DNA

<213> Homo sapiens

<400> 91

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<210> 92

<211> 107

<212> PRT

<213> Homo sapiens

<400> 92

Met	Gly	Lys	Gly	Lys	Val	Thr	Phe	Pro	Asn	Gly	Phe	Thr	Val	Glu	Gly
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1           5           10           15
Ser Phe Gly Ser Gly Ala Gly Arg Gly Leu His Thr Gln Gly Val Leu
                20           25           30
Asp Thr Ala Ala Leu Pro Pro Asp Pro Ser Ser Thr Cys Lys Arg Gln
                35           40           45
Leu Gly Val Gly Ala Phe Pro Gly Lys Ala Ala Gly Arg Glu Ser Thr
                50           55           60
Ala Pro Ser Gly Thr Leu Cys Val Leu Ala Ala Pro Gly Thr Cys Arg
65           70           75           80
Arg Pro Cys Trp Ala Ser Thr Cys Arg Ala Pro Gly Ser Cys Val Gly
                85           90           95
Leu Arg Ile Thr Cys Pro Ala Arg Gly Pro Thr
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<210> 93

<211> 394

<212> DNA

<213> Homo sapiens

<400> 93

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120
ggcgcgctct ggggcctcgc ggatgaagga ggggtggtcg cgcaagagac gccccgcgcc
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240
gctctatttc gaggtatca ggttcggtgt caacaaccgt tatcacggcc agtgggtgac
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aatggaagtt gtcgttaccg gcaagcatac caggggaactt ctgatcgtg cagtcactct
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394

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<210> 94

<211> 109

<212> PRT

<213> Homo sapiens

<400> 94

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Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile
1           5           10           15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg
                20           25           30
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr
                35           40           45
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg
50           55           60
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile
65           70           75           80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro
85           90           95
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg

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100

105

<210> 95
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 95.
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 ccaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa gggaagaaat
 180
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 360
 gctgagcatg gagctcacc ccatgccatag ggtgtgggaa gagggcacag gaggcctcat
 420
 ccattggggga aagggttgag gatggacatg ggtggggaga gggcatagac atcccttctc
 480
 aatctctgtt cccaccacat ttcattaggag atgagttagg agatgacagc t
 531

<210> 96
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Arg Pro Pro Val Pro Ser Ser His Thr Leu Trp His Gly Val Ser
 1 5 10 15
 Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr
 20 25 30
 Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp
 35 40 45
 His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe
 50 55 60
 Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu
 65 70 75 80
 Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val
 85 90 95
 Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg
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 Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu
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<210> 97
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 97

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 cgacatcgtg tctgagacgt cgaagctcag gccagcttt ggctccagg cgcgctcgg
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 cggtcggccc tcttcgggca attgattcag cgcaatcccg gccatcacat gccagcgctt
 240
 gtccagggtc atgaaatcct gggcataggg gcgcgaggag cgcagcggcg aattggacag
 300
 gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt
 360
 gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat
 405

<210> 98

<211> 122

<212> PRT

<213> Homo sapiens

<400> 98

Met	Ala	Ser	Gly	Asp	Leu	Phe	Pro	Gly	Asn	Val	Phe	Ser	Pro	Arg	Val
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Pro	Phe	Pro	Ser	Ser	Asp	Ile	Thr	Pro	Asn	Ile	Glu	Arg	Leu	Ser	Asn
			20					25					30		
Ser	Pro	Leu	Arg	Ser	Ser	Arg	Ala	Tyr	Ala	Gln	Asp	Phe	Met	Thr	Leu
		35				40					45				
Asp	Lys	Arg	Trp	His	Val	Met	Ala	Gly	Ile	Ala	Leu	Asn	Gln	Leu	Pro
	50			55						60					
Gln	Glu	Gly	Gly	Pro	Thr	Glu	Arg	Ala	Trp	Thr	Pro	Lys	Leu	Gly	Leu
65				70				75						80	
Ser	Phe	Asp	Val	Ser	Asp	Thr	Met	Ser	Leu	Tyr	Gly	Ala	Tyr	Ser	Arg
			85					90					95		
Gly	Phe	Ser	Thr	Tyr	Gln	Pro	Ala	Arg	Lys	Ala	Pro	Arg	Ala	Tyr	Gly
			100					105					110		
Pro	Ser	Ala	Ala	Arg	Pro	Ser	Lys	Arg	Glu						
		115					120								

<210> 99

<211> 545

<212> DNA

<213> Homo sapiens

<400> 99

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 120
 tcgatcccat cactcgggat ttgctggaat ccctgggttcg cgaagccggc gaggctgcgg
 180
 tgatcttggg tgcccagcgt cgcggctcga tcgattggct cteccacag atcatccaca
 240

acctggccga acaccatttt gagtcgtcct ctggaggtag tcgatgatga ctgaacgttc
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 ccattccacg atcagggttaa ggtggccggc ggtgggtggt ctcgtcctcg ttccgctgct
 360
 ggtgggtcgcc ggattgggtcc gggacgacct ggcataccac cgaccgggtg ggccgggtga
 420
 aagcggccgt cgtcaacgag gacaaggccg tcaagggtgcg tggacaactg gttccgatgg
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 545

<210> 100
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 100
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 1 5 10 15
 Trp Cys Ser Ala Arg Leu Trp Met Ile Cys Gly Glu Ser Gln Ser Met
 20 25 30
 Arg Pro Arg Arg Trp Ala Pro Lys Ile Thr Ala Ala Ser Pro Ala Ser
 35 40 45
 Arg Thr Arg Asp Ser Ser Lys Ser Arg Val Met Gly Ser Thr Ile Arg
 50 55 60
 Ser Ala Trp Ser Met Arg Asn Ser Arg Gly Arg Leu Leu Gly Arg Arg
 65 70 75 80
 Gly Arg Trp Val Ser Thr Val Ile Ala Glu Arg Ser Ser Ser Thr Thr
 85 90 95
 Ser Gly Ala Asp Ala
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<210> 101
 <211> 619
 <212> DNA
 <213> Homo sapiens

<400> 101
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 120
 aagctgccgg ggggtgactat ctcacccctcg ccacggattc cggacgcaag ggatacacga
 180
 ccgcccgtcc tcacgaggcc ggcggaaaac gctattacca acctggacca gatccgcgaa
 240
 gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatgggtccag
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 aaccgtgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact
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 ggtcatctgg cctgtgggtg taccgatgtc gttgagctgg tgcgtaagta cgccaaccgc
 420

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 619

<210> 102
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 102
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 20 25 30
 Arg Pro Ala Glu Asn Ala Ile Thr Asn Leu Asp Gln Ile Arg Glu Val
 35 40 45
 Cys Ala Ser Arg Asn Val Thr Ala Cys Leu His Pro His Trp Gly Thr
 50 55 60
 Met Val Gln Asn Arg Asp Glu Val Ile Arg Val Leu Glu Asn Ser Ser
 65 70 75 80
 Ile Gly Leu Cys Leu Asp Thr Gly His Leu Ala Cys Gly Gly Thr Asp
 85 90 95
 Val Val Glu Leu Val Arg Lys Tyr Ala Asn Arg Val Asp Ile Val His
 100 105 110
 Ala Lys Asp Val His Lys Glu Met Ala Asp Lys Leu Leu Pro Gly Glu
 115 120 125
 Ile Thr Trp Ser Glu Gly Ile Arg Ala Gly Met Phe Ala Pro Ile Gly
 130 135 140
 Asp Gly Asp Ile Asp Phe Ala Ala Ile Val Arg Leu Leu Asp Glu Ala
 145 150 155 160
 Gly Phe Asp Gly Tyr Tyr Val Leu Glu Gln Asp Ile Met
 165 170

<210> 103
 <211> 321
 <212> DNA
 <213> Homo sapiens

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 actgggggga gaccctgcc gctgggggga gaccgagcc attgggggga gaccctgcc
 180
 atggggaaag acccctgcca ttgggggaga ntacctgcca ttgggggaga tccctgccg
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agtgggttggg gcgaagaccc c
321

<210> 104
<211> 107
<212> PRT
<213> Homo sapiens

<400> 104
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Gly Glu Thr Pro Ala Ile Gly Gly Arg Pro Leu Pro Trp Gly Lys Thr
20 25 30
Pro Ala Met Gly Gln Thr Pro Ala Thr Gly Gly Arg Pro Leu Pro Leu
35 40 45
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp
50 55 60
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg
65 70 75 80
Trp Gly Glu Ile Pro Ala Val Gly Gly Arg Xaa Pro Pro Val Gly Glu
85 90 95
Asp Pro Cys Arg Ser Gly Trp Gly Glu Asp Pro
100 105

<210> 105
<211> 344
<212> DNA
<213> Homo sapiens

<400> 105
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ccgggtcaac gagggtttgg cgcacgggcc actccgtggc gcccgggggtg atgtgcaaca
120
gggcggggccc gcgcgcggcc gggcctgatt ccagcctctc gtgctcgtcc cagtacccat
180
ccagcgcacg gcccagcgg tcggcatccc agccgtgggc gccgtcgcgc gcccagggg
240
cctcaatgtc gtcacggcg gccagttcca cccggcggaa catctcgttg cggaccatga
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cccgaaggc gcgggaattc tcggtcagtt tcggcgggtgc cggc
344

<210> 106
<211> 62
<212> PRT
<213> Homo sapiens

<400> 106
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Arg Ala Arg Pro Ser Thr His Pro Ala His Arg Pro Ser Gly Arg His
20 25 30
Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His

35 40 45
 Arg Arg Pro Val Pro Pro Gly Gly Thr Ser Arg Cys Gly Pro
 50 55 60

<210> 107
 <211> 549
 <212> DNA
 <213> Homo sapiens

<400> 107
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 120
 cacagaccgc aaaataagggtgttttgcctc gccctcctca gttcacgtgg gcaccttgga
 180
 acactgaaga aggcattttc cgaactcact gtcctacgga cttattctcc gcaactgtttt
 240
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 540
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 549

<210> 108
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 108
 Met Lys Leu Lys Gly Cys Pro Phe Leu Ala Gly Thr Leu His Arg Pro
 1 5 10 15
 Glu Asn Lys Gly Phe Cys Ser Ala Leu Leu Ser Ser Arg Gly His Leu
 20 25 30
 Gly Thr Leu Lys Lys Ala Phe Ser Glu Leu Thr Val Leu Arg Thr Tyr
 35 40 45
 Ser Pro His Cys Phe Arg Leu Leu Arg Pro Val Leu Val Thr Asp Arg
 50 55 60
 Ser Arg Gly His Lys Gln Ala Ala Arg Glu Leu Cys Ser Pro Gly Lys
 65 70 75 80
 Ala Phe Leu Cys Ser Leu Asn Val Lys Ala Ser Gly Ser Gly Leu Leu
 85 90 95
 Ser Ser Ser Thr Cys Ala His Leu His Ser Phe Met
 100 105

<210> 109
 <211> 748

<212> DNA

<213> Homo sapiens

<400> 109

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 120
 gatattgggg taagttacca atttacttta cagcccttaa gtaaataatc tgctttcctc
 180
 agcatcatag acttttgaag aggattaatt aagcgcttaa aaaacctgta gactctatta
 240
 cagtcagtga aaggaataat tctctttaca aagtaaatgc agttgtttta ttttagacaa
 300
 gagtgttcta aacttcgtga agagttaagg cttcaacatg aagaggataa gaagtcagca
 360
 atgtctcaac ttttgcagtt gaaagatcga gagaaaaatg cagcaagaga ttcatggcag
 420
 aagaaagtag aagatctctt aaaccagatt tccttgctga aacagaatct ggagatacag
 480
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 540
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 600
 aaagaagcac atgtccttgc atttcaaact atggaagagg aaaaggaaaa ggagcaaaga
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<210> 110

<211> 157

<212> PRT

<213> Homo sapiens

<400> 110

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		20					25						30		
Leu	Gln	Leu	Lys	Asp	Arg	Glu	Lys	Asn	Ala	Ala	Arg	Asp	Ser	Trp	Gln
		35				40						45			
Lys	Lys	Val	Glu	Asp	Leu	Leu	Asn	Gln	Ile	Ser	Leu	Leu	Lys	Gln	Asn
	50				55					60					
Leu	Glu	Ile	Gln	Leu	Ser	Gln	Ser	Gln	Thr	Ser	Leu	Gln	Gln	Leu	Gln
65				70						75				80	
Ala	Gln	Phe	Thr	Gln	Glu	Arg	Gln	Arg	Leu	Thr	Gln	Glu	Leu	Glu	Glu
			85					90						95	
Leu	Glu	Glu	Gln	His	Gln	Gln	Arg	His	Lys	Ser	Leu	Lys	Glu	Ala	His
		100					105						110		
Val	Leu	Ala	Phe	Gln	Thr	Met	Glu	Glu	Lys	Glu	Lys	Glu	Gln	Arg	
		115				120						125			
Ala	Leu	Glu	Asn	His	Leu	Gln	Gln	Lys	His	Ser	Ala	Glu	Leu	Gln	Ser

130 135 140
 Leu Lys Asp Ala His Arg Glu Ser Met Glu Gly Phe Arg
 145 150 155

<210> 111
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 111
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 420
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 429

<210> 112
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 112
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 20 25 30
 Ile Thr Gly Phe Asp Gly Ile Leu Ser Ala Tyr Xaa Arg His Gln His
 35 40 45
 Xaa Thr Leu Ala Glu Ile Ile Ala Pro Phe Gly His Leu Val Met Ile
 50 55 60
 Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu
 65 70 75 80
 Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro
 85 90 95
 Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val
 100 105 110
 Glu Lys Gly Gln Ile Arg Pro Thr Met Thr Arg His Ile Glu Gly Leu
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 Thr Thr Gln His Val Arg Glu Ala Thr Ala Ala Val Glu Ser Gly
 130 135 140

<210> 113
 <211> 382

<212> DNA

<213> Homo sapiens

<400> 113

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 120
 gtccacagcc ccaccttctg ccagctggcg tgcggccagg atgggcagct gaagggcttc
 180
 gcggtgctgg agtatgagac ggctgagatg gcggaggagg cacagcagca ggcggacggc
 240
 ctgtccctgg ggggcagcca cctgcgagtc tccttctgcg cccctgggac ccccgggcgc
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<210> 114

<211> 125

<212> PRT

<213> Homo sapiens

<400> 114

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1				5					10					15	
Trp	Ala	Thr	Met	Arg	Ala	Ala	Ser	Ile	Leu	Arg	Pro	Gly	Val	Pro	Gly
			20					25					30		
Ala	Gln	Lys	Glu	Thr	Arg	Arg	Trp	Leu	Pro	Pro	Arg	Asp	Arg	Pro	Ser
		35					40					45			
Ala	Cys	Cys	Cys	Ala	Ser	Ser	Ala	Ile	Ser	Ala	Val	Ser	Tyr	Ser	Ser
	50					55					60				
Thr	Ala	Lys	Pro	Phe	Ser	Cys	Pro	Ser	Trp	Pro	His	Ala	Ser	Trp	Gln
65					70				75					80	
Lys	Val	Gly	Leu	Trp	Thr	Ala	Asp	Ser	Ala	Arg	His	Arg	Ala	Ser	Thr
			85					90					95		
Ser	Leu	Lys	Pro	Gly	Gly	Arg	Arg	Ser	Thr	Gln	Arg	Gln	Gln	Glu	Trp
			100					105					110		
Arg	Arg	Ala	Gly	Leu	Ser	Ser	Pro	Ala	Ser	Val	Gln	Cys			
		115					120					125			

<210> 115

<211> 4798

<212> DNA

<213> Homo sapiens

<400> 115

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 120
 ccccatcctt cctcccacca acctagagge ttgcttcgt aaatgctggc cctttccttc
 180

atgggctcca ccctctgagt gtgtcatgaa ctcttccact tccttgccct gggtcgtatt
240
gggtccctctg cccgagggtca gagatttggg cgagcccttc tcctccatct tcacagtctc
300
catttaccat tagatgccag gccagacag ttgatgaaaa atgtaagaaa cggaccaag
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tataagaaaa agctagatct gtccatttta tttctagttt ttggaagaga tgtggataca
420
gagaaatatt actctactat tgaaaaaaat atatatcagt ctgattataa atgtcaactc
480
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540
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600
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660
tattactttt ggcagttaat tttaaaaatc accgttttagg ccaaaacaac atgacatttg
720
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780
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840
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900
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960
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1020
atattagttg gggtgataac tgaatggctg tccttctgcc ttcgttactg cttttgtgga
1080
tgttattttc tttgacctt attccacctg tgtgcagtgg agaggatggg tgttgatatt
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1260
tctacccct gccacctctc accttcttcc ctttcacctt tttctgtagc tgaacggaaa
1320
ccaccgctct ttaacatgaa tgcgatgagt gccttatacc acattgcaca gaacgaatcc
1380
cccgtgctcc agtcaggaca ctggtctgag tacttccgga attttgtcga ctctgtctt
1440
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4798

<210> 116

<211> 1062

<212> PRT

<213> Homo sapiens

<400> 116

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			20					25				30	
Cys	His	Leu	Ser	Pro	Ser	Ser	Leu	Ser	Pro	Phe	Ser	Val	Ala
		35					40					45	
Lys	Pro	Pro	Leu	Phe	Asn	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr
		50				55					60		
Ala	Gln	Asn	Glu	Ser	Pro	Val	Leu	Gln	Ser	Gly	His	Trp	Ser
65					70				75				80
Phe	Arg	Asn	Phe	Val	Asp	Ser	Cys	Leu	Gln	Lys	Ile	Pro	Gln
			85						90				95
Pro	Thr	Ser	Glu	Val	Leu	Leu	Lys	His	Arg	Phe	Val	Leu	Arg
			100					105					110
Pro	Pro	Thr	Val	Ile	Met	Asp	Leu	Ile	Gln	Arg	Thr	Lys	Asp
		115					120					125	
Arg	Glu	Leu	Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys	Lys	Ile
	130					135					140		
Gln	Glu	Ala	Pro	Asn	Gly	Pro	Gly	Ala	Glu	Ala	Pro	Glu	Glu
145					150				155				160
Glu	Ala	Glu	Pro	Tyr	Met	His	Arg	Ala	Gly	Thr	Leu	Thr	Ser
				165					170				175
Ser	Ser	His	Ser	Val	Pro	Ser	Met	Ser	Ile	Ser	Ala	Ser	Ser
			180					185				190	
Ser	Ser	Val	Asn	Ser	Leu	Ala	Asp	Ala	Ser	Asp	Asn	Glu	Glu
		195					200				205		
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Pro	Glu
	210					215				220			
Glu	Met	Ala	Met	Met	Gln	Glu	Gly	Glu	His	Thr	Val	Thr	Ser
225					230				235				240
Ser	Ile	Ile	His	Arg	Leu	Pro	Gly	Ser	Asp	Asn	Leu	Tyr	Asp
			245					250					255
Tyr	Gln	Pro	Glu	Ile	Thr	Pro	Ser	Pro	Leu	Gln	Pro	Pro	Ala
		260						265				270	
Ala	Pro	Thr	Ser	Thr	Thr	Ser	Ser	Ala	Arg	Arg	Arg	Ala	Tyr
		275					280					285	
Asn	Arg	Asp	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	Ser	Leu	Val
	290					295				300			
Gln	Ile	Gln	Glu	His	Glu	Gln	Asp	Ser	Ala	Leu	Arg	Glu	Gln
305					310				315				320
Gly	Tyr	Lys	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	Gln	Leu	Leu
			325						330				335
Glu	Ser	Arg	Leu	Arg	Gly	Glu	Arg	Glu	Glu	His	Ser	Ala	Arg
		340					345					350	
Arg	Glu	Leu	Glu	Ala	Gln	Arg	Ala	Gly	Phe	Gly	Ala	Glu	Ala
		355					360				365		
Leu	Ala	Arg	Arg	His	Gln	Ala	Ile	Gly	Glu	Lys	Glu	Ala	Arg
	370					375					380		
Gln	Ala	Glu	Glu	Arg	Lys	Phe	Gln	Gln	His	Ile	Leu	Gly	Gln
385					390				395				400
Lys	Glu	Leu	Ala	Ala	Leu	Leu	Glu	Ala	Gln	Lys	Arg	Thr	Tyr
			405						410				415
Arg	Lys	Glu	Gln	Leu	Lys	Glu	Glu	Leu	Gln	Glu	Asn	Pro	Ser
		420						425			430		
Lys	Arg	Glu	Lys	Ala	Glu	Trp	Leu	Leu	Arg	Gln	Lys	Glu	Gln

481

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<210> 117
<211> 471
<212> DNA
<213> Homo sapiens
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<210> 118
<211> 157
<212> PRT
<213> Homo sapiens
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<400> 118

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Xaa Ala Leu Thr Ile Cys Leu Ala Gly Val Val Ile Cys Ala Val Gly
 1           5           10           15
Val Val Asp Asp Leu Leu Asp Leu Pro Ala Leu Ala Lys Ala Ala Gly
      20           25           30
Gln Val Leu Ala Ala Gly Ile Val Val Thr Gly Gly Val Arg Met Phe
      35           40           45
Trp Ile Pro Leu Pro Asn Ser Ile Ile Ala Leu Gly Thr Pro Thr Ser
      50           55           60
Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn
      65           70           75           80
Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly
      85           90           95
Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp
      100          105          110
Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly
      115          120          125
Ala Cys Leu Gly Phe Leu Pro His Asn Trp His Pro Ala Arg Met Phe
      130          135          140
Met Gly Asp Ser Gly Ala Leu Leu Leu Gly Leu Leu Leu
      145          150          155

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<210> 119

<211> 302

<212> DNA

<213> Homo sapiens

<400> 119

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tagccgaggt cgaggcagta aatctaataa aacttttcgca aaaaattcgg atgtctactc
120
tcagaaaaag actcgaacag tacgaggcac ctccgaagat ttagcacgat cgctccataa
180
gcttcatatg cgcccgtaac ctgcgtatca tgacattgag ggtatgtggg ctttcccagc
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ctttactttt tatctggatc atgcacaagc agaccatac gctgccccaa ataaggcacg
300
cn
302

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<210> 120

<211> 98

<212> PRT

<213> Homo sapiens

<400> 120

```

Met Ser Ser Arg Gly Gly Arg Gly Gly Tyr Tyr Arg Glu Leu
 1           5           10           15
Tyr Gly Ser Arg Gly Arg Gly Ser Lys Ser Asn Glu Thr Phe Ala Lys
      20           25           30
Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr
      35           40           45
Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

```

50 55 60
 Pro Ala Tyr His Asp Ile Glu Gly Met Trp Ala Phe Pro Ala Phe Thr
 65 70 75 80
 Phe Tyr Leu Asp His Ala Gln Ala Asp Pro Tyr Ala Ala Pro Asn Lys
 85 90 95
 Ala Arg

<210> 121
 <211> 318
 <212> DNA
 <213> Homo sapiens

<400> 121
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 120
 tgtgtgagaa ggagtagaag cagctccagt agagtgggcc ttttcatttt tatccagagg
 180
 aaattttagt gctgtggcta ttacttcctt tttttctttt tttttttttg ttttagagaca
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 300
 tgcctcccag gttcaagc
 318

<210> 122
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 122
 Xaa Met Gly Gly Pro Gly Thr Ala Leu Val Pro Leu Phe Phe Leu Gly
 1 5 10 15
 Lys Lys Leu Ser Pro Lys Gly Phe Ala Ala Leu Gln Glu Ser Phe Leu
 20 25 30
 Val Ser Leu Gly Leu Phe Leu Cys Cys Val Arg Arg Ser Arg Ser Ser
 35 40 45
 Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly
 50 55 60
 Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Phe Cys Leu Glu Thr
 65 70 75 80
 Glu Ser Xaa Ser Val Ala Arg Leu Glu
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<210> 123
 <211> 338
 <212> DNA
 <213> Homo sapiens

<400> 123
 acgcgtctag ggtagaaatc aactccagta actgtcatc aacctcagca atgctgggga
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cgggcagagg cagggcagct gtgtgccaca ttctgccag ggctggtcag gccccggctc
 120
 tcaccactcc tcctccctgc tttgaacctg tggaacaaag ggcccttgca cccaactca
 180
 ttctcttttg ccacataagg gcctcaagtc atgctgtccc ctctgcctgg gttgcttttt
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 338

<210> 124
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 124
 Met Leu Gly Thr Gly Arg Gly Arg Ala Ala Val Cys His Ile Pro Ala
 1 5 10 15
 Arg Ala Gly Gln Ala Pro Ala Leu Thr Thr Pro Pro Pro Cys Phe Glu
 20 25 30
 Pro Val Glu Gln Arg Ala Pro Ala Pro Gln Leu Ile Pro Leu Cys His
 35 40 45
 Ile Arg Ala Ser Ser His Ala Val Pro Ser Ala Trp Val Ala Phe Ser
 50 55 60
 Pro Ser Ala Trp Val Thr Val His Thr Thr Gly His Phe Pro Gln Gly
 65 70 75 80
 Arg Ala Leu Thr Ala His Thr Pro Lys His Ala Pro Cys Ser Ser Ile
 85 90 95

<210> 125
 <211> 280
 <212> DNA
 <213> Homo sapiens

<400> 125
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 ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga
 120
 accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca cttttctgca
 180
 tttccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg
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 gcttctgctg tcctggccca ttctggatag gcctgatcta
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<210> 126
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 126
 Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

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      1             5             10             15
Gly Ala Cys Arg Gln Gly Leu Glu Gly Arg Leu Leu Glu Arg Glu Thr
      20             25             30
Arg Pro Ile Cys Leu Ser Gly Asn Leu Gln Pro Pro Thr Gly Ala Asp
      35             40             45
Cys Gln Leu Ser Gly Glu Lys Ser Leu Phe Cys Ile Pro Thr Thr Leu
      50             55             60
Ser Ile Cys Ala Ile Arg Gln Arg Asp Ser Thr His Leu Ile Glu Gly
      65             70             75             80
Phe Cys Cys Pro Gly Pro Phe Trp Ile Gly Leu Ile
      85             90

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<210> 127
 <211> 444
 <212> DNA
 <213> Homo sapiens

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<400> 127
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ctgcaaagcc gtcactgccc tgcggagcag atcacgtccg tcagcatcga catgtcgcca
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gcgttcatca ggggctgcgc cgagcacctg cccaacgcgc gcgtcacctt cgacaagttc
180
cacgtcatcg ggcacgcaa tgcggccgtg gacaggatgc gccgcatcga gcagcgcagc
240
gacaagtccc tcaaggggat gcgctggtcg ctgctgaaga accgcgccag cctcaagccc
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360
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420
cgcgacatgc tcaagcactg gtgc
444

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<210> 128
 <211> 148
 <212> PRT
 <213> Homo sapiens

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<400> 128
Arg Val Ile Ala Val Ala Glu Gly Arg Gly Ala Asp Ser Ile Ala Gln
1             5             10             15
Leu Thr Thr Glu Leu Gln Ser Arg His Cys Pro Ala Glu Gln Ile Thr
      20             25             30
Ser Val Ser Ile Asp Met Ser Pro Ala Phe Ile Arg Gly Cys Ala Glu
      35             40             45
His Leu Pro Asn Ala Arg Val Thr Phe Asp Lys Phe His Val Ile Gly
      50             55             60
His Ala Asn Ala Ala Val Asp Arg Met Arg Arg Ile Glu Gln Arg Ser
      65             70             75             80
Asp Lys Ser Leu Lys Gly Met Arg Trp Ser Leu Leu Lys Asn Arg Ala
      85             90             95
Ser Leu Lys Pro Glu Ala Ala Ala Asp Leu Asp Ala Leu Ile Ala Arg

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100 105 110
 Met Ala Thr Val Arg Thr Ala Arg Ala Trp Val Tyr Lys Glu Gln Leu
 115 120 125
 Arg Glu Ile Leu Ala Arg Lys Gln Ile Asn Val Ala Arg Asp Met Leu
 130 135 140
 Lys His Trp Cys
 145

<210> 129
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 129
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 ttggacgaga ttattgacgt ctttgacgcc gtcattggtg cccgtggcga tatggccgtc
 120
 gagtgccgc tgcaggaagt tccgtgatc caaaagcaga tcatcgagaa ggctcgttta
 180
 caggctaagc ccgtcattgt ggccaccag atgcttgagt cgatgatcca cgctccccgt
 240
 ccgaccgcg ctgaggccgc cgacgtcgcg aacgccatcc ttgacggcgc g
 291

<210> 130
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 130
 Glu Glu Gly Arg Thr Val Pro Val Ile Ala Lys Leu Glu Lys Pro Gln
 1 5 10 15
 Ala Ile Glu Asn Leu Asp Glu Ile Ile Asp Val Phe Asp Ala Val Met
 20 25 30
 Val Ala Arg Gly Asp Met Ala Val Glu Cys Pro Leu Glu Glu Val Pro
 35 40 45
 Leu Ile Gln Lys Gln Ile Ile Glu Lys Ala Arg Leu Gln Ala Lys Pro
 50 55 60
 Val Ile Val Ala Thr Gln Met Leu Glu Ser Met Ile His Ala Pro Arg
 65 70 75 80
 Pro Thr Arg Ala Glu Ala Ala Asp Val Ala Asn Ala Ile Leu Asp Gly
 85 90 95
 Ala

<210> 131
 <211> 416
 <212> DNA
 <213> Homo sapiens

<400> 131
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attccaccgg tgctctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc
 120
 cgcggtgtct tccgctacgc cgaacgtctg gtaggccacg acctggctct gcggatgcag
 180
 ggggcattgc ggatgcgggt ctacgaccgg ctgtcacgta ccnaccctgc tgggnnacgt
 240
 cgccgggggtg acctgctggg acgggttact gccgacgtcg acgcggtgtt ggacatgggc
 300
 gtgcgggtga tcgttccggc gtgcgcgtca agcctcgtca tcattggcac cacggctcctt
 360
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 416

<210> 132

<211> 126

<212> PRT

<213> Homo sapiens

<400> 132

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Arg	Ala	Ala	Glu	Ile	Pro	Pro	Val	Leu	Tyr	Leu	Glu	Ala	Ala	Ala	Val
			20					25					30		
Gly	Val	Arg	Phe	Phe	Gly	Ile	Ser	Arg	Gly	Val	Phe	Arg	Tyr	Ala	Glu
		35				40					45				
Arg	Leu	Val	Gly	His	Asp	Leu	Ala	Leu	Arg	Met	Gln	Gly	Ala	Leu	Arg
	50					55				60					
Met	Arg	Val	Tyr	Asp	Arg	Leu	Ser	Arg	Thr	Xaa	Pro	Ala	Gly	Xaa	Arg
65					70					75				80	
Arg	Arg	Gly	Asp	Leu	Leu	Val	Arg	Val	Thr	Ala	Asp	Val	Asp	Ala	Val
			85					90					95		
Leu	Asp	Met	Val	Val	Arg	Val	Ile	Val	Pro	Ala	Cys	Ala	Ser	Ser	Leu
		100						105					110		
Val	Ile	Ile	Gly	Thr	Thr	Val	Leu	Leu	Cys	Pro	Arg	Glu	Gly		
		115					120						125		

<210> 133

<211> 327

<212> DNA

<213> Homo sapiens

<400> 133

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 120
 gccgaaattg cgaaggcgct agaaaccgct gacgttggtga tcggttctgt ccttattccg
 180
 ggtagttcta ccccgaagct tggtactacc gatatgggtg ctcacatgca gcctgggtct
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 tacgatgacc ccactttcac tgtgcac
 327

<210> 134
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 134
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 Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg
 20 25 30
 Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu
 35 40 45
 Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr
 50 55 60
 Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser
 65 70 75 80
 Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser
 85 90 95
 His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His
 100 105

<210> 135
 <211> 560
 <212> DNA
 <213> Homo sapiens

<400> 135
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 ttacactcag ggctacagcc acggggggct gaggcccaag gctgcaatct cgggggaagg
 120
 ggaagttggc ttttcttggt ggattggaaa catcctcttg gaggcaaaga ctttctcttg
 180
 atcttacaga cttcccgga ttttagatt agaattattgg gggcaaagga ggctgtcttg
 240
 ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag
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 tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt
 360
 ccccatctc ccatggataa gtacgttcta gaacattctc ttgggtcta atactctgaa
 420
 atgacatctt gtcttcatgc tcgagagaga attacttcac tggctccact tggagtgcc
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 560

<210> 136
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 136

Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
 1 5 10 15
 Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
 20 25 30
 Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
 35 40 45
 Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
 50 55 60
 Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
 65 70 75 80
 Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
 85 90 95
 Ile Ser Ser Gly
 100

<210> 137

<211> 429

<212> DNA

<213> Homo sapiens

<400> 137

accggttgga tggcctgcag gccaaagcgt tcctgcaaac tcagcaggcc ttcagcgcaa
 60
 gaggcaaaca gctggtcgcg cacctgcttg aggtccaccg attgcgcata gcccttgagc
 120
 aaggcgcgcc agttggtttt gtcggccact tggctgcgga acaggtcttc gacaaaaccg
 180
 gactgctggc gggctgcaac gcgcatgata ggcagcgctt ggctggcgcc ctggctcgagc
 240
 cagcgctcgc gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
 300
 aggtacacca catggtcggc catgcagaat gtttcgcccc agccgggata acggcaagt
 360
 ccggcgctgt aatggcaacg ttcggggctc atgatgcaca ggtcacactg ggccagcttg
 420
 gtcatgccc
 429

<210> 138

<211> 141

<212> PRT

<213> Homo sapiens

<400> 138

Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
 1 5 10 15
 Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
 20 25 30
 Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
 35 40 45
 Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
 50 55 60
 Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln

```

65              70              75              80
Gln Ser Gly Phe Val Glu Asp Leu Phe Arg Ser Gln Val Ala Asp Lys
              85              90              95
Thr Asn Trp Arg Ala Leu Leu Lys Gly Asp Ala Gln Ser Val Asp Leu
              100             105             110
Lys Gln Val Arg Asp Gln Leu Phe Ala Ser Cys Ala Glu Gly Leu Leu
              115             120             125
Ser Leu Gln Glu Arg Phe Gly Leu Gln Ala Ile Gln Pro
              130             135             140

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<210> 139
 <211> 341
 <212> DNA
 <213> Homo sapiens

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<400> 139
acgcgtcgtt tgaaggcttg atccgcacgt ccaattcgct ttgcgccaat gcgccgcagc
60
ttgtgaacag cagaatcaag ccgctggtaa atcttctctg gagcttcata ggccggggatg
120
ctacacgagc tggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc
180
tttgcagcct gtaacgactg agggttcgga tggaaaaaca catgctccag gatggggaccg
240
acggccactt caccgatctc ttcatagccc tggcgtttgt agaaatccag gtagcgcgaa
300
tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t
341

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<210> 140
 <211> 113
 <212> PRT
 <213> Homo sapiens

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<400> 140
Met Thr Arg Thr His Gln Ala Ser Cys Ser Thr Leu Ala Ile Arg Ala
1              5              10              15
Thr Trp Ile Ser Thr Asn Ala Arg Ala Met Lys Arg Ser Val Lys Trp
              20              25              30
Pro Ser Val Pro Ser Trp Ser Met Cys Phe Ser Ile Arg Thr Leu Ser
              35              40              45
Arg Tyr Arg Leu Gln Arg Phe Glu Thr Glu Leu Phe Arg Gln Phe Arg
50             55             60
Val Gln Ser Val Ser Pro Ala Arg Val Ala Ser Pro Pro Met Lys Leu
65             70             75             80
Pro Gly Arg Phe Thr Ser Gly Leu Ile Leu Leu Phe Thr Ser Cys Gly
              85             90             95
Ala Leu Ala Gln Ser Glu Leu Asp Val Arg Ile Lys Pro Ser Asn Asp
              100            105            110
Ala

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<210> 141
 <211> 324

<212> DNA

<213> Homo sapiens

<400> 141

gaattcctct tggatagctt cgggtaaatg ggtacagcaa atatcaggag cgcaaccgca
 60
 acctttactt actggtacat gaacaccatt tacattacag ctatcgtagt caccaccagt
 120
 catgtgaaca gacacataac tgaaagggtt ataaaccaca gtctcacggt acgtatgacc
 180
 gtcaactgtg aacaccgcta agtaatagcc tgcgggggct tgcataaact cctttgacca
 240
 tgcgtaataa atacgtccgt cattagtcac acctgatggg gcgaaacaaa aagaacggca
 300
 gcagttatca ccgcccatat gcgt
 324

<210> 142

<211> 106

<212> PRT

<213> Homo sapiens

<400> 142

Met	Gly	Gly	Asp	Asn	Cys	Cys	Arg	Ser	Phe	Cys	Phe	Ala	Pro	Ser	Gly
1				5				10					15		
Val	Thr	Asn	Asp	Gly	Arg	Ile	Tyr	Tyr	Ala	Trp	Ser	Lys	Glu	Phe	Met
		20					25					30			
Gln	Ala	Pro	Ala	Gly	Tyr	Tyr	Leu	Ala	Val	Phe	Thr	Val	Asp	Gly	His
	35					40					45				
Thr	Tyr	Arg	Glu	Thr	Val	Val	Tyr	Lys	Pro	Phe	Ser	Tyr	Val	Ser	Val
	50				55					60					
His	Met	Thr	Trp	Gly	Glu	Tyr	Asp	Ser	Cys	Asn	Val	Asn	Gly	Val	His
65				70				75					80		
Val	Pro	Val	Ser	Lys	Gly	Cys	Gly	Cys	Ala	Pro	Asp	Ile	Cys	Cys	Thr
			85				90						95		
His	Leu	Pro	Glu	Ala	Ile	Gln	Glu	Glu	Phe						
		100					105								

<210> 143

<211> 1325

<212> DNA

<213> Homo sapiens

<400> 143

nacgcgtgga tctgccagct gagcctggag ctgtgcaggc agctgccctg ctacgatgag
 60
 gcaccccagg agaagaactt cctgtacaaa tgcataggca ccaccctggg tgctgcttca
 120
 agtaaggagg tggtagaggaa gcaccttcaa gagctgctgg agacggccag ataccaggag
 180
 gaggcagaac gcgagggcct cgctgctgc ttcgggatct gtgccatctc ccacctcgag
 240
 gacacgctgg ccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc
 300

attctcaaca tttttaagga tcgaagtgag aacgaagtgg agaaggtgaa gagtgtcttg
 360
 atcctgtgct atgggcacgt ggcgccccgg gccccccggg agctgggtgct ggccaaggta
 420
 gagtgcagaca tcctccggaa catcntgccg gcacttcagc acnncaagga cccagccctg
 480
 aagctgtgcc ttgtccagag tgtgtgcatg gtcagccgcg ccatctgcag cagcaccag
 540
 gctggctcct tccacttcac ccggaaagca gagctggtgg cacagatgat ggagttcatc
 600
 agggcagagc ccccgactc cttgaggaca cctattcgga agaaagccat gctcacctgc
 660
 acttacttgg tctccgtgga gccagcgctg gacgagcagg cccgggcgga tgtgatccat
 720
 ggctgcctgc acagcatcat ggccctgctg cctgagccca aggaggagga cggaggctgc
 780
 cagaagtccc tgtatctgga gacactgcac gcccttgagg atctgctgac gagcctcctg
 840
 cagcgggaaca tgacccccca aggctgcag atcatgattg agcacctgag cccatggatc
 900
 aagtccccaa gaggtcacgt agcggcgctg gccctaggcc tgagcgccct cctcgtgcgc
 960
 tacttcctgg agcacctgcg tgtcagtggc gcccaagtag ataccaggtt tccatctgag
 1020
 cccaggatcc tgtgcaatgg ccctgggtgcc cttccacaac ctgggccttc tcacggcct
 1080
 cttctcccca cgggtgtgcgg acctgtggcc tgccaccgc caggaggccg tggactgtgt
 1140
 ctactccctg ctgtacctcc agctcggcta tgagggttc tcccgggact accgcgatga
 1200
 cgtggcggag cggctcctca gcctcaagga cggcctcgtg caccctgacc ccgccattct
 1260
 cttccacacc tgccacagtg taggccagat tattgccaag cgcctcccc cagcccttca
 1320
 cgcgt
 1325

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Xaa	Ala	Trp	Ile	Cys	Gln	Leu	Ser	Leu	Glu	Leu	Cys	Arg	Gln	Leu	Pro
1			5					10					15		
Cys	Tyr	Asp	Glu	Ala	Pro	Gln	Glu	Lys	Asn	Phe	Leu	Tyr	Lys	Cys	Ile
		20						25				30			
Gly	Thr	Thr	Leu	Gly	Ala	Ala	Ser	Ser	Lys	Glu	Val	Val	Arg	Lys	His
		35					40					45			
Leu	Gln	Glu	Leu	Leu	Glu	Thr	Ala	Arg	Tyr	Gln	Glu	Glu	Ala	Glu	Arg
		50				55					60				
Glu	Gly	Leu	Ala	Cys	Cys	Phe	Gly	Ile	Cys	Ala	Ile	Ser	His	Leu	Glu
65				70					75					80	
Asp	Thr	Leu	Ala	Gln	Leu	Glu	Asp	Phe	Val	Arg	Ser	Glu	Val	Phe	Arg

[illegible]

<210> 145

<211> 802

<212> DNA

<213> Homo sapiens

<400> 145

cggccgtcta ggtccggctc agtgcgctgt tgctcgccgt agaacacgag gctgcgcaag
60 cataagcaga cgtagagagt ggtcacatcc atgtcgatgg tgtgcgcgta atgaaggctc
120 acatcaccct ggtgaaggcc tgcaccacta gcgtcggcac catttccccg cgtcggacaa
180 gacatcatgc cccatatctt gacagaatgt ctgacatgag tatgccacgc cgagcagcac
240

cagaggacga caccgatctg gcgagcgccg cccgttcacg gcgcagatac ctcacccctg
 300
 tcatttggg cggtatcgte gctgtcctcg gactaggcat tttcgggtat cttgcgtggg
 360
 ggtcattgtg cgatcaagct gccgggggtct gtcagcgtgg tgaacccggt atgtactggg
 420
 gttcgggtgg ctctctggcc attctcggac tcattatcgg ggtcttgacg cagatctggc
 480
 tggagaagcg ctggtggcac atgcttgcca tcgtcatccc ggctgttttc atcgtcgccg
 540
 gtatcttttt ctggctcgcc gtctaagaag gggcgtcaca gattccacaa acgacacagg
 600
 tattgatctc cgttttatcg gctcctagca gccgtgggtca acgtatcgct atcaagcgat
 660
 acaggactcg tcgttcgcat cgttggtgtg ctgctgggaa acaatcccag cgatctactc
 720
 ggctaccgcc agacagttca ctcacaaccc ctcacgccgg cgcagacatc aaatcccatt
 780
 ctcgatagac ggcccacacc ac
 802

<210> 146

<211> 151

<212> PRT

<213> Homo sapiens

<400> 146

Met	Lys	Val	Tyr	Ile	Thr	Leu	Val	Lys	Ala	Cys	Thr	Thr	Ser	Val	Gly
1				5					10					15	
Thr	Ile	Ser	Pro	Arg	Arg	Thr	Arg	His	His	Ala	Pro	Tyr	Leu	Asp	Arg
			20					25					30		
Met	Ser	Asp	Met	Ser	Met	Pro	Arg	Arg	Ala	Ala	Pro	Glu	Asp	Asp	Thr
		35				40						45			
Asp	Leu	Ala	Asp	Ala	Ala	Arg	Ser	Trp	Arg	Arg	Tyr	Leu	Ile	Leu	Val
	50					55					60				
Ile	Cys	Gly	Val	Ile	Val	Ala	Val	Leu	Gly	Leu	Gly	Ile	Phe	Gly	Tyr
65				70				75						80	
Leu	Ala	Trp	Trp	Ser	Leu	Cys	Asp	Gln	Ala	Ala	Gly	Val	Cys	Gln	Arg
			85					90					95		
Gly	Glu	Pro	Val	Met	Tyr	Trp	Cys	Ser	Val	Val	Ser	Leu	Ala	Ile	Leu
			100				105					110			
Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Gln	Ile	Trp	Leu	Glu	Lys	Arg	Trp
	115					120					125				
Trp	His	Met	Leu	Ala	Ile	Val	Ile	Pro	Ala	Val	Phe	Ile	Val	Ala	Gly
	130				135						140				
Ile	Phe	Phe	Trp	Leu	Ala	Val									
145					150										

<210> 147

<211> 368

<212> DNA

<213> Homo sapiens

<400> 147

acgcgtgaaa acggtatgac tcttctggcc ttagtagatc tgtctaaaaa acccgatgag
 60
 ttacacagt gggcattagt agcccgcgat gttcatgaca ttcctgggtct acgaaaagtt
 120
 attggtcaga aagtaccttg tggtgcagtg acgggggtcgg aaaagggtgct tcataaaaaa
 180
 gattactggg atctagcaac acctatgccca attgcgtggg gtacaacgga ccgaacagtt
 240
 attgctgatg cacgacgtac aatccccacc acggagtggg atatccttgc aagactacgt
 300
 ccacgcctag aagagggttcg caagcaacgt aatgatgtat tgctcctcaa cgaggaggat
 360
 ccccccta
 368

<210> 148

<211> 117

<212> PRT

<213> Homo sapiens

<400> 148

Met	Thr	Leu	Leu	Ala	Leu	Val	Asp	Leu	Ser	Lys	Lys	Pro	Asp	Glu	Phe
1				5					10					15	
Thr	Gln	Trp	Ala	Leu	Val	Ala	Arg	Asp	Val	His	Asp	Ile	Pro	Gly	Leu
			20					25					30		
Arg	Lys	Val	Ile	Gly	Gln	Lys	Val	Pro	Cys	Val	Ala	Val	Thr	Gly	Ser
		35					40					45			
Glu	Lys	Val	Leu	His	Lys	Lys	Asp	Tyr	Trp	Asp	Leu	Ala	Thr	Pro	Met
	50					55					60				
Pro	Ile	Ala	Trp	Gly	Thr	Thr	Asp	Arg	Thr	Val	Ile	Ala	Asp	Ala	Arg
65					70				75					80	
Arg	Thr	Ile	Pro	Thr	Thr	Glu	Trp	Asp	Ile	Leu	Ala	Arg	Leu	Arg	Pro
			85						90				95		
Arg	Leu	Glu	Glu	Val	Arg	Lys	Gln	Arg	Asn	Asp	Val	Leu	Leu	Leu	Asn
			100					105					110		
Glu	Glu	Asp	Pro	Pro											
			115												

<210> 149

<211> 407

<212> DNA

<213> Homo sapiens

<400> 149

nngctagcat ggaccctagt cacacaggca gccatacccg aggtcaaagt gacccatttt
 60
 cctaataatgg ccgctcagat ccaatacttt gaagattcgt ccgtgggttat atggcacgat
 120
 gcggtggatg gstatcgtgta ccgaagtgcg gatgaaggca agtcgtgggc cccaattaag
 180
 gggcctgaac agggtcaggc gcaccttttc gtgctccatc cctacgacaa gactcaagcg
 240
 tatattctga cgcgcagcac tcagcattgg cgcacgtcga accgtggcga gacgtggcag
 300

tcattctcaa cgctcatcc gcctacgacc ttgaaagcta tgctcttgga ctttcatccg
 360
 acgcatcatg actggatcct tttcacgggc caggcttgca cggtaaa
 407

<210> 150
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 150
 Xaa Leu Ala Trp Thr Leu Val Thr Gln Ala Ala Ile Pro Glu Val Lys
 1 5 10 15
 Val Thr His Phe Pro Asn Met Ala Ala Gln Ile Gln Tyr Phe Glu Asp
 20 25 30
 Ser Ser Val Val Ile Trp His Asp Ala Val Asp Gly Ile Val Tyr Arg
 35 40 45
 Ser Ala Asp Glu Gly Lys Ser Trp Ala Pro Ile Lys Gly Pro Glu Gln
 50 55 60
 Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala
 65 70 75 80
 Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly
 85 90 95
 Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Leu Lys
 100 105 110
 Ala Met Pro Leu Asp Phe His Pro Thr His His Asp Trp Ile Leu Phe
 115 120 125
 Thr Gly Gln Ala Cys Thr Val
 130 135

<210> 151
 <211> 448
 <212> DNA
 <213> Homo sapiens

<400> 151
 accggtgtcc gtggctattg ccccgaaatgg tccccatccg cgccccggg aactccctcg
 60
 gcttttcgcg catccaggtc ccagcccca gctactggtg cgccccgagc ccctaggtgc
 120
 cagagcggtg gtcggccggg ctccctgcca gtctcggtc ctccctctc cccaccagaa
 180
 ggaaaaactt gggcccttcg agaaccctgt ggaatgttct ttgtaatcaa ctgtacatcc
 240
 gcttccacgg cacggcctcg tgcaaaatcg cgggtttcgg ggccttgag caaattgcgc
 300
 ttgtcagcgg cgacgtcagg aggacaagg gaggggttcg cggctgaaac tgcagcttcg
 360
 cagcacagag ccattttagg ctgctcccca cctcgcgggg cccatgggaa gccggccccg
 420
 ggagggcgcg gctgcatgga tattcgac
 448

<210> 152

<211> 149
 <212> PRT
 <213> Homo sapiens

<400> 152
 Thr Gly Val Arg Gly Tyr Cys Pro Glu Trp Ser Pro Ser Ala Ser Pro
 1 5 10 15
 Gly Thr Pro Ser Ala Phe Arg Ala Ser Arg Ser Pro Ala Pro Ala Thr
 20 25 30
 Gly Ala Pro Arg Ala Pro Arg Cys Gln Ser Gly Gly Arg Pro Gly Ser
 35 40 45
 Cys Pro Val Ser Ala Pro Pro Ser Ser Pro Pro Glu Gly Lys Thr Trp
 50 55 60
 Ala Leu Arg Glu Pro Cys Gly Met Phe Phe Val Ile Asn Cys Thr Ser
 65 70 75 80
 Ala Ser Thr Ala Arg Pro Arg Ala Lys Ser Arg Val Ser Gly Pro Trp
 85 90 95
 Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly
 100 105 110
 Phe Ala Ala Glu Thr Ala Ala Ser Gln His Arg Ala Ile Leu Gly Cys
 115 120 125
 Ser Pro Pro Arg Gly Ala His Gly Lys Pro Ala Pro Gly Gly Arg Gly
 130 135 140
 Cys Met Asp Ile Arg
 145

<210> 153
 <211> 440
 <212> DNA
 <213> Homo sapiens

<400> 153
 nnntgggtcc atgtatgtgt gtgtatatga gggagacacg caggtgtgtg tccgagtgtg
 60
 tgtccatggg tccatgtatg tgtgtgtata tgtgggggaa caggtgtgtg tccgagtgtg
 120
 tgcattgggtc cgtgtatatg cgtgtatatata tgcgggggata tgtatatgtg tgtgtgtatg
 180
 aacaggtgta agtgggggagc actcaggtgt gtctgtgtgt gttcgtgtac acgtgtgtaa
 240
 gtgggtgacc atgaaggggt gtgtgtgtcc gtgtgtaggt ttgcgtgcat gcacacatgc
 300
 atgtgtgtac tggggcatcc aagcccctgg tctccactcc attccaccct acgcctacct
 360
 ccttgatctc tgcgcccagc cttggctgtg ctcccctgct gtagtcacgt ggggtgtctgc
 420
 acgtgggtgt ctgcacgcgt
 440

<210> 154
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 154

Gly Arg His Ala Gly Val Cys Pro Ser Val Cys Pro Trp Val His Val
 1 5 10 15
 Cys Val Cys Ile Cys Gly Gly Thr Gly Val Cys Pro Ser Val Cys Met
 20 25 30
 Gly Pro Cys Ile Cys Val Tyr Ile Cys Gly Asp Met Tyr Met Cys Val
 35 40 45
 Cys Met Asn Arg Cys Lys Trp Gly Ala Leu Arg Cys Val Cys Val Cys
 50 55 60
 Ser Cys Thr Arg Val
 65

<210> 155

<211> 344

<212> DNA

<213> Homo sapiens

<400> 155

acgcgtatcg accaccatgt cgtcgtcacc acggcaagcg ctctcggcgg gcgagaacga
 60
 gtgaacatgg ccgagttgat ggccgatgcc gcgaccggca cgaaaccgtc ctacctacag
 120
 cgatcttctt cctcgatcac ctcgtttgaa gtggacaggg aacaaagaca ctcagacaac
 180
 gcgccgcagg aagtaaaaag ttcgctctcc gatcacggcc gtcgcgcgag tgcacagggg
 240
 gaactgggca cctcgcaagc tacgccaccg cgatccatgc ccccgcccgt atcttcgcgc
 300
 tcctctacct ccccttacc gatcagcatt atatccgac taga
 344

<210> 156

<211> 92

<212> PRT

<213> Homo sapiens

<400> 156

Met Ala Glu Leu Met Ala Asp Ala Ala Thr Gly Thr Lys Pro Ser Tyr
 1 5 10 15
 Leu Gln Arg Ser Ser Ser Ile Thr Ser Phe Glu Val Asp Arg Glu
 20 25 30
 Gln Arg His Ser Asp Asn Ala Pro Gln Glu Val Lys Ser Ser Leu Ser
 35 40 45
 Asp His Gly Arg Arg Ala Ser Ala Gln Gly Glu Leu Gly Thr Ser Gln
 50 55 60
 Ala Thr Pro Pro Arg Ser Met Pro Pro Pro Val Ser Ser Ala Ser Ser
 65 70 75 80
 Thr Ser Pro Leu Pro Ile Ser Ile Ile Ser Asp Leu
 85 90

<210> 157

<211> 6816

<212> DNA

<213> Homo sapiens

<400> 157
nnagatctcc aaagaaccaa aaggatcaat atttctggat tcctgtatgg gtgtcgttca
60
gaacaacaaa gtcaggcggtt ttgcttttga gctcaagatg caggacaaaa gtagttatct
120
cttggcagca gacagtgaag tggaaatgga agaattggatc acaattctaa ataagatcct
180
ccagctcaac tttgaagctg caatgcaaga aaagcgaaat ggcgactctc acgaagatga
240
tgaacaaagc aaattggaag gttctggttc cggtttagat agctacctgc cggaacttgc
300
caagagtgc agagaagcag aaatcaaact gaaaagtga agcagagtca aactttttta
360
tttggaccca gatgccaga agcttgactt ctcatcagct gagccagaag tgaagtcatt
420
tgaagagaag tttggaaaaa ggatccttgt caagtgcatt gatttatctt tcaatttgca
480
atgctgtgtt gccgaaaatg aagaaggacc cactacaaat gttgaacctt tctttgttac
540
tctatccctg tttgacataa aatacaaccg gaagatttct gccgatttcc acgtagacct
600
gaaccatttc tcagtggaggc aaatgatcgc caccacgtcc ccggcgctga tgaatggcag
660
tgggccgaaa cccaatctgc cctcaggggc atccttcacg aagccgccat gcagtatccg
720
aagcagggaa tattttcagt cacttgctct catccagata tatttcttgt ggccagaatt
780
gaaaaagtcc ttcaggggag catcacacat tgcgctgagc catatatgaa aagttcagac
840
tcttctaagg tggcccgaaa ggtgctgaag aatgccaaag aggcagcca aagactagga
900
cagtatagaa tgccatttgc ttgggcagca aggacattgt ttaaggatgc atctggaaat
960
cttgacaaaa atgccagatt ttctgccatc tacaggcaag acagcaataa gctatccaat
1020
gatgacatgc tcaagttact tgcagacttt cggaaacctg agaagatggc taagctccca
1080
gtgatttttag gcaatctaga cattacaatt gataatgttt cctcagactt ccctaattat
1140
gttaattcat catacattcc cacaaaaaa tttgaaacct gcagtaaaac tcccatcacg
1200
tttgaagtgg aggaatttgt gcctgcata ccaaaacaca ctcagcctta caccatctac
1260
accaatcacc tttacgttta tcctaagtac ttgaaatacg acagtcagaa gtcttttgcc
1320
aaggctagaa atattgcat ttgcattgaa ttcaaagatt cagatgagga agactctcag
1380
ccccttaagt gcatttatgg cagacctggt gggccagttt tcacaagaag cgcctttgct
1440
gcagttttac accatcacca aaaccagaa ttttatgatg agattaaaat agagttgccc
1500
actcagctgc atgaaaagca ccacctgttg ctacattct tccatgtcag ctgtgacaac
1560

tcaagtaaag gaagcacgaa gaagagggat gtcgttgaaa cccaagttgg ctactcctgg
1620
cttccccctcc tgaaagacgg aaggggtggtg acaagcgagc agcacatccc ggtctcggcg
1680
aaccttcctt cgggctatct tggctaccag gagcttggga tgggcaggca ttatgggtccg
1740
gaaattaaat gggtagatgg aggcaagcca ctgctgaaaa tttccactca tctgggtttct
1800
acagtgtata ctcaggatca gcattttacat aattttttcc agtactgtca gaaaaccgaa
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<210> 158

<211> 1572

<212> PRT

<213> Homo sapiens

<400> 158

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			20					25					30		
Asp	Phe	Arg	Lys	Pro	Glu	Lys	Met	Ala	Lys	Leu	Pro	Val	Ile	Leu	Gly
			35				40					45			
Asn	Leu	Asp	Ile	Thr	Ile	Asp	Asn	Val	Ser	Ser	Asp	Phe	Pro	Asn	Tyr
	50					55					60				
Val	Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys
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Thr	Pro	Ile	Thr	Phe	Glu	Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys
			85					90					95		
His	Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro
			100					105					110		
Lys	Tyr	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn
		115					120					125			
Ile	Ala	Ile	Cys	Ile	Glu	Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln
	130				135						140				
Pro	Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg
145				150					155					160	
Ser	Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr
			165					170					175		
Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His
			180					185					190		
Leu	Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly
		195					200					205			
Ser	Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp
	210					215					220				
Leu	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile
225				230					235					240	
Pro	Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu
			245					250					255		
Gly	Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly

505

690	695	700
Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser		
705	710	715
Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu		720
	725	730
Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn		735
	740	745
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu		750
	755	760
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu		765
	770	775
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe		780
785	790	795
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg		800
	805	810
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly		815
	820	825
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp		830
	835	840
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu		845
	850	855
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe		860
865	870	875
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys		880
	885	890
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr		895
	900	905
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe		910
	915	920
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys		925
	930	935
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr		940
945	950	955
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr		960
	965	970
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser		975
	980	985
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe		990
	995	1000
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu		1005
	1010	1015
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg		1020
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Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn		1040
	1045	1050
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr		1055
	1060	1065
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg		1070
	1075	1080
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val		1085
	1090	1095
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val		1100
1105	1110	1115
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg		1120

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 1155 1160 1165
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 1285 1290 1295
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 1315 1320 1325
 Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
 1330 1335 1340
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 1345 1350 1355 1360
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 1365 1370 1375
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 1380 1385 1390
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 1395 1400 1405
 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
 1410 1415 1420
 Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 1425 1430 1435 1440
 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 1445 1450 1455
 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 1460 1465 1470
 Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
 1475 1480 1485
 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
 1490 1495 1500
 Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
 1505 1510 1515 1520
 Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu
 1525 1530 1535
 Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala
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1555
Ser Ser Val Val
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1560

1565

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<211> 540
<212> DNA
<213> Homo sapiens

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<210> 160
<211> 110
<212> PRT
<213> Homo sapiens

<400> 160
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Thr Pro Gly Thr Ala Gln Arg Cys Met Cys His Ser Val Val Cys Phe
20 25 30
Asn Gln Gly Ala Leu Trp Gln Gly Leu Gly Gly Thr Ser Gln Arg Ala
35 40 45
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly
50 55 60
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg
65 70 75 80
Thr His Gln Ala Leu Ser Leu Val Ala Phe Pro Asp Asn Leu Tyr Pro
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Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe
100 105 110

<210> 161
<211> 351
<212> DNA
<213> Homo sapiens

<400> 161
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<210> 162
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 162
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 Phe Ala Gly Arg Arg Ala Trp Leu Ala Ala Thr Met Lys Gly Asp Asp
 20 25 30
 Ser Ser Lys Ile Thr His Lys Ile Ala Arg Ala Lys Arg Glu Gly Arg
 35 40 45
 Val Trp Trp Ser Phe Glu Tyr Phe Pro Pro Arg Thr Pro Gln Gly Met
 50 55 60
 Gln Asn Leu Tyr Asp Arg Ile Glu Arg Met Ser Gln Leu Gly Pro Glu
 65 70 75 80
 Phe Val Asp Ile Thr Trp Asn Ala Gly Gly Arg Thr Ser Asp Met Thr
 85 90 95
 Thr Gln Leu Val Lys Thr Val His Ala Tyr Phe Gly Val Glu Thr Cys
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 Met His Leu Thr Cys
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<210> 163
 <211> 360
 <212> DNA
 <213> Homo sapiens

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 180
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 240
 gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgcy
 300

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360

<210> 164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 164

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Ala	Gly	Gly	Val	Asp	Thr	Tyr	Thr	Leu	Arg	Gln	Pro	Ile	Gly	Val	Cys
			20					25					30		
Ala	Gly	Ile	Thr	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro	Leu	Trp	Met
		35					40					45			
Phe	Pro	Met	Ala	Ile	Ala	Cys	Gly	Asn	Thr	Phe	Val	Leu	Lys	Pro	Ser
	50					55					60				
Glu	Gln	Asp	Pro	Leu	Ser	Thr	Met	Leu	Leu	Val	Glu	Leu	Ala	Leu	Glu
65				70						75				80	
Ala	Gly	Val	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	His	Gly	Gly	Lys	Asp
			85					90						95	
Val	Val	Asp	Ala	Leu	Cys	Thr	His	Lys	Asp	Ile	Lys	Ala	Val	Ser	Phe
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<210> 165

<211> 728

<212> DNA

<213> Homo sapiens

<400> 165

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120
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180
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240
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600
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660

gtggcaggtt ttgaaaaagt cgctgtgcat ggtcaagtgc cactggaaag agaagcagga
 720
 ctacgcgt
 728

<210> 166
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 166
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 20 25 30
 Arg Ala Arg Gly Asn Ser Phe Thr Lys Phe Gly Asn Arg Asn Val Phe
 35 40 45
 Met Lys Asp Asn Ser Ser Ser Ser Thr Asp Ser Arg Ser Arg Ser
 50 55 60
 Ser Ser Arg Ser Pro Thr Arg His Phe Arg Arg Ser Asp Ser His Ser
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 Asp Ser Asp Ser Ser Tyr Ser Gly Asn Glu Cys His Pro Val Gly Arg
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 Arg Asn Pro Pro Pro Lys Gly Arg Gly Gly Arg Gly Ala His Met Asp
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 Arg Gly Arg Gly Arg Ala Gln Arg Gly Lys Arg His Asp Leu Ala Pro
 115 120 125
 Thr Lys Arg Ser Arg Lys Lys Met Ala Ala Leu Glu Cys Glu Asp Pro
 130 135 140
 Glu Arg Glu Leu Lys Lys Gln Lys Arg Ala Ala Arg Phe Gln His Gly
 145 150 155 160
 His Ser Arg Arg Leu Arg Leu Glu Pro Leu Val Leu Gln Met Ser Ser
 165 170 175
 Leu Glu Ser Ser Gly Ala Asp Pro Asp Trp Gln Glu Leu Gln Ile Val
 180 185 190
 Gly Thr Cys Pro Asp Ile Thr Lys His Tyr Leu Arg Leu Thr Cys Ala
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 Pro Asp Pro Ser Thr Val Arg Pro Val Ala Phe Pro Val Ala Gly Phe
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 Leu Arg

<210> 167
 <211> 510
 <212> DNA
 <213> Homo sapiens

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<210> 168

<211> 128

<212> PRT

<213> Homo sapiens

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Gly	Ala	Gly	Gln	Ala	Asn	Val	Cys	Asp	Val	Val	Thr	Ser	Thr	Val	Cys
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<210> 169

<211> 537

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

<400> 170

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<213> Homo sapiens

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 35 40 45
 Lys Gly Phe Ile Lys Ala Gln Val Val Ser Phe Gly Asp Leu Val Glu
 50 55 60
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 gacaaaatct aacgtgacat cagatcgaaa ggttatagaa ataaaactaa tgagatctaa
 8460
 aaaaaaaaaa aaaaaaaaaa aaaa
 8484

<210> 176

<211> 1393

<212> PRT

<213> Homo sapiens

<400> 176

Met	Ala	Arg	Glu	Gln	Leu	Arg	Gln	Val	Tyr	Ser	Met	Thr	Ala	Tyr	Ser
1			5						10					15	
Cys	Pro	Ser	Ser	Ser	Ile	Ser	Phe	Met	Leu	Glu	Trp	Thr	Val	Ala	Cys
		20						25					30		
Ser	Met	Tyr	Leu	Ala	Met	Pro	Val	Thr	Asn	Ala	Phe	Leu	Ser	Ser	Lys
		35					40					45			
Phe	Val	Ser	Lys	Leu	Ala	Trp	Tyr	Met	Met	Glu	Glu	Gly	Gly	Gly	Ser
		50					55				60				
Met	His	Gly	Cys	Trp	Ser	Gly	Arg	Gly	Ser	Ser	Ser	Ser	Arg	Ser	Thr
65					70					75				80	
Leu	Asp	Arg	Ala	Ser	Ser	Arg	Val	Thr	Cys	Val	Val	Met	Ala	Ala	Val
			85						90					95	
Ser	Val	Phe	Cys	Thr	Gly	Ser	Ala	Ala	Gly	Pro	Gly	Glu	Gly	Pro	Glu
			100						105					110	
Ala	Thr	Ala	Gly	Pro	Arg	Ala	Gly	Ala	Gln	Asp	Ala	Leu	Pro	Arg	Ser

521

545					550					555				560	
Asp	Lys	Tyr	Ser	Asn	Lys	Asp	Cys	Pro	Asp	Ser	Ala	Glu	Glu	Tyr	Glu
				565						570				575	
Arg	Ala	Thr	Arg	Tyr	Asn	Tyr	Thr	Ser	Glu	Glu	Lys	Phe	Ala	Leu	Val
				580					585				590		
Glu	Val	Ile	Ala	Met	Ile	Lys	Gly	Leu	Gln	Val	Leu	Met	Gly	Arg	Met
				595				600					605		
Glu	Ser	Val	Phe	Asn	His	Ala	Ile	Arg	His	Thr	Val	Tyr	Ala	Ala	Leu
				610			615				620				
Gln	Asp	Phe	Ser	Gln	Val	Thr	Leu	Arg	Glu	Pro	Leu	Arg	Gln	Ala	Ile
625					630					635					640
Lys	Lys	Lys	Lys	Asn	Val	Ile	Gln	Ser	Val	Leu	Gln	Ala	Ile	Arg	Lys
				645					650					655	
Thr	Val	Cys	Asp	Trp	Glu	Thr	Gly	His	Glu	Pro	Phe	Asn	Asp	Pro	Ala
				660				665					670		
Leu	Arg	Gly	Glu	Lys	Asp	Pro	Lys	Ser	Gly	Phe	Asp	Ile	Lys	Val	Pro
				675				680					685		
Arg	Arg	Ala	Val	Gly	Pro	Ser	Ser	Thr	Gln	Leu	Tyr	Met	Val	Arg	Thr
				690			695					700			
Met	Leu	Glu	Ser	Leu	Ile	Ala	Asp	Lys	Ser	Gly	Ser	Lys	Lys	Thr	Leu
705					710					715					720
Arg	Ser	Ser	Leu	Glu	Gly	Pro	Thr	Ile	Leu	Asp	Ile	Glu	Lys	Phe	His
				725					730					735	
Arg	Glu	Ser	Phe	Tyr	Thr	His	Leu	Ile	Asn	Phe	Ser	Glu	Thr	Leu	
				740				745					750		
Gln	Gln	Cys	Cys	Asp	Leu	Ser	Gln	Leu	Trp	Phe	Arg	Glu	Phe	Phe	Leu
				755				760					765		
Glu	Leu	Thr	Met	Gly	Arg	Arg	Ile	Gln	Phe	Pro	Ile	Glu	Met	Ser	Met
				770			775				780				
Pro	Trp	Ile	Leu	Thr	Asp	His	Ile	Leu	Glu	Thr	Lys	Glu	Ala	Ser	Met
785					790					795					800
Met	Glu	Tyr	Val	Leu	Tyr	Ser	Leu	Asp	Leu	Tyr	Asn	Asp	Ser	Ala	His
				805					810					815	
Tyr	Ala	Leu	Thr	Arg	Phe	Asn	Lys	Gln	Phe	Leu	Tyr	Asp	Glu	Ile	Glu
				820				825					830		
Ala	Glu	Val	Asn	Leu	Cys	Phe	Asp	Gln	Phe	Val	Tyr	Lys	Leu	Ala	Asp
				835				840					845		
Gln	Ile	Phe	Ala	Tyr	Tyr	Lys	Val	Met	Ala	Gly	Ser	Leu	Leu	Leu	Asp
				850			855				860				
Lys	Arg	Leu	Arg	Ser	Glu	Cys	Lys	Asn	Gln	Gly	Ala	Thr	Ile	His	Leu
865					870					875					880
Pro	Pro	Ser	Asn	Arg	Tyr	Glu	Thr	Leu	Leu	Lys	Gln	Arg	His	Val	Gln
				885					890					895	
Leu	Leu	Gly	Arg	Ser	Ile	Asp	Leu	Asn	Arg	Leu	Ile	Thr	Gln	Arg	Val
				900				905					910		
Ser	Ala	Ala	Met	Tyr	Lys	Ser	Leu	Glu	Leu	Ala	Ile	Gly	Arg	Phe	Glu
				915				920					925		
Ser	Glu	Asp	Leu	Thr	Ser	Ile	Val	Glu	Leu	Asp	Gly	Leu	Leu	Glu	Ile
				930			935				940				
Asn	Arg	Met	Thr	His	Lys	Leu	Leu	Ser	Arg	Tyr	Leu	Thr	Leu	Asp	Gly
945					950					955					960
Phe	Asp	Ala	Met	Phe	Arg	Glu	Ala	Asn	His	Asn	Val	Ser	Ala	Pro	Tyr
				965					970					975	
Gly	Arg	Ile	Thr	Leu	His	Val	Phe	Trp	Glu	Leu	Asn	Tyr	Asp	Phe	Leu

980 985 990
 Pro Asn Tyr Cys Tyr Asn Gly Ser Thr Asn Arg Phe Val Arg Thr Val
 995 1000 1005
 Leu Pro Phe Ser Gln Glu Phe Gln Arg Asp Lys Gln Pro Asn Ala Gln
 1010 1015 1020
 Pro Gln Tyr Leu His Gly Ser Lys Ala Leu Asn Leu Ala Tyr Ser Ser
 1025 1030 1035 1040
 Ile Tyr Gly Ser Tyr Arg Asn Phe Val Gly Pro Pro His Phe Gln Val
 1045 1050 1055
 Ile Cys Arg Leu Leu Gly Tyr Gln Gly Ile Ala Val Val Met Glu Glu
 1060 1065 1070
 Leu Leu Lys Val Val Lys Ser Leu Leu Gln Gly Thr Ile Leu Gln Tyr
 1075 1080 1085
 Val Lys Thr Leu Met Glu Val Met Pro Lys Ile Cys Arg Leu Pro Arg
 1090 1095 1100
 His Glu Tyr Gly Ser Pro Gly Ile Leu Glu Phe Phe His His Gln Leu
 1105 1110 1115 1120
 Lys Asp Ile Val Glu Tyr Ala Glu Leu Lys Thr Val Cys Phe Gln Asn
 1125 1130 1135
 Leu Arg Glu Val Gly Asn Ala Ile Leu Phe Cys Leu Leu Ile Glu Gln
 1140 1145 1150
 Ser Leu Ser Leu Glu Glu Val Cys Asp Leu Leu His Ala Ala Pro Phe
 1155 1160 1165
 Gln Asn Ile Leu Pro Arg Val His Val Lys Glu Gly Glu Arg Leu Asp
 1170 1175 1180
 Ala Lys Met Lys Arg Leu Glu Ser Lys Tyr Ala Pro Leu His Leu Val
 1185 1190 1195 1200
 Pro Leu Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg
 1205 1210 1215
 Glu Gly Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met
 1220 1225 1230
 Phe Glu Val Ile Leu Thr Arg Ile Arg Ser Phe Leu Asp Asp Pro Ile
 1235 1240 1245
 Trp Arg Gly Pro Leu Pro Ser Asn Gly Val Met His Val Asp Glu Cys
 1250 1255 1260
 Val Glu Phe His Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile
 1265 1270 1275 1280
 Pro Val Gly Thr His Glu Phe Thr Val Glu Gln Cys Phe Gly Asp Gly
 1285 1290 1295
 Leu His Trp Ala Gly Cys Met Ile Ile Val Leu Leu Gly Gln Gln Arg
 1300 1305 1310
 Arg Phe Ala Val Leu Asp Phe Cys Tyr His Leu Leu Lys Val Gln Lys
 1315 1320 1325
 His Asp Gly Lys Asp Glu Ile Ile Lys Asn Val Pro Leu Lys Lys Met
 1330 1335 1340
 Val Glu Arg Ile Arg Lys Phe Gln Ile Leu Asn Asp Glu Ile Ile Thr
 1345 1350 1355 1360
 Ile Leu Asp Lys Tyr Leu Lys Ser Gly Asp Gly Glu Gly Thr Pro Val
 1365 1370 1375
 Glu His Val Arg Cys Phe Gln Pro Pro Ile His Gln Ser Leu Ala Ser
 1380 1385 1390
 Ser

<210> 177
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 177
 acgcgtgatg tcacactgcc tctgccgctg ggtcctaatt cgattgcacg caccatggct
 60
 gcagttcgtg gcgcgcatag tttctggcat gcttcgcgca tcctggagac cgatcccgcc
 120
 gctgccgtga aaccgcctaa aaatgtgaag cgattgccca aagccgtgtc cgtggagcaa
 180
 atgcaaaagc tccttgccat acccagtctt aagactccta ccggcctgcg taatcgagcg
 240
 atacttgagt tcttatatgc taccggcgcg cgcgtgagcg agatgctggc aacagacctg
 300
 gacgatatac acctggggcga aaaaccccgcg gatgaaaacg gggaatctat tgcacttccc
 360
 gggatatgtc gccttttttg aaagggaggt aaagagcggt tagtcccttt gggatcc
 417

<210> 178
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 178
 Thr Arg Asp Val Thr Leu Pro Leu Pro Leu Gly Pro Asn Ser Ile Ala
 1 5 10 15
 Arg Thr Met Ala Ala Val Arg Gly Ala His Ser Phe Trp His Ala Ser
 20 25 30
 Arg Ile Leu Glu Thr Asp Pro Ala Ala Val Lys Pro Pro Lys Asn
 35 40 45
 Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu
 50 55 60
 Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala
 65 70 75 80
 Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu
 85 90 95
 Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu
 100 105 110
 Asn Gly Glu Ser Ile Ala Leu Pro Gly Tyr Val Arg Leu Phe Gly Lys
 115 120 125
 Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser
 130 135

<210> 179
 <211> 362
 <212> DNA
 <213> Homo sapiens

<400> 179
 acgcgtcgaa ggtgccggtg ggggcatca ataacatcgc gcaatccctg gaagagcctc
 60

aggtgattgc ccgtgggttg atggtggaag atccccgcatc cccaagaatc cgggaattcg
 120
 ccattggggcc gggcagcccg aatccaaaat gtcggggcac gccagtgagg agtatggtaa
 180
 ggggcccggca ccgatgttgg nggcagcata cggatggaag tgctgggcga ggcctgggt
 240
 ttgccggcag agcaactggg gcagctcaag gcgggcgggg tgatcgagca gttggattga
 300
 gcaatggcgg ccgcgaagcc cgccatttac cttgatgact gtttagcgcg cggattcttt
 360
 aa
 362

<210> 180
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Ala Gly Phe Ala Ala Ala Ile Ala Gln Ser Asn Cys Ser Ile Thr
 1 5 10 15
 Pro Pro Ala Leu Ser Cys Pro Ser Cys Ser Ala Gly Lys Pro Arg Arg
 20 25 30
 Ser Pro Ser Thr Ser Ile Arg Met Leu Pro Pro Thr Ser Val Pro Ala
 35 40 45
 Pro Tyr His Thr Pro Thr Gly Arg Ala Pro Thr Phe Trp Ile Arg Ala
 50 55 60
 Ala Arg Pro Asn Gly Glu Phe Pro Asp Ser Trp Gly Cys Gly Ile Phe
 65 70 75 80
 His His Gln Pro Thr Gly Asn His Leu Arg Leu Phe Gln Gly Leu Arg
 85 90 95
 Asp Val Ile Asp Arg Pro His Arg His Leu Arg Arg
 100 105

<210> 181
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 181
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 60
 ccgattcact tgtcgggtaca ggccaatacg gtgaattggg ccagcgtcga gttctggcaa
 120
 cagcaaggta tctgccgggt aatcctgtcg cgggaattgt cactggaaga aatcggcgaa
 180
 atccgccaac aggtgccggc catggagctg gaagtgtttg tgcacgggtgc cctgtacatg
 240
 gcctattccg ggcgtgtttt gttgtccggc tatatgaaca agcgcgatgc caaccaa
 297

<210> 182
 <211> 99
 <212> PRT

<213> Homo sapiens

<400> 182

Ala Leu Ile Met Ser Asp Pro Gly Leu Ile Met Leu Val Arg Arg His
 1 5 10 15
 Phe Pro Cys Met Pro Ile His Leu Ser Val Gln Ala Asn Thr Val Asn
 20 25 30
 Trp Ala Ser Val Glu Phe Trp Gln Gln Gly Ile Cys Arg Val Ile
 35 40 45
 Leu Ser Arg Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln
 50 55 60
 Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met
 65 70 75 80
 Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp
 85 90 95
 Ala Asn Gln

<210> 183

<211> 351

<212> DNA

<213> Homo sapiens

<400> 183

cgggagctca ccatgaagcc gaccggctcg ggggatgtgg cgaacaaggt catcacccat
 60
 attccgttta acatcgtctc ccaggcgact catccattcc ttcgtacctt ggacgatgtc
 120
 aagcgcacat ctttggcgac cgacgggctc ggccaccagg tcctgctcaa gggctaccag
 180
 gccgagggcc acgactacgc acaccccgac tacggcgcca acgtctccca ccgtgccggc
 240
 gggatgaagg atctcgagaa gctcaccgag tcgggcaggc agtggaacac cgatttcggc
 300
 attcacgtca acctggtgga gtcctatcct gaggcgaatc acttcggcga c
 351

<210> 184

<211> 117

<212> PRT

<213> Homo sapiens

<400> 184

Arg Asp Val Thr Met Lys Pro Thr Gly Ser Gly Asp Val Ala Asn Lys
 1 5 10 15
 Val Ile Thr His Ile Pro Phe Asn Ile Val Ser Gln Ala Thr His Pro
 20 25 30
 Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp
 35 40 45
 Gly Leu Gly His Gln Val Leu Leu Lys Gly Tyr Gln Ala Glu Gly His
 50 55 60
 Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly
 65 70 75 80
 Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

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      85              90              95
Thr Asp Phe Gly Ile His Val Asn Leu Val Glu Ser Tyr Pro Glu Ala
      100              105              110
Asn His Phe Gly Asp
      115

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<210> 185
 <211> 396
 <212> DNA
 <213> Homo sapiens

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<400> 185
cgcggtgggtc tcagtaaaga aaatttggtg cctagaggat gcaccattag aaacacagag
60
gctgttggtg gcattgtggt ttatgcaggc catgaaacca aagcaatgct gaacaacagt
120
gggccacggt ataagcgcag caaattagaa agaagagcaa acacagatgt cctctggtgt
180
gtcatgcttc tggtcataat gtgcttaact ggcgcagtag gtcattggaat ctggctgagc
240
aggatatgaaa agatgcattt tttcaatggt cccgagcctg atggacatat catatcacca
300
ctgttggcag gattttatat gttttggacc gtgatcattt tgttacaggt cttgattcct
360
atttctctct atgtttccat cgaaattgtg aagctt
396

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<210> 186
 <211> 132
 <212> PRT
 <213> Homo sapiens

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<400> 186
Arg Val Gly Leu Ser Lys Glu Asn Leu Leu Leu Arg Gly Cys Thr Ile
1      5      10      15
Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu
20     25     30
Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys
35     40     45
Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu
50     55     60
Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser
65     70     75     80
Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His
85     90     95
Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile
100    105    110
Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu
115    120    125
Ile Val Lys Leu
130

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<210> 187
 <211> 423

<212> DNA

<213> Homo sapiens

<400> 187

cgagtgtctca ccgcgtcagc cgtcatgcgt ccactgagg ctgttgcttc tcggtcggca
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 gaacctcgac gagttcagcg gatcctggac cagcgcgagt gggctggcgt ctctgttctc
 120
 gatgagcattc gtcgtttgct tggcacgggc ggcgatcaag aggtcatcga ggctgctcgc
 180
 cgcggagatc gcagtattgc tgacgcgggtg gaaactaacg gcattcctcac ggcgcggacc
 240
 gacactccgt tgtccgagct ctctgctccg accagcaacg ccagggtgcc gttggccggt
 300
 gtcgacgagg acttccacct catgggtgtc atctctcggg tgacctgct cgacgcgatg
 360
 tcacgagctc gcgacgaggc aggagaggga tctgtcatgt ccttgagaga caccggaaag
 420
 ctt
 423

<210> 188

<211> 141

<212> PRT

<213> Homo sapiens

<400> 188

Arg	Val	Leu	Thr	Ala	Ser	Ala	Val	Met	Arg	Pro	Thr	Glu	Ala	Val	Val
1				5				10					15		
Ser	Arg	Ser	Ala	Glu	Pro	Arg	Arg	Val	Gln	Arg	Ile	Leu	Asp	Gln	Arg
		20					25					30			
Glu	Trp	Ala	Gly	Val	Phe	Val	Val	Asp	Glu	His	Arg	Arg	Leu	Leu	Gly
	35					40					45				
Thr	Val	Gly	Asp	Gln	Glu	Val	Ile	Glu	Ala	Ala	Arg	Arg	Gly	Asp	Arg
	50					55					60				
Ser	Ile	Ala	Asp	Ala	Val	Glu	Thr	Asn	Gly	Ile	Leu	Thr	Ala	Arg	Thr
65				70				75						80	
Asp	Thr	Pro	Leu	Ser	Glu	Leu	Phe	Ala	Pro	Thr	Ser	Asn	Ala	Arg	Val
			85					90					95		
Pro	Leu	Ala	Val	Val	Asp	Glu	Asp	Phe	His	Leu	Met	Gly	Val	Ile	Ser
	100							105					110		
Arg	Val	Thr	Leu	Leu	Asp	Ala	Met	Ser	Arg	Ala	Arg	Asp	Glu	Ala	Gly
	115						120					125			
Glu	Gly	Ser	Val	Met	Ser	Leu	Glu	Asn	Thr	Gly	Lys	Leu			
	130					135						140			

<210> 189

<211> 429

<212> DNA

<213> Homo sapiens

<400> 189

ngatgggttta ccaacatatg cacgggttcga gcggcaatag ctctcgggg gctggcagtg
 60

aaatgtttga agatgccggc gtttcgggcc tcaacttggt tcgatgccgt gggtccaccg
 120
 atttcgccga tgcggctcat cgcacgggta agaagtttcg tccagataac ccaggacaga
 180
 gcaaggtata tcaggctcag aaccaggaaa agcagggcct taccacagtg ccccatatag
 240
 accgcgctag ctacggcaaa aggcgcgccc agtgggggtcc aggacagcac tttcatggct
 300
 gaagggagcg catcccnagc ttcgcctagc cccagagcta acccagcgac cagtggacca
 360
 gcgccccatca tcagtaggaa ccctacgata atcagccctt gttttacccc tggaatggag
 420
 ctgatttcn
 429

<210> 190

<211> 123

<212> PRT

<213> Homo sapiens

<400> 190

Met	Met	Gly	Ala	Gly	Pro	Leu	Val	Ala	Gly	Leu	Ala	Leu	Gly	Leu	Gly
1				5					10					15	
Glu	Ala	Xaa	Asp	Ala	Leu	Pro	Ser	Ala	Met	Lys	Val	Leu	Ser	Trp	Thr
			20					25					30		
Pro	Leu	Gly	Ala	Pro	Phe	Ala	Val	Ala	Ser	Ala	Val	Tyr	Met	Gly	His
		35				40					45				
Trp	Gly	Lys	Ala	Leu	Leu	Phe	Leu	Val	Leu	Ser	Leu	Ile	Tyr	Leu	Ala
	50				55					60					
Leu	Ser	Trp	Val	Ile	Trp	Thr	Lys	Leu	Leu	Asn	Arg	Ala	Met	Ser	Arg
65				70					75					80	
Ile	Gly	Glu	Ile	Gly	Gly	Thr	Thr	Ala	Ser	Lys	Gln	Val	Glu	Ala	Gly
			85					90					95		
Asn	Ala	Gly	Ile	Phe	Lys	His	Phe	Thr	Ala	Ser	Pro	Arg	Gly	Ala	Ile
		100					105						110		
Ala	Ala	Arg	Thr	Val	His	Met	Leu	Val	Asn	His					
		115					120								

<210> 191

<211> 4845

<212> DNA

<213> Homo sapiens

<400> 191

ccgccccggg ccatggcgac actcagcttc gtcttctctgc tgctgggggc agtgtctctgg
 60
 cctccggctt ctgcctccgg ccaggagttc tggccccggac aatcggcggc cgatattctg
 120
 tcgggggagg cttcccgcag acggtatctt ctgtatgacg tcaaccccc ggaaggcttc
 180
 aacctgcgca gggatgtcta tatccgaatc gcctctctcc tgaagactct gctgaagacg
 240
 gaggagtggg tgcttgtcct gcctccatgg ggccgcctct atcactggca gagtctctgac
 300

atccaccagg tccggattcc ctggtctgag ttttttgatc ttccaagtct caataaaaaac
360
atccccgtca tcgagtatga gcagttcatc gcagaatctg gtggggccctt tattgaccag
420
gtttacgtcc tgcaaagtta cgcagagggg tggaagaag ggacctggga agagaagggtg
480
gacgagcggc cgtgtattga tcagctcctg tactcccagg acaagcacga gtactacaga
540
ggatgggtttt ggggttatga ggagaccagg ggtctaaacg tctcctgtct gtccgtccag
600
ggctcagcct ccatcggtggc gccctgctg ctgagaaaca catcagcccg gtccgtgatg
660
ttagacagag ccgagaacct acttcacgac cactatggag ggaaagaata ctgggatacc
720
cgtcgcagca tgggtgtttgc caggcacctg cgggaggtgg gagacgagtt caggagcaga
780
catctcaact ccacggacga cgcagacagg atccccctcc aggaggactg gatgaagatg
840
aagggtcaagc tgggctccgc gctagggggc ccctacctgg gagtccacct gagaagaaaa
900
gatttcatct ggggtcacag acaggatgta cccagtctgg aaggggccgt gaggaagatc
960
cgagcctca tgaagacca ccggctggac aagggtgtttg tggccacaga tgccgtcaga
1020
aaggaatatg aagagctaaa aaagctgtta cccgagatgg tgaggtttga acccacgtgg
1080
gaggagctgg agctctacaa ggacggaggc gttgcgatta ttgaccagtg gatctgcgca
1140
cacgccaggc gcctgcccac gtcactgtcg gccgagagcg ggtcgggtgg ctttcaaagg
1200
ttcttctgtc ccaagtactc ggtgtcagag cagatggctg cctgtgttca cagtggatc
1260
ttccatactg ttgacctcct cgtctgagtc tcctgtagca tctggttcag tgtttccctg
1320
ggctgaagtt aattgttcat cttgcccctt tagttctcat gcacagaatt cctccatagc
1380
aggctgttgg catagctggc ctctgtctcag aacctcttct tgtgtcgcat tttcccatca
1440
ttcccggttt ctgcccctgt ctgcccctg ccctgagagt tgcccggtgc ctggacttgg
1500
gcatgtcctt gttgctgtgt tgttgagcat ccgtgagcgt ccccgaggcc gggagcgtgg
1560
gccctcgtgt gatcattctc gtggggctgc catgagcgtc cccaaggctg ggagcatggg
1620
ccctcgtgtg atcgttcttg tggggctgcc gtgagcgtcc ccgaggccgg gagcgtggggc
1680
cctcgtgtga tcattctcgt ggggctgccg tgagcgtccc agaggccggg agcgtggggc
1740
ctgctgcag tcattcctct ggggttctg tgggaggtac gcctgggctc ctgttcctcc
1800
aaagacctgc ctgcccctc gcataggaga tgaaggctgg ggttaggggtg aaacgggttg
1860
agttaaatgg aaaatgaaag tagagggaaat gatcttccc gtggttagca ctgtgcacac
1920

gcgtgctct ctgtgggtta gtctgtctct ctctgccc aggaatgctg agcgccctga
1980
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<210> 192

<211> 428

<212> PRT

<213> Homo sapiens

<400> 192

Pro Pro Gly Ala Met Ala Thr Leu Ser Phe Val Phe Leu Leu Leu Gly
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 Ala Val Ser Trp Pro Pro Ala Ser Ala Ser Gly Gln Glu Phe Trp Pro
 20 25 30
 Gly Gln Ser Ala Ala Asp Ile Leu Ser Gly Ala Ala Ser Arg Arg Arg

35				40				45							
Tyr	Leu	Leu	Tyr	Asp	Val	Asn	Pro	Pro	Glu	Gly	Phe	Asn	Leu	Arg	Arg
50						55					60				
Asp	Val	Tyr	Ile	Arg	Ile	Ala	Ser	Leu	Leu	Lys	Thr	Leu	Leu	Lys	Thr
65					70					75					80
Glu	Glu	Trp	Val	Leu	Val	Leu	Pro	Pro	Trp	Gly	Arg	Leu	Tyr	His	Trp
				85					90					95	
Gln	Ser	Pro	Asp	Ile	His	Gln	Val	Arg	Ile	Pro	Trp	Ser	Glu	Phe	Phe
				100					105				110		
Asp	Leu	Pro	Ser	Leu	Asn	Lys	Asn	Ile	Pro	Val	Ile	Glu	Tyr	Glu	Gln
		115					120						125		
Phe	Ile	Ala	Glu	Ser	Gly	Gly	Pro	Phe	Ile	Asp	Gln	Val	Tyr	Val	Leu
	130					135					140				
Gln	Ser	Tyr	Ala	Glu	Gly	Trp	Lys	Glu	Gly	Thr	Trp	Glu	Glu	Lys	Val
145					150					155					160
Asp	Glu	Arg	Pro	Cys	Ile	Asp	Gln	Leu	Leu	Tyr	Ser	Gln	Asp	Lys	His
				165					170					175	
Glu	Tyr	Tyr	Arg	Gly	Trp	Phe	Trp	Gly	Tyr	Glu	Glu	Thr	Arg	Gly	Leu
				180					185				190		
Asn	Val	Ser	Cys	Leu	Ser	Val	Gln	Gly	Ser	Ala	Ser	Ile	Val	Ala	Pro
		195					200						205		
Leu	Leu	Leu	Arg	Asn	Thr	Ser	Ala	Arg	Ser	Val	Met	Leu	Asp	Arg	Ala
	210					215					220				
Glu	Asn	Leu	Leu	His	Asp	His	Tyr	Gly	Gly	Lys	Glu	Tyr	Trp	Asp	Thr
225					230					235					240
Arg	Arg	Ser	Met	Val	Phe	Ala	Arg	His	Leu	Arg	Glu	Val	Gly	Asp	Glu
				245					250					255	
Phe	Arg	Ser	Arg	His	Leu	Asn	Ser	Thr	Asp	Asp	Ala	Asp	Arg	Ile	Pro
				260					265				270		
Phe	Gln	Glu	Asp	Trp	Met	Lys	Met	Lys	Val	Lys	Leu	Gly	Ser	Ala	Leu
		275					280						285		
Gly	Gly	Pro	Tyr	Leu	Gly	Val	His	Leu	Arg	Arg	Lys	Asp	Phe	Ile	Trp
	290					295					300				
Gly	His	Arg	Gln	Asp	Val	Pro	Ser	Leu	Glu	Gly	Ala	Val	Arg	Lys	Ile
305					310					315					320
Arg	Ser	Leu	Met	Lys	Thr	His	Arg	Leu	Asp	Lys	Val	Phe	Val	Ala	Thr
				325					330					335	
Asp	Ala	Val	Arg	Lys	Glu	Tyr	Glu	Glu	Leu	Lys	Lys	Leu	Leu	Pro	Glu
				340					345				350		
Met	Val	Arg	Phe	Glu	Pro	Thr	Trp	Glu	Glu	Leu	Glu	Leu	Tyr	Lys	Asp
				355					360				365		
Gly	Gly	Val	Ala	Ile	Ile	Asp	Gln	Trp							

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<210> 193
<211> 350
<212> DNA
<213> Homo sapiens
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<400> 193

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 gcgcagctgt acgacgagcc cttcgtcgtc gcgctgcggg cgtcgcaccc gctggccgac
 120
 cgtgccagca tcagccccga ggaggtcaag ggcgagacca tgttgatgtt gggcacgggc
 180
 ccctgggttc cccggggccc cggtgggggt ttggcccga tttggcgcgt ttctccagcg
 240
 ccgttaaggg catacgccgc agtttcgagg gctcgtcgtt ggagaccatc aagcacatcg
 300
 tggcttcggg catggcgtga cggtggtgcc gcagctgtcc gtgccgcgcg
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<210> 194

<211> 116

<212> PRT

<213> Homo sapiens

<400> 194

Ala	Gly	Glu	Leu	Asp	Cys	Ala	Ile	Met	Ala	Glu	Pro	Phe	Pro	Asp	Thr
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Gly	Leu	Ala	Thr	Ala	Gln	Leu	Tyr	Asp	Glu	Pro	Phe	Val	Val	Ala	Leu
			20					25						30	
Arg	Ala	Ser	His	Pro	Leu	Ala	Asp	Arg	Ala	Ser	Ile	Ser	Pro	Glu	Glu
		35					40					45			
Val	Lys	Gly	Glu	Thr	Met	Leu	Met	Leu	Gly	Thr	Gly	Pro	Trp	Phe	Pro
	50				55					60					
Arg	Ala	Arg	Gly	Gly	Gly	Leu	Ala	Arg	Ile	Trp	Arg	Val	Ser	Pro	Ala
65					70					75				80	
Pro	Leu	Arg	Ala	Tyr	Ala	Ala	Val	Ser	Arg	Ala	Arg	Arg	Trp	Arg	Pro
			85						90					95	
Ser	Ser	Thr	Ser	Trp	Leu	Arg	Ala	Trp	Arg	Asp	Gly	Gly	Ala	Ala	Ala
			100					105						110	
Val	Arg	Ala	Ala												
			115												

<210> 195

<211> 495

<212> DNA

<213> Homo sapiens

<400> 195

acgcgtgaac gcgacggctt ggcgatcgga ggcgtcggcc ccgctcgttga gtgggcccgtt
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 gaaatgggtc gcttcgacga aagcgagact ctcgaccgcc ttgcatcggg cgtccttgaa
 120
 ccagaacttg gcgacgattt ggccgccgtc ctgctcgatt ctcacgggt tgctgtcatc
 180
 agcgagggat cgaactggct tgcctcgcta cccgtgatcg taggtcgcaa cacggaacag
 240
 tttcgagca taccagacct tgcccgcgac cggatcgaca aactgcacca gttgagccat
 300

cgcgaaatag cacgaaatcg cgagctcctg cgtgcccgcg ctgcgtcggg gcaggtgcgg
 360
 cactgccacg gcgacgcaca cctcggcaac atcgatcatga ttgacggcaa gccggctcctg
 420
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 480
 ttccctctga tggat
 495

<210> 196
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 196
 Thr Arg Glu Arg Asp Gly Leu Ala Ile Gly Gly Val Gly Pro Val Val
 1 5 10 15
 Glu Trp Ala Val Glu Met Val Arg Phe Asp Glu Ser Glu Thr Leu Asp
 20 25 30
 Arg Leu Ala Ser Gly Val Leu Glu Pro Glu Leu Gly Asp Asp Leu Ala
 35 40 45
 Ala Val Leu Leu Asp Ser His Arg Val Ala Val Ile Ser Glu Gly Ser
 50 55 60
 Asn Trp Leu Ala Ser Leu Pro Val Ile Val Gly Arg Asn Thr Glu Gln
 65 70 75 80
 Phe Arg Ser Ile Pro Asp Leu Ala Arg Asp Arg Ile Asp Lys Leu His
 85 90 95
 Gln Leu Ser His Arg Glu Ile Ala Arg Asn Arg Glu Leu Leu Arg Ala
 100 105 110
 Arg Ala Ala Ser Gly Gln Val Arg His Cys His Gly Asp Ala His Leu
 115 120 125
 Gly Asn Ile Val Met Ile Asp Gly Lys Pro Val Leu Phe Asp Ala Ile
 130 135 140
 Glu Phe Asp Pro Asp Ile Ala Thr Thr Asp Val Leu Tyr Asp Phe Ala
 145 150 155 160
 Phe Pro Leu Met Asp
 165

<210> 197
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 197
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 aaaggtatca atccagatga aactgaaggt gaacgtcacg caagcgatga tgagccattc
 120
 tcttcattag cattcaaaat tgcaactgac ccattcgtag gtaacttaac cttcttccgt
 180
 gtgtactcag gtgtaattaa ctctggtgat acagtattaa actctgtacg tcaaaaacgt
 240
 gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt
 300

cgtgcgggcg atatcgctgc agcaatcggc ttaaaagatg taactacggg tgaaccatta
 360
 tgtgtgtcg atgcaccaat cattcttgag cgtatggaat tc
 402

<210> 198
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 198
 Gln Ala Met Leu Asp Ala Val Val Glu Tyr Leu Pro Ala Pro Thr Asp
 1 5 10 15
 Ile Pro Ala Ile Lys Gly Ile Asn Pro Asp Glu Thr Glu Gly Glu Arg
 20 25 30
 His Ala Ser Asp Asp Glu Pro Phe Ser Ser Leu Ala Phe Lys Ile Ala
 35 40 45
 Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe Arg Val Tyr Ser Gly
 50 55 60
 Val Ile Asn Ser Gly Asp Thr Val Leu Asn Ser Val Arg Gln Lys Arg
 65 70 75 80
 Glu Arg Phe Gly Arg Ile Val Gln Met His Ala Asn Lys Arg Glu Glu
 85 90 95
 Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala Ala Ile Gly Leu Lys
 100 105 110
 Asp Val Thr Thr Gly Glu Pro Leu Cys Ala Val Asp Ala Pro Ile Ile
 115 120 125
 Leu Glu Arg Met Glu Phe
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<210> 199
 <211> 507
 <212> DNA
 <213> Homo sapiens

<400> 199
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 tatcgcaaa agaccaagcg accctggacg ttctagacag aactctgcta cgaggcctga
 120
 caatagtga atccccgaga acccagctat ggaagggttt ccagatgctc gaaggcctgt
 180
 cataccagag gttagggttaa actgtatgga gactttcgag gtgaaagttg actcgccggt
 240
 aaagcctgct cctaaagagg atttagatct gatagatcta tcctcagatt caacctcggg
 300
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 360
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 420
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 480
 cagcctgagc acagctccgc ttgtaca
 507

<210> 200
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 200
 Met Glu Gly Glu Glu Ala Ala Phe Leu Pro Glu Gly Pro Ser Ser Pro
 1 5 10 15
 Trp Phe Ile Val Ser Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu
 20 25 30
 Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile
 35 40 45
 Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg
 50 55 60
 Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr
 65 70 75 80
 Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu
 85 90 95
 Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu
 100 105 110
 Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu
 115 120 125
 Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser
 130 135 140
 His Arg Ser Met His Asp Phe Thr Arg
 145 150

<210> 201
 <211> 527
 <212> DNA
 <213> Homo sapiens

<400> 201
 gatgtggcta ttatccctgt ttcccaggtg agaaacaggg tcagtgatag agctgggtag
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 tgtgcctgca ggctcaccag ccagtcacct cctcaccaag gatgatgttc tccgtgggtga
 120
 gctggtcctt ggtctcctgg aactcgtggc gcacctgggc cagctgcgcc tcgaaggcat
 180
 ccttctccat ctctttggct agctgcaagt tctggagctg ctcgttgagg tctgtgatct
 240
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 300
 ccagctgctc aaactcctgg cggaacatct tctcctgcac agccagctca tcccacttcc
 360
 gctggtaccg ggctagccgg tctccaggt ctcggtatct gatgtggtag aactccttca
 420
 tctccttggc cagaggcggc tccacggcca ccaccggctc cttcttgccc cttttcttct
 480
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 527

<210> 202

<211> 70
 <212> PRT
 <213> Homo sapiens

<400> 202
 Gly Arg Pro Gln Ser Pro Ser Cys Tyr Trp Pro Ala Ala Gln Thr Pro
 1 5 10 15
 Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly
 20 25 30
 Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr
 35 40 45
 Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Pro Ala Pro
 50 55 60
 Ser Cys Pro Leu Ser Ser
 65 70

<210> 203
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 203
 ngtgcaccgg tggatcatgga caacgcgcgcc tacgtggtct acacctcggg atccaccggc
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 cgacccaagg gagttgtcgt caccacacacc ggactcgaca gcttcgcact cgaccagcag
 120
 cgtcgattcc acgcagatca ccactctcga accctgcact tcgccacccc cagcttcgac
 180
 ggagccgtct tcgagtacct gcaggcattc ggtgtcggag ccaccatggt gatcggtccc
 240
 accgacatct acggcgggcgc cgaactggca agtctcatcc gccgcgaaca cgtcactcac
 300
 gcgt
 304

<210> 204
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 204
 Xaa Ala Pro Val Val Met Asp Asn Ala Ala Tyr Val Val Tyr Thr Ser
 1 5 10 15
 Gly Ser Thr Gly Arg Pro Lys Gly Val Val Val Thr His Thr Gly Leu
 20 25 30
 Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His
 35 40 45
 Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe
 50 55 60
 Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro
 65 70 75 80
 Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu
 85 90 95
 His Val Thr His Ala

100

<210> 205
 <211> 356
 <212> DNA
 <213> Homo sapiens

<400> 205
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 gcacaattaa atacagtgtt aactttatctt tcaccacaat caaaagataa agatttaatac
 120
 atgccagatc aacaagaaga aatagatatt ctgattgcaa ccgactgtat ttcagaagga
 180
 cagaacttac aagattgtga ttacttaata aactatgaca ttcattggaa tccagttcgt
 240
 atcattcaaa gatttggacg gattgatcga attggttcga agaataaatg tgtacaatta
 300
 gttaactttt ggccagatat tacattagat gaatatattg atctaaaggg acgcgt
 356

<210> 206
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 206
 Xaa Asn Ser Ala Met Ile Thr Gly Ser Ile Glu Gly Lys Thr Thr Ile
 1 5 10 15
 Glu Gly Ile Asn Ala Gln Leu Asn Thr Val Leu Thr Leu Phe Ser Pro
 20 25 30
 Gln Ser Lys Asp Lys Asp Leu Ile Met Pro Asp Gln Gln Glu Glu Ile
 35 40 45
 Asp Ile Leu Ile Ala Thr Asp Cys Ile Ser Glu Gly Gln Asn Leu Gln
 50 55 60
 Asp Cys Asp Tyr Leu Ile Asn Tyr Asp Ile His Trp Asn Pro Val Arg
 65 70 75 80
 Ile Ile Gln Arg Phe Gly Arg Ile Asp Arg Ile Gly Ser Lys Asn Lys
 85 90 95
 Cys Val Gln Leu Val Asn Phe Trp Pro Asp Ile Thr Leu Asp Glu Tyr
 100 105 110
 Ile Asp Leu Lys Gly Arg
 115

<210> 207
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 207
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 catggtgtgt gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcactg
 120

tgtgtggtgt gtagcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt
 180
 gtgcacatgt gcactgtgtg gtgtgtatgc atggtgtgtg cacgtgtgca ctgtgtatgc
 240
 atgngtgtgt gcatgtgtgc actgtgtatg catagtgtgc acgtgtgcac tgtgtggtgt
 300
 gtagcatgg taatgtgcac gtgt
 324

<210> 208
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 208
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met His Gly Val Cys Thr Cys Xaa Thr Val Cys Gly Cys
 20 25 30
 Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val
 35 40 45
 Cys Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Met Cys
 50 55 60
 Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys
 65 70 75 80
 Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys
 85 90 95
 Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys
 100 105

<210> 209
 <211> 168
 <212> DNA
 <213> Homo sapiens

<400> 209
 nnctccagag gttatgaggt tggaagcccg gtttttttca ggtgcagaaa aggctaccat
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 attcaagggt ccacgactcg cacctgcctt gccaatntaa catggagtgg gatacagacc
 120
 gaatgtatac ctcatgcctg cagacagcca gaaaccccg cacacgcg
 168

<210> 210
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 210
 Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg
 1 5 10 15
 Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn
 20 25 30
 Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

35 40 45
Gln Pro Glu Thr Pro Ala His Ala
50 55

<210> 211
<211> 354
<212> DNA
<213> Homo sapiens

<400> 211
tacatgggct ttgacacagt ggtggctgaa gctgcactaa ggggtgtttgg aggcaatgtc
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cagctggcag ctcagaccct tgcacaccat ggaggaagcc tcccacccga cctgcagtcc
120
tcaggagagg actcctcccc cacaccgtcc acatccccat ctgactctgc agggacctct
180
agtgcctcga cagatgaaga catggagacg gaggctgtca acgaaatcct ggaggacatt
240
ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgct
300
gaatacttgt cctgcgttga aagtataagt tctgccngca aagaacaact gatc
354

<210> 212
<211> 118
<212> PRT
<213> Homo sapiens

<400> 212
Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe
1 5 10 15
Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly
20 25 30
Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr
35 40 45
Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr
50 55 60
Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile
65 70 75 80
Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu
85 90 95
Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala
100 105 110
Xaa Lys Glu Gln Leu Ile
115

<210> 213
<211> 669
<212> DNA
<213> Homo sapiens

<400> 213
attgcccaat ctcagagtgt ccaggaaagc ctggagagcc tggtgcagtc tattggggaa
60

gttgaacaaa acctggaagg gaaacaggtg tcatcactct catcaggagt catccaggaa
 120
 gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag
 180
 gccacccgtg agatggtgac ccgattcatg gagacagcag acagtactac agcagcagtg
 240
 ctgcagggca aactggcaga ggtgagccag cggttcgaac agctctgtct acagcagcaa
 300
 gaaaaggaga gctccctaaa gaagcttcta cccagggcag agatgtttga acacctctct
 360
 ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca
 420
 gatcaagata ttacacattt cttccaacag atccaggagc tcaatttggga aatggaagac
 480
 caacaggaga acctagatac tcttgagcac ctggtcactg aactgagctc ttgtggcttt
 540
 gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag
 600
 ctacagaaga cagttaaaga gagagagaaa gatgcatcat cttgccagga acagttggat
 660
 gaattccgg
 669

<210> 214

<211> 223

<212> PRT

<213> Homo sapiens

<400> 214

Ile	Ala	Gln	Ser	Gln	Ser	Val	Gln	Glu	Ser	Leu	Glu	Ser	Leu	Leu	Gln
1			5					10					15		
Ser	Ile	Gly	Glu	Val	Glu	Gln	Asn	Leu	Glu	Gly	Lys	Gln	Val	Ser	Ser
		20					25					30			
Leu	Ser	Ser	Gly	Val	Ile	Gln	Glu	Ala	Leu	Ala	Thr	Asn	Met	Lys	Leu
		35				40					45				
Lys	Gln	Asp	Ile	Ala	Arg	Gln	Lys	Ser	Ser	Leu	Glu	Ala	Thr	Arg	Glu
	50					55				60					
Met	Val	Thr	Arg	Phe	Met	Glu	Thr	Ala	Asp	Ser	Thr	Thr	Ala	Ala	Val
65				70					75					80	
Leu	Gln	Gly	Lys	Leu	Ala	Glu	Val	Ser	Gln	Arg	Phe	Glu	Gln	Leu	Cys
		85						90					95		
Leu	Gln	Gln	Gln	Glu	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Leu	Leu	Pro	Gln
		100						105					110		
Ala	Glu	Met	Phe	Glu	His	Leu	Ser	Gly	Lys	Leu	Gln	Gln	Phe	Met	Glu
	115						120					125			
Asn	Lys	Ser	Arg	Met	Leu	Ala	Ser	Gly	Asn	Gln	Pro	Asp	Gln	Asp	Ile
	130					135				140					
Thr	His	Phe	Phe	Gln	Gln	Ile	Gln	Glu	Leu	Asn	Leu	Glu	Met	Glu	Asp
145				150					155					160	
Gln	Gln	Glu	Asn	Leu	Asp	Thr	Leu	Glu	His	Leu	Val	Thr	Glu	Leu	Ser
		165						170					175		
Ser	Cys	Gly	Phe	Ala	Leu	Asp	Leu	Cys	Gln	His	Gln	Asp	Arg	Val	Gln
	180						185					190			
Asn	Leu	Arg	Lys	Asp	Phe	Thr	Glu	Leu	Gln	Lys	Thr	Val	Lys	Glu	Arg

	195		200		205									
Glu	Lys	Asp	Ala	Ser	Ser	Cys	Gln	Glu	Gln	Leu	Asp	Glu	Phe	Arg
	210					215						220		

<210> 215
 <211> 814
 <212> DNA
 <213> Homo sapiens

<400> 215
 aaatttcgta cccgctccgg cacagtacga gcccttgacg atgtgagcct ggctattaag
 60
 agaggttcca tctcagccgt tatcgggcac tccggagccg gcaaattccac cctgggttcg
 120
 ctcatcaacg gattagagac tcccacgcgt ggccgcgtct tggtagacgg caccgacgtc
 180
 tcgcagctct cggacaaaagc gatgcgcccg ctacgcgcag acatcgggat gatcttccaa
 240
 cagttcaacc tatteggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg
 300
 gctcattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag cttcgtcggg
 360
 ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcgggtt
 420
 ggtattgccc gagcgctagc aactaaacca tcgattttgt tggctgacga gtccacctcg
 480
 gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa
 540
 ctaggggtga cggtcgtcgt catcaccac gagatggagg tcgtccgctc gattgcccag
 600
 caggtctcgg tactagcagc tggccatctc gtcgagtctg gaagcgcgcg ccaggtcttc
 660
 gctcatccac agtcagagac caccagcgt ttctggcgga cgattatcgg ccagcaccg
 720
 agtggggagg aacaggcacg gttgcagtcg gaaaaccag atgcacgact cgtcgacgtc
 780
 agttcggtgg ccagtcactc gttcggtgac gcgt
 814

<210> 216
 <211> 271
 <212> PRT
 <213> Homo sapiens

<400> 216
 Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser
 1 5 10 15
 Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly
 20 25 30
 Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro
 35 40 45
 Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser
 50 55 60
 Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln

65					70					75					80
Gln	Phe	Asn	Leu	Phe	Gly	Ser	Arg	Thr	Ile	Tyr	Asp	Asn	Val	Ala	Tyr
				85					90					95	
Pro	Leu	Lys	Leu	Ala	His	Trp	Lys	Lys	Ala	Asp	Glu	Lys	Lys	Arg	Val
			100					105					110		
Thr	Glu	Leu	Leu	Ser	Phe	Val	Gly	Leu	Thr	Ser	Lys	Ala	Trp	Asp	His
		115					120				125				
Pro	Asp	Gln	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Val	Gly	Ile	Ala	Arg
	130				135						140				
Ala	Leu	Ala	Thr	Lys	Pro	Ser	Ile	Leu	Leu	Ala	Asp	Glu	Ser	Thr	Ser
145				150					155						160
Ala	Leu	Asp	Pro	Glu	Thr	Thr	Ala	Asp	Val	Leu	Ser	Leu	Leu	Lys	Arg
			165					170						175	
Val	Asn	Ala	Glu	Leu	Gly	Val	Thr	Val	Val	Val	Ile	Thr	His	Glu	Met
		180					185				190				
Glu	Val	Val	Arg	Ser	Ile	Ala	Gln	Gln	Val	Ser	Val	Leu	Ala	Ala	Gly
		195					200				205				
His	Leu	Val	Glu	Ser	Gly	Ser	Ala	Arg	Gln	Val	Phe	Ala	His	Pro	Gln
	210				215					220					
Ser	Glu	Thr	Thr	Gln	Arg	Phe	Leu	Ala	Thr	Ile	Ile	Gly	Gln	His	Pro
225				230						235					240
Ser	Gly	Glu	Glu	Gln	Ala	Arg	Leu	Gln	Ser	Glu	Asn	Pro	Asp	Ala	Arg
			245					250						255	
Leu	Val	Asp	Val	Ser	Ser	Val	Ala	Ser	His	Ser	Phe	Gly	Asp	Ala	
		260						265					270		

<210> 217
 <211> 500
 <212> DNA
 <213> Homo sapiens

<400> 217
 nnacgcgtcg cgatgaaaga ggcgctgaaa ggtgccatcc agattccaac agtgactttt
 60
 agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
 120
 tttcctacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtatagccac
 180
 ctgttcacta tccaaggctc ggaccccagc ttgcagccct acctgctgat ggctcacttt
 240
 gatgtggtgc ctgcccctga agaaggctgg gaggtgcccc cattctctgg gttggagcgt
 300
 gatggcgtca tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
 360
 caggccttgg agctcctgct gatcaggaag tacatcccc gaagatcttt cttcatttct
 420
 ctgggccatg atgaggagtc atcagggaca ggggctcaga g gatctcagc cctgctacag
 480
 tcaaggggcg tccagctagc
 500

<210> 218
 <211> 166
 <212> PRT

<213> Homo sapiens

<400> 218

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Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
 1           5           10           15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
           20           25           30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
           35           40           45
Phe Ile Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile
           50           55           60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
65           70           75           80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
           85           90           95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
           100          105          110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Leu Ile
           115          120          125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
           130          135          140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
145          150          155          160
Ser Arg Gly Val Gln Leu
           165

```

<210> 219

<211> 361

<212> DNA

<213> Homo sapiens

<400> 219

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acgcgttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccataca
60
caagggtccgc acgctcccat gtccctcggt ttgcacagtt cttttgcgcc gcattatggc
120
gaagcgcgtc agattgcgcc tgatatcaag cgcatacagg tcaacaaccc cagccccttc
180
acttttttcg gcaccaacag ttatctgatc ggccgcgata cgctggcatt gatcgatccc
240
gggtccgcttg acgaggecca tcacgcggcg ctgctgctg ccattgccgg ccggccggtc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtcgacac gggtttgaaa
360
g
361

```

<210> 220

<211> 102

<212> PRT

<213> Homo sapiens

<400> 220

```

Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

```

```

      1             5             10             15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
      20             25             30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
      35             40             45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
      50             55             60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
65             70             75             80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
      85             90             95
Ile Pro Val Ser Thr Arg
      100

```

<210> 221
 <211> 401
 <212> DNA
 <213> Homo sapiens

```

<400> 221
agatctctgt gtcgtcggct gcaaagagga tgagcccaga tgcatatcag gggctccctc
60
ccacatccca cctgctcggg cagcccacgg cagcccacaca ctgctgcagc acacctcgtc
120
gcagctctgg ttctctctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgctggc ccagtgaacca ccccccagg gcataccctc ctacagagca
240
ttcccaaaaa aggctagagt agacaccagc ctgctccgta gggggcctcc accccattct
300
ccaaggcctc caccagggga cgcttggtga accagcatcc aggctggcc cacctccctg
360
ctcagagtcc atgttctgtg acaagggtgg caactgggat t
401

```

<210> 222
 <211> 124
 <212> PRT
 <213> Homo sapiens

```

<400> 222
Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
1             5             10             15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
      20             25             30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
      35             40             45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
      50             55             60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
65             70             75             80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
      85             90             95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu

```

100 105 110
 Gly Ser Ser Ser Leu Gln Pro Thr Thr Gln Arg Ser
 115 120

<210> 223
 <211> 331
 <212> DNA
 <213> Homo sapiens

<400> 223
 tcatgaaatc tgtgggcagt gacccaggag ggtatgggca ggcccaacca ggttggtgtg
 60
 cccttgaagc cccacagacc tgccagggca gcagggcagt tgggagccgg agaacctgag
 120
 aaccaagcca ggctgcatgc aggaggctgg cacgtgaacg ctgcaggtgt tgccggcagc
 180
 cgtggtgcct ggcagatagt gttcgacccc cnaggacctt cttgctgggc agcccagtc
 240
 aaaagctggt cccgcttaag ccacccccac cgccttggcc acacctggca catgggtgaa
 300
 gcaagggcat ttcccggggc ttctgttcc c
 331

<210> 224
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 224
 Met Pro Leu Leu His Pro Cys Ala Arg Cys Gly Gln Gly Gly Gly Gly
 1 5 10 15
 Gly Leu Ser Gly Asn Ser Phe Trp Thr Gly Leu Pro Ser Lys Lys Val
 20 25 30
 Leu Gly Gly Arg Thr Leu Ser Ala Arg His His Gly Cys Arg Gln His
 35 40 45
 Leu Gln Arg Ser Arg Ala Ser Leu Leu His Ala Ala Trp Leu Gly Ser
 50 55 60
 Gln Val Leu Arg Leu Pro Thr Ala Leu Leu Pro Trp Gln Val Cys Gly
 65 70 75 80
 Ala Ser Arg Ala His Gln Pro Gly Trp Ala Cys Pro Tyr Pro Pro Gly
 85 90 95
 Ser Leu Pro Thr Asp Phe Met
 100

<210> 225
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 225
 tgatcacggg cgtgagccac cagcccagca tcccttgctt ttcattcgca cctccacctc
 60
 cagaatgacc ctcatccct cctgcacaga cggtgacagc agtaactcct acaaacacca
 120

ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct
 180
 caaatcctcc agggctgect gctatggggg agggaggcac actttgcttg gctctcaagg
 240
 cctcagccag ccgggtccaa accaactccc agcctggcct caccatccca ccgccaacc
 300
 ttgctcaca ctggccccctc ttcttgggaac atgggcctn
 339

<210> 226

<211> 91

<212> PRT

<213> Homo sapiens

<400> 226

Met	Thr	Leu	Ile	Pro	Ser	Cys	Thr	Asp	Gly	Asp	Ser	Ser	Asn	Ser	Tyr
1				5					10					15	
Lys	His	His	Gln	Thr	Asp	Leu	Gln	Glu	Gln	Arg	Asn	Ser	Gln	Ser	Arg
			20					25					30		
Phe	His	Pro	Arg	Arg	Ala	Leu	Lys	Ser	Ser	Arg	Ala	Ala	Cys	Tyr	Gly
		35					40					45			
Gly	Gly	Arg	His	Thr	Leu	Leu	Gly	Ser	Gln	Gly	Leu	Ser	Gln	Pro	Gly
	50					55					60				
Pro	Asn	Gln	Leu	Pro	Ala	Trp	Pro	His	His	Pro	Thr	Ala	Lys	Pro	Leu
65				70					75					80	
Leu	Thr	Leu	Ala	Pro	Leu	Pro	Gly	Thr	Trp	Ala					
				85					90						

<210> 227

<211> 353

<212> DNA

<213> Homo sapiens

<400> 227

gtcgaccctc tcgattgtgg cgaactccat ggctgctgcg ggctgctgta ggctctcgag
 60
 tagctcgacg tcgggttcgc gagggctcgc agcgtggcca tgctgcttct tggatggttc
 120
 gggcaactcc tcgggggatt cgagcagttc ttggcgcacc tgctctggcg tcatcccgga
 180
 ggccaggccg acaagtgctg cctcctgccca cccgctgagc gacgctgcca tgttgagtac
 240
 ggcgtcttca ctggtcaggg cgagcgcggt atcgaccagg ttggcgtcca ggccgagaga
 300
 cagcatgtct gctcagtcgc ggtgatgact ggagtggcgg tctcctgcac ggg
 353

<210> 228

<211> 102

<212> PRT

<213> Homo sapiens

<400> 228

Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

```

      1             5             10             15
Leu Thr Ser Glu Asp Ala Val Leu Asn Met Ala Ala Ser Leu Ser Gly
      20             25             30
Trp Gln Glu Ala Ala Leu Val Gly Leu Ala Ser Gly Met Thr Pro Glu
      35             40             45
Gln Val Arg Gln Glu Leu Leu Glu Ser Pro Glu Glu Leu Pro Glu Pro
      50             55             60
Ser Lys Lys Gln His Gly His Ala Ala Ser Pro Arg Glu Pro Asp Val
      65             70             75             80
Glu Leu Leu Glu Ser Leu Arg Arg Pro Ala Ala Met Glu Phe Ala
      85             90             95
Thr Ile Glu Gly Val Asp
      100

```

<210> 229
 <211> 743
 <212> DNA
 <213> Homo sapiens

<400> 229
 nnggctaggg acacggcctc ctctcaaca ggagtgctt gtgcaggctc aggggcatca
 60
 tcaaagataa cacagggtcg gtcaggggct gctggctgct cctgccccag gactggctcc
 120
 aggatgggca aggtctgctc cctggtagcc agggggagag ggaaggag caccagggag
 180
 tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag
 240
 agtaaagtgt ctgccccagg ggtgtcaca gccaggacc gggtagttgg aaagccagcc
 300
 cagcttggca ctacgaggag ccaggaggca gatgttcagg actgggagtt cagaaagagg
 360
 gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaaag
 420
 agagattcac tgggtaccta cagtagtcca gatgtaagcc ttggggactg ggaatttggg
 480
 aagagagatt ctctgggtgc ttatgccagc caagatgcca acgagcaggg ccaagatttg
 540
 gggaagaggg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag
 600
 tttcagaaga gagatgtgtc actcggcacc tatggcagcc gggctgcgga gccacaggaa
 660
 caggagtttg ggaagagcgc ttggataagg gactacagca gtggtggcag ctccaggacc
 720
 cttgacgccc aggacagaag ctt
 743

<210> 230
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 230
 Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

1	5	10	15
Ser Gly Ala	Ser Ser Lys Ile Thr	Gln Gly Trp	Ser Gly Ala Ala Gly
20	25	30	
Cys Ser Cys	Pro Arg Thr Gly Ser	Arg Met Gly	Lys Ala Ala Ser Leu
35	40	45	
Val Ala Arg	Gly Arg Gly Glu Gly	Ser Thr Arg	Glu Trp Ala Ser Arg
50	55	60	
Cys Gly Ile	Gly Gln Glu Glu Met	Glu Ala Ser	Ser Ser Gln Asp Gln
65	70	75	80
Ser Lys Val	Ser Ala Pro Gly Val	Leu Thr Ala	Gln Asp Arg Val Val
85	90	95	
Gly Lys Pro	Ala Gln Leu Gly Thr	Gln Arg Ser	Gln Glu Ala Asp Val
100	105	110	
Gln Asp Trp	Glu Phe Arg Lys Arg	Asp Ser Gln	Gly Thr Tyr Ser Ser
115	120	125	
Arg Asp Ala	Glu Leu Gln Asp Gln	Glu Phe Gly	Lys Arg Asp Ser Leu
130	135	140	
Gly Thr Tyr	Ser Ser Arg Asp Val	Ser Leu Gly	Asp Trp Glu Phe Gly
145	150	155	160
Lys Arg Asp	Ser Leu Gly Ala Tyr	Ala Ser Gln	Asp Ala Asn Glu Gln
165	170	175	
Gly Gln Asp	Leu Gly Lys Arg Asp	His His Gly	Arg Tyr Ser Ser Gln
180	185	190	
Asp Ala Asp	Glu Gln Asp Trp Glu	Phe Gln Lys	Arg Asp Val Ser Leu
195	200	205	
Gly Thr Tyr	Gly Ser Arg Ala Ala	Glu Pro Gln	Glu Gln Glu Phe Gly
210	215	220	
Lys Ser Ala	Trp Ile Arg Asp Tyr	Ser Ser Gly	Gly Ser Ser Arg Thr
225	230	235	240
Leu Asp Ala	Gln Asp Arg Ser		
245			

<210> 231
 <211> 431
 <212> DNA
 <213> Homo sapiens

<400> 231
 acgcgttggc caccgagagg ctggcgaggg tgtgcagcac ggcgcagtgt ggcaggggtcc
 60
 caggggtgcag cctgcgcagc agctcctcca tcaccttgct gatgaactgt cttcccacgg
 120
 ccaccaggac gccactcgcc gcctgctgcc agtcccagac caggtccttc gtcttggtca
 180
 tctcgctgga ggccaggagg atgatggtgc tggctgtgtc cttgtccagc tcttgggcgc
 240
 gactgctcag gaccctctcc atggccctca ggaccgctgc tcggtatggg tgtgccagct
 300
 tgtcatgctg ccgcagatac tcctcgcagg cacggagcgt ctccaccctg ctggacgcc
 360
 tcaccgataa ggaccccctg gtgcaggagc aggtctgcag tgccctgtgc tccctcgggg
 420
 aggtgcggcc g
 431

<210> 232
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 232
 Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu
 1 5 10 15
 Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg
 20 25 30
 Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp
 35 40 45
 Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr
 50 55 60
 Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val
 65 70 75 80
 Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg
 85 90 95
 Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu
 100 105 110
 Ala Ser Leu Ser Val Ala Asn Ala
 115 120

<210> 233
 <211> 606
 <212> DNA
 <213> Homo sapiens

<400> 233
 acgcgttcag ggatgccaga aatctaactg ggtaataaaa agctgggaga acattccaga
 60
 aaggtgggca cccttagcat tcccaaaaag caccagccct cctcatcctt ccagcttct
 120
 gtgctggaat gcacccccat cggaaggct cgaaaactca ggacacatta ggatcacctg
 180
 gaaagcattt gtcaaaacgc atctccctgc gggtcagggt ccaagttaa atcaaacttc
 240
 aggtgatgct gactcagggt gctccagaaa cacctgggga agcagcactt tggaggctgc
 300
 ctctcacatc caccacacag caagtgggca gggagctagg taaatctcct tccagttga
 360
 gaaggggctc ggagcaggca cagagaagag atacccttag aatgcaagtt gttagctgc
 420
 gaaagtccag cctgcaggct tcctgggcaa gctagtgggc tgaagtatgc cacagcaaca
 480
 ggcttctaga gccggctgcc cagctcctac tctgcctctg ccactcactg actgtgtggt
 540
 cttgagcagg tcacctgtct gacttggtga gagctgacag gcatcacctg ttagaggctt
 600
 acgcgt
 606

<210> 234

<211> 108
 <212> PRT
 <213> Homo sapiens

<400> 234

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Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser
 1             5             10             15
Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln
      20             25             30
Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr
      35             40             45
Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln
      50             55             60
Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly
65             70             75             80
Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln
      85             90             95
Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser
      100             105

```

<210> 235
 <211> 328
 <212> DNA
 <213> Homo sapiens

<400> 235

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120
ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atggctcaag
180
aaagaggaaa aagaagggca acttcaggat taaccactgg ggacctgaac ctaactgaaa
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300
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328

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<210> 236
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 236

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Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln
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Gln Tyr Arg Ala Glu Asn Gln Ile Leu Leu Lys Glu Ile Glu Ser Leu
      20             25             30
Glu Glu Glu Arg Leu Asp Leu Lys Lys Lys Ile Arg Gln Met Ala Gln
      35             40             45
Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu
      50             55             60
Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys

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65 70 75 80
Leu Asp Leu Leu Ser Leu Lys Asn Met Ser Glu Ala Gln Ser Lys Asn
 85 90 95
Glu

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<210> 237
<211> 2059
<212> DNA
<213> Homo sapiens
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<400> 237

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120
gatgtcagac tgcacatgaa atcgggttacg gtaccccgagg atcatcgcta ccgagtacac
180
cccgaacagc acccgctggg cgccgatcag cgtgagggag tgccccacca gtggcacttt
240
tcttagatag cggaacccat ccaccacatc ccagtcacc gttctcatcg tccgggaacg
300
atccaccagt ggcgggcccaa gctcccgacg tgaaaactgc agcccctagg cgaccgagac
360
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420
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480
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540
aaccacgca ccaaggcggt gagcaaaaac cggttcaggc tcatcgcgat gagcaacca
600
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660
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720
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 2059

<210> 238

<211> 129

<212> PRT

<213> Homo sapiens

<400> 238

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Val	Leu	Asp	Gly	Pro	Cys	Ser	Cys	Gly	Ser	Trp	Val	Ser	Ser	Glu	Leu
		20						25					30		
Asp	Ile	Asn	Ala	Trp	Ile	Leu	Gln	Pro	Ala	Leu	Pro	Ser	Phe	Arg	Arg
		35					40					45			
Gln	Glu	Ser	Pro	Gly	His	Ser	Pro	Pro	Gly	Pro	Pro	Gln	Glu	Gly	Met
	50					55					60				
Lys	Gly	Met	Pro	Ser	Ser	Leu	Val	Pro	Arg	Ala	Gln	Pro	Ser	Pro	Ser
65				70					75					80	
Pro	Pro	Gly	Gln	Gly	Gln	Cys	Gly	Ile	Phe	Arg	Phe	Arg	Pro	Leu	Trp
			85				90							95	
Ala	Glu	Pro	Pro	Cys	Glu	Cys	Ser	Tyr	Cys	Leu	Cys	Val	Ala	Val	Thr
		100					105					110			
Ser	Ile	Cys	Leu	Leu	Leu	Ile	Cys	Gln	Pro	Ile	Ala	Ala	Gly	Ser	Thr
		115					120					125			
Phe															

<210> 239
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 239
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 120
 ggtagctg cctcctcca cttctgcttc tcggcggttac cccataccgt attggccgcg
 180
 tggtcacctt tgaatgcagc catgtcgtcg tctccgtatc gaaatgatgt gccatcgaag
 240
 atgccgacct cagcatcggc atctgcagtg atgagtgcgt atcgcgccac acgaaacgcc
 300
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 360
 ggtagctgtat ataaagcaaa ggaacttn
 388

<210> 240
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 240
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 Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val
 20 25 30
 Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Ser Pro Tyr
 35 40 45
 Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala
 50 55 60
 Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val
 65 70 75 80
 Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly
 85 90 95
 Arg Val Tyr Lys Ala Lys Glu Leu
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<210> 241
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 241
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 tcccatctgg gggcccttag cacagtcctt gggacccac atgctgcctt tcaggctgat
 180

gtgggcaaac tcggcagccc agcctactcc cgggccatgg gccaccatct cagcttcctt
 240
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 300
 gggaaacggg ttgacttgca caaccagcac
 330

<210> 242
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 242
 Met Ala Pro Val Pro Pro Met Pro Leu Leu Leu Leu Ile Gln Ser Thr
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 Arg Leu Ser Pro Arg Glu Ala Glu Met Val Ala His Gly Pro Gly Val
 20 25 30
 Gly Trp Ala Ala Glu Phe Ala His Ile Ser Leu Lys Gly Ser Met Trp
 35 40 45
 Gly Pro Arg Asp Cys Ala Lys Gly Pro Gln Met Gly Arg Ala Lys Gly
 50 55 60
 Ala Trp Glu Gly Arg Cys Phe Pro Gln Ala Arg Pro Gly Ser Ser Ile
 65 70 75 80
 Pro Arg Ser Glu Ala Ser Ser Thr Ala Ser Val Pro Ala Ala Phe Asn
 85 90 95
 Ser Ala Pro Arg
 100

<210> 243
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 243
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 120
 cccgtactgc tacacatgct agatattctc ccctccttgc ggactacagt ggtgatggtg
 180
 caggcagaag tagccgatcg attggctgcc acaccaggca gccgcattta cgggtgtcccc
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 300
 ttctggccgg ctcccaatgt tgattctggn
 330

<210> 244
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 244
 Xaa Pro Ser Leu Arg Val Ile Thr Lys Asp Ala Met His Val Thr Ala

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      1           5           10           15
Glu Glu Ile Leu His Thr Gly His Pro Ala Pro Thr Ala Leu Val Ala
      20           25           30
Asn Leu Pro Tyr Asn Val Ala Val Pro Val Leu Leu His Met Leu Asp
      35           40           45
Ile Leu Pro Ser Leu Arg Thr Thr Val Val Met Val Gln Ala Glu Val
      50           55           60
Ala Asp Arg Leu Ala Ala Thr Pro Gly Ser Arg Ile Tyr Gly Val Pro
65           70           75           80
Ser Val Lys Val Asn Phe Tyr Gly Thr Val Ser Arg Ala Gly Ala Ile
      85           90           95
Gly Arg Asn Val Phe Trp Pro Ala Pro Asn Val Asp Ser Gly
      100           105           110

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<210> 245
 <211> 355
 <212> DNA
 <213> Homo sapiens

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<400> 245
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120
gcgtgttgca gaaacagaag ttgaccgtcg gaggtaggcg gcattcgctt cggatcgaag
180
cgtcccgagg catccatctc gagttgacga cgaaaatctt tccagtccac gccgtagggg
240
ganttgcaa ccacagcatc gaatttgtcc agaaggaagt ggtcgttggt gagggatttg
300
ccccattcaa tacgcgcac ttcccggaag cgcgcctcta ttgcggccaa cgcgt
355

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<210> 246
 <211> 101
 <212> PRT
 <213> Homo sapiens

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<400> 246
Met Arg Val Leu Asn Gly Ala Ile Pro Ser Pro Thr Thr Thr Ser Phe
      1           5           10           15
Trp Thr Asn Ser Met Leu Trp Leu Pro Xaa Pro Pro Thr Ala Trp Thr
      20           25           30
Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
      35           40           45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
      50           55           60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
65           70           75           80
Ile Arg Ala Arg His Cys Phe Gln Val Thr Pro Ala Glu Val Asn Pro
      85           90           95
Lys Leu Gly Gly Gly
      100

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<210> 247
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 247
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 120
 ttcttccact gctacaagcg cggagtggac cgcgtgttcg ttgaccaccc actgttctctg
 180
 gagagggttt ggggaaagac cgaggagaag atctacgggc ctgacgctgg aacggactac
 240
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 300
 ctgagcctca acaacaaccc atacttctcc gga
 333

<210> 248
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 248
 Met Ala Ala Asn Gly His Arg Val Met Val Val Ser Pro Arg Tyr Asp
 1 5 10 15
 Gln Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ser Glu Ile Lys Met
 20 25 30
 Gly Asp Arg Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys Arg Gly
 35 40 45
 Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp
 50 55 60
 Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr
 65 70 75 80
 Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu
 85 90 95
 Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser Gly
 100 105 110

<210> 249
 <211> 5503
 <212> DNA
 <213> Homo sapiens

<400> 249
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 120
 tcgccacgca ccgcatgcc cctgaacccc agccccgatg gtgaggccta cacactggct
 180
 tcgagaccac ccgtccgcct caatgatgtc atgctcaggc tggtagcgga gctgcgctgg
 240

cagaagttcg tcatgttcta cgacagcgag tatgatatacc gtgggcttca aagctttctg
300
gaccaggcct cgcggtggg ccttgacgtc tctttacaaa aggtggacaa gaacattagc
360
cacgtattca ccagcctgtt caccacgatg aagacagagg agctgaatcg ctaccgggac
420
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480
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 5503

<210> 250

<211> 927

<212> PRT

<213> Homo sapiens

<400> 250

Met	Thr	Gln	Gly	Ile	Leu	Ala	Leu	Val	Thr	Ser	Thr	Gly	Cys	Ala	Ser
1				5					10					15	
Ala	Asn	Ala	Leu	Gln	Ser	Leu	Thr	Asp	Ala	Met	His	Ile	Pro	His	Leu
			20					25					30		
Phe	Val	Gln	Arg	Asn	Pro	Gly	Gly	Ser	Pro	Arg	Thr	Ala	Cys	His	Leu
		35					40					45			
Asn	Pro	Ser	Pro	Asp	Gly	Glu	Ala	Tyr	Thr	Leu	Ala	Ser	Arg	Pro	Pro
	50				55						60				
Val	Arg	Leu	Asn	Asp	Val	Met	Leu	Arg	Leu	Val	Thr	Glu	Leu	Arg	Trp
65				70					75					80	
Gln	Lys	Phe	Val	Met	Phe	Tyr	Asp	Ser	Glu	Tyr	Asp	Ile	Arg	Gly	Leu
			85					90						95	
Gln	Ser	Phe	Leu	Asp	Gln	Ala	Ser	Arg	Leu	Gly	Leu	Asp	Val	Ser	Leu
			100					105					110		
Gln	Lys	Val	Asp	Lys	Asn	Ile	Ser	His	Val	Phe	Thr	Ser	Leu	Phe	Thr
			115					120					125		
Thr	Met	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Tyr	Arg	Asp	Thr	Leu	Arg	Arg
	130					135					140				
Ala	Ile	Leu	Leu	Leu	Ser	Pro	Gln	Gly	Ala	His	Ser	Phe	Ile	Asn	Glu
145					150					155				160	
Ala	Val	Glu	Thr	Asn	Leu	Ala	Ser	Lys	Asp	Ser	His	Trp	Val	Phe	Val
			165					170					175		
Asn	Glu	Glu	Ile	Ser	Asp	Pro	Glu	Ile	Leu	Asp	Leu	Val	His	Ser	Ala
			180					185					190		
Leu	Gly	Arg	Met	Thr	Val	Val	Arg	Gln	Ile	Phe	Pro	Ser	Ala	Lys	Asp
			195				200					205			
Asn	Gln	Lys	Cys	Thr	Arg	Asn	Asn	His	Arg	Ile	Ser	Ser	Leu	Leu	Cys
	210					215					220				
Asp	Pro	Gln	Glu	Gly	Tyr	Leu	Gln	Met	Leu	Gln	Ile	Ser	Asn	Leu	Tyr
225					230					235				240	
Leu	Tyr	Asp	Ser	Val	Leu	Met	Leu	Ala	Asn	Ala	Phe	His	Arg	Lys	Leu
				245				250						255	
Glu	Asp	Arg	Lys	Trp	His	Ser	Met	Ala	Ser	Leu	Asn	Cys	Ile	Arg	Lys

563

690 695 700
 Arg Ile Leu Glu Leu Gln Asp Thr Gly Asp Leu Asp Val Leu Lys Gln
 705 710 715 720
 Lys Trp Trp Pro His Met Gly Arg Cys Asp Leu Thr Ser His Ala Ser
 725 730 735
 Ala Gln Ala Asp Gly Lys Ser Leu Lys Leu His Ser Phe Ala Gly Val
 740 745 750
 Phe Cys Ile Leu Ala Ile Gly Leu Leu Leu Ala Cys Leu Val Ala Ala
 755 760 765
 Leu Glu Leu Trp Trp Asn Ser Asn Arg Cys His Gln Glu Thr Pro Lys
 770 775 780
 Glu Asp Lys Glu Val Asn Leu Glu Gln Val His Arg Arg Met Asn Ser
 785 790 795 800
 Leu Met Asp Glu Asp Ile Ala His Lys Gln Ile Ser Pro Ala Ser Ile
 805 810 815
 Glu Leu Ser Ala Leu Glu Met Gly Gly Leu Ala Pro Thr Gln Thr Leu
 820 825 830
 Glu Pro Thr Arg Glu Tyr Gln Asn Thr Gln Leu Ser Val Ser Thr Phe
 835 840 845
 Leu Pro Glu Gln Ser Ser His Gly Thr Ser Arg Thr Leu Ser Ser Gly
 850 855 860
 Pro Ser Ser Asn Leu Pro Leu Pro Leu Ser Ser Ser Ala Thr Met Pro
 865 870 875 880
 Ser Met Gln Cys Lys His Arg Ser Pro Asn Gly Gly Leu Phe Arg Gln
 885 890 895
 Ser Pro Val Lys Thr Pro Ile Pro Met Ser Phe Gln Pro Val Pro Gly
 900 905 910
 Gly Val Leu Pro Glu Ala Leu Asp Thr Ser His Gly Thr Ser Ile
 915 920 925

<210> 251

<211> 291

<212> DNA

<213> Homo sapiens

<400> 251

nngatcagcc gcgggggtccg cgccctcgat tcggcggtgg agaccgagag tctgcgtgag
 60
 gacgtcaacg cgctcgaacg gctgcggttg gccgtgcgcg ccagcgtggt catcctcatc
 120
 gagtaccacc attcgggtgac cctgctgctg cgggtgcgcg ggaactcacc tctggaacga
 180
 gaggccctcg aggcccgccg ccgtatcgat gcgaaggttc ccgctctcgt cgagagcgcc
 240
 atcgccgagg gtggtctgcg ctcggatttc actcccgggc tcatcacgcg t
 291

<210> 252

<211> 97

<212> PRT

<213> Homo sapiens

<400> 252

Xaa Ile Ser Arg Gly Val Arg Ala Leu Asp Ser Ala Val Glu Thr Glu

1 5 10 15
 Ser Leu Arg Glu Asp Val Asn Ala Leu Glu Arg Leu Arg Leu Ala Val
 20 25 30
 Arg Ala Ser Val Val Ile Leu Ile Glu Tyr His His Ser Val Thr Leu
 35 40 45
 Leu Leu Arg Val Arg Gly Asn Ser Pro Leu Glu Arg Glu Ala Leu Glu
 50 55 60
 Ala Arg Arg Arg Ile Asp Ala Lys Val Pro Ala Leu Val Glu Ser Ala
 65 70 75 80
 Ile Ala Glu Gly Gly Leu Arg Ser Asp Phe Thr Pro Gly Leu Ile Thr
 85 90 95
 Arg

<210> 253
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 253
 gtgcacggat gggagcgcctc gcgcgcgtgc tggcgccttc acagcccggc gagcggcggtg
 60
 cgctcacggc cctgtaccga ccgatctcgc aaccttcgcg agaccgatcc accaaccgcg
 120
 cccacatgtc ggcagtgatg gcgggcacct tgcgggagaa ggccgggaag gtcgagcgag
 180
 ccaatgaccg tcgcacggtc ggcacgctcc acgagcggga cgagaagctc gcggcaggac
 240
 gctcactcgt cgcggtgtcc tccgcggtct ccatcacctg ccctgcgaca tggaacgccc
 300
 acgacttcgg acggcgactc gacgcgt
 327

<210> 254
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 254
 Met Gly Ala Leu Ala Arg Val Leu Val Pro Ser Gln Pro Gly Glu Arg
 1 5 10 15
 Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
 20 25 30
 Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
 35 40 45
 Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
 50 55 60
 Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Gly Arg Ser Leu
 65 70 75 80
 Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
 85 90 95
 Ala His Asp Phe Gly Arg Arg Leu Asp Ala
 100 105

<210> 255
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 255
 ctagaaatgg ctggctacga atacatggaa gctgaaaata gccacaagc ccacgaaatt
 60
 atcgtggacc atagacctga cttaatctta tgtgattgga tgatgccagg agggagtggc
 120
 atcgagctaa ctcgtcgctt aaagaaagac agcacgacag cagaaatccc tgttatttta
 180
 ctaacggcca aaagtgaaga agacaataaa attcaaggct tagaagtcgg tgcagatgac
 240
 tacatcacta aacctttctc tcctcgtgaa ctagtagcac gcctcaaggc ggtattacgc
 300
 cgagcgactc cacaaggtat tgatgatcct attgaaattg atggtttaac gcttgatccc
 360
 attagccaac gc
 372

<210> 256
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 256
 Leu Glu Met Ala Gly Tyr Glu Tyr Met Glu Ala Glu Asn Ser Gln Gln
 1 5 10 15
 Ala His Glu Ile Val Asp His Arg Pro Asp Leu Ile Leu Cys Asp
 20 25 30
 Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys
 35 40 45
 Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Leu Thr Ala Lys
 50 55 60
 Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp
 65 70 75 80
 Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys
 85 90 95
 Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu
 100 105 110
 Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg
 115 120

<210> 257
 <211> 639
 <212> DNA
 <213> Homo sapiens

<400> 257
 nnacgcgtag cggtcgaggt tgcggacacc atgcccgaa cgggcctgct cgccatcgag
 60
 gcacccatgg gacacggcaa gaccgaggcc gccctcatgt gcgcacaggt gctcgccgaa
 120

cgggttcgggc tcggcggcat cttcttcggt ctaccgacga tggccacgtc caatcccatg
 180
 ttcgggtcgag ttcgggaatg gctggacgct gtgccagcca aggaccgctc aagcatttcc
 240
 ctgggtcact cgaaagctgg actcaacgag gagtaccagc agctcatgcc gtggaacgcc
 300
 accatggccg tctacgacga aggtgcccgc acgcagcgtg aagcttcggc gatcgtccat
 360
 gagtggttct tgggcccga ggcgcgcgatc ctggccgacc acgtcgtcgg gaccatcgac
 420
 caggcactgt tcaccggtct caaagccaag catgtggtgt tacgccacct cggctctggcg
 480
 agcaaggctc tcatcattga tgaggtccac gccgcgcgacg tctatatgcg cgaatacctc
 540
 aaggctcgtc tcgaatggct cgggcgcctac cgcacgccag tcatcctcat gtccgcgacg
 600
 ctgccaccgg cccaacgtca tgaactcgcg ctagcgtac
 639

<210> 258

<211> 213

<212> PRT

<213> Homo sapiens

<400> 258

Xaa	Arg	Val	Ala	Val	Glu	Val	Ala	Asp	Thr	Met	Pro	Glu	Pro	Gly	Leu
1			5						10					15	
Leu	Ala	Ile	Glu	Ala	Pro	Met	Gly	His	Gly	Lys	Thr	Glu	Ala	Ala	Leu
		20						25					30		
Met	Cys	Ala	Gln	Val	Leu	Ala	Glu	Arg	Phe	Gly	Leu	Gly	Gly	Ile	Phe
		35					40					45			
Phe	Gly	Leu	Pro	Thr	Met	Ala	Thr	Ser	Asn	Pro	Met	Phe	Gly	Arg	Val
	50					55					60				
Arg	Glu	Trp	Leu	Asp	Ala	Val	Pro	Ala	Lys	Asp	Pro	Ser	Ser	Ile	Ser
65				70					75					80	
Leu	Ala	His	Ser	Lys	Ala	Gly	Leu	Asn	Glu	Glu	Tyr	Gln	Gln	Leu	Met
			85					90						95	
Pro	Trp	Asn	Ala	Thr	Met	Ala	Val	Tyr	Asp	Glu	Gly	Ala	Gly	Thr	Gln
		100						105					110		
Arg	Glu	Ala	Ser	Ala	Ile	Val	His	Glu	Trp	Phe	Leu	Gly	Arg	Lys	Arg
		115					120					125			
Ala	Ile	Leu	Ala	Asp	His	Val	Val	Gly	Thr	Ile	Asp	Gln	Ala	Leu	Phe
	130					135					140				
Thr	Gly	Leu	Lys	Ala	Lys	His	Val	Val	Leu	Arg	His	Leu	Gly	Leu	Ala
145				150					155					160	
Ser	Lys	Val	Val	Ile	Ile	Asp	Glu	Val	His	Ala	Ala	Asp	Val	Tyr	Met
			165					170						175	
Arg	Glu	Tyr	Leu	Lys	Val	Val	Leu	Glu	Trp	Leu	Gly	Ala	Tyr	Arg	Thr
		180					185					190			
Pro	Val	Ile	Leu	Met	Ser	Ala	Thr	Leu	Pro	Pro	Ala	Gln	Arg	His	Glu
		195					200					205			
Leu	Ala	Leu	Ala	Tyr											
		210													

<210> 259
 <211> 252
 <212> DNA
 <213> Homo sapiens

<400> 259
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
 60
 ncatgggtgtg tgcacgtgtg cnaactgtgta tgcattggtaa tgtgcacgtg tgcantgtg
 120
 tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtgggggt gtatgcatgg
 180
 tgtgtgcaca tgagcactgt gtggtgtgta tgcattggtgn ggtgcacgtg tgcactgtgt
 240
 atgcaatggt gt
 252

<210> 260
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 260
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val
 35 40 45
 Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met
 50 55 60
 Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys
 65 70 75 80
 Met Gln Trp Cys

<210> 261
 <211> 1202
 <212> DNA
 <213> Homo sapiens

<400> 261
 gctagcccgg tcgcgttcgt cgtcgatttg ctggcggcag tcccctcgat cgtcttcggt
 60
 ctgtggggcg gcacgtctct cggatcgteg ggaatcatca acggttacgc gggggcctta
 120
 ttcaaagcgc tcggctggat tccgatcttt tccgaagatc cgtcgtggtc ctcggtact
 180
 ggcacggtct accttgccag tctcgtcctg gccatcatga tcctgccaat tatcactgct
 240
 gttagccgcg acgtcatgcc ccgaacgccc catgatcaag tcgaggccgc gctcgccttc
 300
 ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtccggcatc
 360

atttccggat ccattgttggg tctaggacgc gccctcggcg agaccctggc tgtcacccctc
 420
 atcctgcaga cgatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc
 480
 ggtggtgaga cattcgcgctc gaagattgcc ggtaacttct ccgaggccat tagcgatccc
 540
 acctcgctgg gtgccctcgt ggcgtcggcc ctggccctgt tcgtcattac cttcgtggtc
 600
 aacgcgactg cccggttgat tgcggcgaag ggggttaagc gatgagcgcc accaccctg
 660
 accacatcac ccaccatggc gacaacacgc ccggacagct agatctctcc cgcccgctctg
 720
 gtaaacggac tatcaagagc ggctgcgcct caacattcat gatcgtggcc accgtactgg
 780
 ctgttatccc actggcctgg ctgctcttcg cggccgtccg gcgcggcacc ggatcactat
 840
 tccacgcgtc gtggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg
 900
 ccatccacgc tatcgtcgga acccttgaaa ttggccttat tacatcgatt atctcggtac
 960
 cgatcgctct gatgaccgcg atcttcttag tcgagtacgc ccgcggaact aagatcgcca
 1020
 aggtcattag cttcgcgcgc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct
 1080
 tcgtcttcgc cgtagtcggt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt
 1140
 tggecctcat gatcctcatg gttccgacgg tgctgcgac aaccgaggaa atgctcaage
 1200
 tt
 1202

<210> 262

<211> 214

<212> PRT

<213> Homo sapiens

<400> 262

Ala	Ser	Pro	Val	Ala	Phe	Val	Val	Asp	Leu	Leu	Ala	Ala	Val	Pro	Ser
1			5					10					15		
Ile	Val	Phe	Gly	Leu	Trp	Gly	Gly	Ile	Val	Phe	Gly	Ser	Ser	Gly	Ile
		20					25					30			
Ile	Asn	Gly	Tyr	Ala	Gly	Ala	Leu	Phe	Lys	Ala	Leu	Gly	Trp	Ile	Pro
	35					40					45				
Ile	Phe	Ser	Glu	Asp	Pro	Ser	Trp	Ser	Ser	Ala	Thr	Gly	Thr	Val	Tyr
	50				55					60					
Leu	Ala	Ser	Leu	Val	Leu	Ala	Ile	Met	Ile	Leu	Pro	Ile	Ile	Thr	Ala
65				70				75					80		
Val	Ser	Arg	Asp	Val	Met	Pro	Arg	Thr	Pro	His	Asp	Gln	Val	Glu	Ala
		85					90					95			
Ala	Leu	Ala	Leu	Gly	Ser	Thr	Arg	Trp	Glu	Val	Ile	Lys	Leu	Ala	Val
	100						105					110			
Phe	Pro	His	Ser	Arg	Ser	Gly	Ile	Ile	Ser	Gly	Ser	Met	Leu	Gly	Leu
	115					120					125				
Gly	Arg	Ala	Leu	Gly	Glu	Thr	Leu	Ala	Val	Thr	Leu	Ile	Leu	Gln	Thr

```

      130              135              140
Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val
145              150              155              160
Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala
      165              170              175
Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala
      180              185              190
Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala
      195              200              205
Ala Lys Gly Val Lys Arg
      210

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<210> 263
 <211> 424
 <212> DNA
 <213> Homo sapiens

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<400> 263
acgcgtgagt gctctgcgct ggaaacaacg gtgatagagc ccatccgcgc tgaactttcc
60
gacgtggtgc tcgtgaacaa gctcgaaaag tatgtacgcg aacgtacctc ggaagacggt
120
gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcacgac gatcctgctg
180
tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaaag
240
gcttatatgg cctcgccatt ccgtgccaat ttggacctgg catacccatc ttcgacgcca
300
caggcccagt ccagccggc gatgccgcgc tgggagacag ggacctcagc cagtagcatg
360
gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgct gcagaagcac
420
gann
424

```

<210> 264
 <211> 99
 <212> PRT
 <213> Homo sapiens

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<400> 264
Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile
1      5      10      15
Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His
      20      25      30
Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn
      35      40      45
Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro
      50      55      60
Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp
65      70      75      80
Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln
      85      90      95
Lys His Xaa

```

<210> 265
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 265
 ncgtacggcc ctggcgctccg catggacgag ggataccatt ccggcatgac ggtgccgggt
 60
 gccttcgact ccctcatcgg caagctcacc atcactgggtg atagccgtga gcaagccctg
 120
 gctcgagctg cccgcgccct cgacgaaatc gtcacgacg gcatgccgac ggtcattccc
 180
 tttcaccagg cgggtggttca cgacccggct ttcactgccg ccgacggctg cttcggcgct
 240
 tttaccgact ggatcgaaac cgagttcgac aacaagatcg agccatacac cgggtctctg
 300
 ggcgagctcg ccaattccga gcctcctcgt gaggtcgtcg tcgaggtaa cggtaaacgc
 360

<210> 266
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 266
 Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met
 1 5 10 15
 Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr
 20 25 30
 Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Ala Arg Ala Leu Asp
 35 40 45
 Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala
 50 55 60
 Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val
 65 70 75 80
 Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr
 85 90 95
 Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val
 100 105 110
 Val Val Glu Val Asn Gly Lys Arg
 115 120

<210> 267
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 267
 natcctcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg
 60
 ttaacgcac ctagtcaatc caccgatggc gaccctggca aaaaatacga ggtgacttgg
 120

ctagatctcg ggcaccttca ccctagtcgg cggggactcg tcactatcac cacaactgtc
 180
 gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa
 240
 aaacttttcg aagctcgcca ttaccgccag attccgatgc ttgcatcacg tcatggctgg
 300
 acagctccat tcattggtga gaccggcgca gcccatgcca tcgaggatgc gatgggcatt
 360
 accatcccaa ctgcgtggc atggatacga acctgctcg ctgagttcag cagaatcacc
 420
 tcacacttca catttttgtc atgggtaggc catcactgtg atgatgccgg c
 471

<210> 268

<211> 157

<212> PRT

<213> Homo sapiens

<400> 268

Xaa	Pro	Gln	Arg	Val	Phe	Ser	Ser	Thr	Arg	Lys	Ile	Met	Phe	Val	Ile
1				5				10					15		
Gly	Ser	Met	Pro	Leu	Thr	His	Pro	Ser	Gln	Ser	Thr	Asp	Gly	Asp	Pro
			20					25					30		
Gly	Lys	Lys	Tyr	Glu	Val	Thr	Trp	Leu	Asp	Leu	Gly	His	Leu	His	Pro
		35				40						45			
Ser	Arg	Pro	Gly	Leu	Val	Thr	Ile	Thr	Thr	Thr	Val	Asp	Asp	Asp	Val
	50					55					60				
Ile	Thr	Ser	Ser	Gln	Val	Asn	Val	Gly	Asn	Leu	His	Arg	Gly	Asp	Glu
65				70					75					80	
Lys	Leu	Phe	Glu	Ala	Arg	Asp	Tyr	Arg	Gln	Ile	Pro	Met	Leu	Ala	Ser
			85					90					95		
Arg	His	Gly	Trp	Thr	Ala	Pro	Phe	Ile	Gly	Glu	Thr	Gly	Ala	Ala	His
			100					105					110		
Ala	Ile	Glu	Asp	Ala	Met	Gly	Ile	Thr	Ile	Pro	Thr	Arg	Val	Ala	Trp
		115				120						125			
Ile	Arg	Thr	Leu	Leu	Ala	Glu	Phe	Ser	Arg	Ile	Thr	Ser	His	Phe	Thr
	130					135					140				
Phe	Leu	Ser	Trp	Val	Gly	His	His	Cys	Asp	Asp	Ala	Gly			
145					150						155				

<210> 269

<211> 387

<212> DNA

<213> Homo sapiens

<400> 269

acgcgtgtcg tgtttccaga aaaaaccaat aaattagagt ttatggtaga agtgattgct
 60
 gatatgacgg taatcaatcc atttgatttc tttgtggaaa gctacgcaga agactaccca
 120
 tttgcttatg acaaagctct taaaaaagag ttagaacctt atttacaggt ttctgaacct
 180
 tgttcgttac tcgacaaatg gctgtctggt gttgatcgtg aaaaaacacc gatcaatgat
 240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatggat tcgcttagaa
 300
 ccgggcgttc agtcacctga agaaacgctc acattaatga aaggctcttg tcgcgatacc
 360
 tcgggggttat tgggtcaaact actacgc
 387

<210> 270

<211> 129

<212> PRT

<213> Homo sapiens

<400> 270

Thr	Arg	Val	Val	Phe	Pro	Glu	Lys	Thr	Asn	Lys	Leu	Glu	Phe	Met	Val
1				5					10					15	
Glu	Val	Ile	Ala	Asp	Met	Thr	Val	Ile	Asn	Pro	Phe	Asp	Phe	Phe	Val
		20					25					30			
Glu	Ser	Tyr	Ala	Glu	Asp	Tyr	Pro	Phe	Ala	Tyr	Asp	Lys	Ala	Leu	Lys
	35					40					45				
Lys	Glu	Leu	Glu	Pro	Tyr	Leu	Gln	Val	Ser	Glu	Pro	Cys	Ser	Leu	Leu
	50				55					60					
Asp	Lys	Trp	Leu	Ser	Gly	Val	Asp	Arg	Glu	Lys	Thr	Pro	Ile	Asn	Asp
65					70				75					80	
Phe	Leu	Val	Ala	Ile	Asn	Ser	Arg	Leu	Ala	Gly	Asp	Ile	Gly	Tyr	Gly
			85					90					95		
Ile	Arg	Leu	Glu	Pro	Gly	Val	Gln	Ser	Pro	Glu	Glu	Thr	Leu	Thr	Leu
		100					105					110			
Met	Lys	Gly	Ser	Cys	Arg	Asp	Thr	Ser	Gly	Leu	Leu	Val	Gln	Ile	Leu
		115					120					125			

Arg

<210> 271

<211> 443

<212> DNA

<213> Homo sapiens

<400> 271

gccggcacca acggaaagtc ctctaccgcg cgcattggctg attcgctttt gcgtgccttc
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 caccgcccag tgggttttgg aaccagccca cacctgcagc gcgttactga gcgcatcggc
 120
 attgatggcc agcccattca cccgcgcgat tatgtacgca tctggcacga gattaagcca
 180
 tttgtggaaa tggtcgatgc cgaatcggac gtgcctatgt ctaagtccga ggtcttcgtg
 240
 ggctgtcct atgctgcgtt tgccgacgcc cccggggacg tcgctgtcgt cgaagtcggc
 300
 cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattaccccg
 360
 gtgggcatgg accacacgga ttacctgggg gagacgatca ctgaaatcgc aggcgagaaa
 420
 gctggcatta ttaagccacg cgt
 443

<210> 272
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 272
 Ala Gly Thr Asn Gly Lys Ser Ser Thr Ala Arg Met Val Asp Ser Leu
 1 5 10 15
 Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu
 20 25 30
 Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro
 35 40 45
 Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met
 50 55 60
 Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val
 65 70 75 80
 Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val
 85 90 95
 Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn
 100 105 110
 Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr
 115 120 125
 Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile
 130 135 140
 Lys Pro Arg
 145

<210> 273
 <211> 864
 <212> DNA
 <213> Homo sapiens

<400> 273
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 60
 aagagaagcc aaagcccccc cccccacct caaaggctcg gaagtctggc atccctactt
 120
 ccgagcctgg atcccagtaa ggatcttgcc ctccctgcaa caccgagtgc cttagacagc
 180
 tgctgctga gaactggcct ccagccggtg tcctcattcc atggggctcc ctgctgactg
 240
 catttctga tctgggatga tgtttaccag cccaaaacca gtcattgtct tccaaaagct
 300
 tctctttgat agaattttga ggccatgcca cctcccttcc agtccacatg gaattccaga
 360
 atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaatgtca
 420
 gcctgtacgg cagagacatg gtggtctgca caagcctgga caagttcttc catattgatg
 480
 gtgggagcaa cccctgtaat ctactccttg gaaggatttt ttgctttgct tatgaaaagc
 540
 tgtgcttgag acttaggtac ttttctcacg tggacacact gatcccatcc catattgcat
 600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatcatat ctttctgatg
 660
 tctattgtat ctcttttgag gaaaagaaca cacattttta atggagattg gctgctttca
 720
 ggtatgtgtg tctatcattg aaagagcatg gactcaaaca tcagccctga gttcttgagt
 780
 ccaccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac
 840
 tcctgactaa tgcccttcac gcgt
 864

<210> 274
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 274
 Met Trp Thr Gly Arg Glu Val Ala Trp Pro Gln Asn Ser Ile Lys Glu
 1 5 10 15
 Lys Leu Leu Glu His Asp Trp Phe Trp Ala Gly Lys His His Pro
 20 25 30
 Arg Ser Gly Asn Ala Val Ser Arg Glu Pro His Gly Met Arg Thr Pro
 35 40 45
 Ala Gly Gly Gln Phe Ser Gly Ser Ser Cys Leu Arg His Ser Val Leu
 50 55 60
 Gln Gly Gly Gln Asp Pro Tyr Trp Asp Pro Gly Ser Glu Val Gly Met
 65 70 75 80
 Pro Asp Phe Arg Ala Phe Glu Val Gly Gly Gly Phe Gly Phe Ser
 85 90 95
 Ser Thr Ala Gly Ser Glu Leu Gln Ser Arg Thr Gln Asn Leu Lys
 100 105 110
 Gln Ser Tyr Phe
 115

<210> 275
 <211> 911
 <212> DNA
 <213> Homo sapiens

<400> 275
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 60
 ttatttttcag gaatgaaagg aattaccag ccttctgctt ttatacctac agctgaaagt
 120
 aattcctttc agcctcaggt gaagactttg ccattctcaa ttgatgctaa acagcagttg
 180
 caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccctt gccaggagaa
 240
 tctgcagcaa aaaagtcaga aagtgtaca agcaatggag tgactaatct tcctaattgga
 300
 aatccttcaa tcctttctcc tcaacctatt ggtatcggtg tggcagctgt ccctagtccc
 360
 attccggtcc agcggactag gcaattggta acttcaccga gtccaatgag ttcttctnga
 420

cggcaaagtt cttccctca atgtacaggt ggtcactcag cacatgcagt ctgtgaaaca
 480
 ggcaccaaag actccccaga acgttccagc agtcctggtg ggaatcggtc tgcccggcac
 540
 cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgctctcca
 600
 actactgtcc tctttactag tagtcccatc aaaactgctg ttgtaccgcg ttcacacatg
 660
 agttctctaa atgtggtgaa aatgacaaca atatccctca caccagcaa cagtaacacc
 720
 cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt
 780
 gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctctggggtc caggagcagc
 840
 agtgcggggg gaacatctgc tgtggaagtc aaagtggaac ccgaaacatc atcagatgag
 900
 catcctgtac a
 911

<210> 276
 <211> 279
 <212> PRT
 <213> Homo sapiens

<400> 276
 Met Lys Gly Ile Thr Gln Pro Ser Ala Phe Ile Pro Thr Ala Glu Ser
 1 5 10 15
 Asn Ser Phe Gln Pro Gln Val Lys Thr Leu Pro Ser Pro Ile Asp Ala
 20 25 30
 Lys Gln Gln Leu Gln Arg Lys Ile Gln Lys Lys Gln Gln Glu Gln Lys
 35 40 45
 Leu Gln Ser Pro Leu Pro Gly Glu Ser Ala Ala Lys Lys Ser Glu Ser
 50 55 60
 Ala Thr Ser Asn Gly Val Thr Asn Leu Pro Asn Gly Asn Pro Ser Ile
 65 70 75 80
 Leu Ser Pro Gln Pro Ile Gly Ile Val Val Ala Ala Val Pro Ser Pro
 85 90 95
 Ile Pro Val Gln Arg Thr Arg Gln Leu Val Thr Ser Pro Ser Pro Met
 100 105 110
 Ser Ser Ser Xaa Arg Gln Ser Ser Ser Pro Gln Cys Thr Gly Gly His
 115 120 125
 Ser Ala His Ala Val Cys Glu Thr Gly Thr Lys Asp Ser Pro Glu Arg
 130 135 140
 Ser Ser Ser Pro Gly Gly Asn Arg Ser Ala Arg His Arg Tyr Pro Gln
 145 150 155 160
 Ile Leu Pro Lys Pro Ala Asn Thr Ser Ala Leu Thr Ile Arg Ser Pro
 165 170 175
 Thr Thr Val Leu Phe Thr Ser Ser Pro Ile Lys Thr Ala Val Val Pro
 180 185 190
 Ala Ser His Met Ser Ser Leu Asn Val Val Lys Met Thr Thr Ile Ser
 195 200 205
 Leu Thr Pro Ser Asn Ser Asn Thr Pro Leu Lys His Ser Ala Ser Val
 210 215 220
 Ser Ser Ala Thr Gly Thr Thr Glu Glu Ser Arg Ser Val Pro Gln Ile

<400> 278																
Met	Ser	Glu	Val	Pro	Asp	Glu	Leu	Val	Val	Leu	Arg	Gly	Ala	Ile	Asp	
1				5					10					15		
Asn	Met	Asp	Ala	Leu	Ile	His	Leu	Leu	Ala	Glu	Arg	Phe	Arg	Ile		
			20				25					30				
Thr	Arg	Glu	Val	Gly	Arg	Leu	Lys	Ala	Glu	Cys	Gly	Leu	Pro	Pro	Ala	
		35				40					45					
Asp	Pro	Ala	Arg	Glu	Ala	Glu	Gln	Ile	Ala	Arg	Leu	Arg	Gln	Leu	Ala	
	50				55					60						
Val	Glu	Ser	Asn	Leu	Asp	Pro	Glu	Phe	Ala	Gln	Lys	Val	Ile	Thr	Phe	
65				70					75					80		
Ile	Val	Ala	Glu	Val	Val	Arg	His	His	Glu	Ala	Ile	Ala	Asp	Asp	Ser	

85 90 95
 Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly
 100 105 110
 Ser Gly Ser
 115

<210> 279
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 279
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 taccacaatc cttaaaaaga aaagaaagaa aggcataatgg aaccacctagt tacctctcat
 120
 ccagcttcaa aattgtcagt gcatgggtcaa tcttgtctta tctgcccctc acccaccctt
 180
 ttccagaaag aagaccaga ggattccaca tctgcctgga aaccacgacc agtctcgact
 240
 ggaagttggt gttaatgttg catgtattca taaaacctct aggcatttct agtgtccctc
 300
 agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt
 348

<210> 280
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 280
 Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr
 1 5 10 15
 Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp
 20 25 30
 Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg
 35 40 45
 Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp
 50 55 60
 Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser
 65 70 75 80
 Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu
 85 90 95
 Pro Lys Ile

<210> 281
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 281
 agatctgcgc agatcgataa tggattaaag actcttgacg ctggagtcac cgagatgaac
 60

aacaagggtgt tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccagggtg
 120
 aattctgcgt taggaantgc cgactcagcg gcagagaaga cgtcgagcgc cgttactcag
 180
 acgcgcgtgg gtgcccaggc gattaccggc gctgctcaaa atgtcatggc tgattcccaa
 240
 gctgtcaact cagccatggt tccgcttatt aataacgtga caaagaatct tcctaccttg
 300
 caaaaacagg ccaggaatct cgtgtcagtg aacggtaccc tgcagaaccc caacggtgat
 360
 tctgtcatta agattcaaca gacc
 384

<210> 282
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 282
 Met Asn Asn Lys Val Leu Gly Ala Thr Lys Ala Val Gly Asp Ser Thr
 1 5 10 15
 Thr Thr Val Asn Gln Val Asn Ser Ala Leu Gly Xaa Ala Asp Ser Ala
 20 25 30
 Ala Glu Lys Thr Ser Ser Ala Val Thr Gln Thr Arg Val Gly Ala Gln
 35 40 45
 Ala Ile Thr Gly Ala Ala Gln Asn Val Met Ala Asp Ser Gln Ala Val
 50 55 60
 Asn Ser Ala Met Val Pro Leu Ile Asn Asn Val Thr Lys Asn Leu Pro
 65 70 75 80
 Thr Leu Gln Lys Gln Ala Arg Asn Leu Val Ser Val Asn Gly Thr Leu
 85 90 95
 Gln Asn Pro Asn Gly Asp Ser Val Ile Lys Ile Gln Gln Thr
 100 105 110

<210> 283
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 283
 cgcgtagacc aatgtgagac ggccgtcacc aagggcatgc gcgacaagtc gggttggtagc
 60
 ggaccggata ttgtgcgtcg cgagctgcgc catgtcgtga cgagcggcac gattgtcgat
 120
 ggaagcgtac tggctgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc
 180
 tctgatggcc tatccgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga
 240
 tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgttctcta
 300
 cgcacaaagg aagtcttgca tgaaaaaggg gtcattgttc cttccacgct gcgcttgatc
 360
 cgcaacgcgg tgcccaccac ctgccaaatt accatgctca agcctgatac cgaattgtcg
 420

gagaga
426

<210> 284
<211> 142
<212> PRT
<213> Homo sapiens

<400> 284
Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys
1 5 10 15
Ser Val Gly Ser Gly Pro Asp Ile Val Arg Arg Glu Leu Arg His Val
20 25 30
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu
35 40 45
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu
50 55 60
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Ala Thr Ala Glu Phe Arg
65 70 75 80
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu
85 90 95
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met
100 105 110
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys
115 120 125
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg
130 135 140

<210> 285
<211> 345
<212> DNA
<213> Homo sapiens

<400> 285
acgcgtgcag tcccttaccg acatgctggc agatgagctc gacggcagcc gcttcaccgg
60
cgattttctca gaaatctaca aacgtcagaa ctcgatcttc ggcgatgtaa ggaataactt
120
ttacaaaaaa ggataccgca tcatcaacgt agcgaatggt gtattgcgca agatttcact
180
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgttcttcc gcggtgtggc
240
gcatttcgaa ctcggtgcgtt tgtttgcaca accctgggggt tatacttcgg acaattcaca
300
ctacggcatc ccgctccgca atgaaatcgt aattggttct attcn
345

<210> 286
<211> 107
<212> PRT
<213> Homo sapiens

<400> 286
Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

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      1           5           10           15
Glu Ile Tyr Lys Arg Gln Asn Ser Ile Phe Gly Asp Val Arg Asn Asn
      20           25           30
Phe Tyr Lys Lys Gly Tyr Arg Ile Ile Asn Val Ala Asn Gly Val Leu
      35           40           45
Arg Lys Ile Ser Leu Val Ser Ala Gly Asn Ala Asp Asn Val Lys Gly
      50           55           60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe Glu Leu Val Arg Leu
      65           70           75           80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr Gly Ile
      85           90           95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile
      100           105

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<210> 287

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 287

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nnttaactgc ccctttgcag tctttattct gggacattag cactgtcttg ttatcttgct
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tcagttgagg gattcgggac aatagcagtg ctgatggtaa tgttgccgat ttccctgttt
120
gttttgcagg tcacggccag gggctttggg ccgctgttac agtttgccta cactgccaaag
180
ctgttactca gcagagaaaa catccgcgag gtcacccgct gtgctgagtt cctgcgcagtg
240
cacaacctgg aggactcctg cttcagcttc ctgcagaccc agctcctgaa cagtgaggat
300
ggcctgtttg tgtgccggaa ggatgctgcg tgccagcgcc cacacgagga ctgcgagaac
360
tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
420
gcttgcccca gggaccagat gcttcagag cccatcagct ttgaggccgc cgccatcccc
480
gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
540
agctcagaaa aggacgcgtt aacgcagtac ccagataca agaaatacca gcttgcatgt
600
accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
660
gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagttag
720
ccgcccagtg aagagaatga ggaagagagc atcacgctct gcctgtcttg agatgagcct
780
gacgccaagg acagagcggg ggatgtcgag atggaccgga aacagcccag ccctgcccct
840
acccccacgg ccccagctgg ggccgctgct ctggagagat ccaggagcgt ggctcgcgcc
900
tcctgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtcttg cctgcccagt
960
acatctcagc agcactttgc caggagtcca gcctgccctt ttgacaaggg gatcactcag
1020

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ggtgacctta aaactgacta cacccttttc acaggggaatt atggacagcc ccacgtgggc
 1080
 cagaaggagg tgtccaactt caccatgggg tcgcccctca gggggcctgg gttggaggct
 1140
 ctctgtaaac aggagggaga gctggaccgg aggagcgtga tcttctcctc cagcgcttgt
 1200
 gaccaagtga gcacctcggt gcattcttat tctgggggtga gcagtttggg caaagacctc
 1260
 tctgagccgg tgccaaaggg tctgtgggtg ggagccggcc agtccctccc cagctcgcag
 1320
 gcctactccc acgggtgggt gatggccgac cacttgccag gaaggatgcg gcccaacac
 1379

<210> 288

<211> 428

<212> PRT

<213> Homo sapiens

<400> 288

Met	Val	Met	Leu	Ala	Ile	Ser	Leu	Phe	Val	Leu	Gln	Val	Thr	Ala	Arg
1				5					10					15	
Gly	Phe	Gly	Pro	Leu	Leu	Gln	Phe	Ala	Tyr	Thr	Ala	Lys	Leu	Leu	Leu
			20					25					30		
Ser	Arg	Glu	Asn	Ile	Arg	Glu	Val	Ile	Arg	Cys	Ala	Glu	Phe	Leu	Arg
		35				40						45			
Met	His	Asn	Leu	Glu	Asp	Ser	Cys	Phe	Ser	Phe	Leu	Gln	Thr	Gln	Leu
	50					55					60				
Leu	Asn	Ser	Glu	Asp	Gly	Leu	Phe	Val	Cys	Arg	Lys	Asp	Ala	Ala	Cys
65				70					75					80	
Gln	Arg	Pro	His	Glu	Asp	Cys	Glu	Asn	Ser	Ala	Gly	Glu	Glu	Glu	Asp
			85					90						95	
Glu	Glu	Glu	Glu	Thr	Met	Asp	Ser	Glu	Thr	Ala	Lys	Met	Ala	Cys	Pro
			100					105					110		
Arg	Asp	Gln	Met	Leu	Pro	Glu	Pro	Ile	Ser	Phe	Glu	Ala	Ala	Ala	Ile
		115				120						125			
Pro	Val	Ala	Glu	Lys	Glu	Glu	Ala	Leu	Leu	Pro	Glu	Pro	Asp	Val	Pro
	130					135					140				
Thr	Asp	Thr	Lys	Glu	Ser	Ser	Glu	Lys	Asp	Ala	Leu	Thr	Gln	Tyr	Pro
145				150					155					160	
Arg	Tyr	Lys	Lys	Tyr	Gln	Leu	Ala	Cys	Thr	Lys	Asn	Val	Tyr	Asn	Ala
			165					170						175	
Ser	Ser	His	Ser	Thr	Ser	Gly	Phe	Ala	Ser	Thr	Phe	Arg	Glu	Asp	Asn
		180					185						190		
Ser	Ser	Asn	Ser	Leu	Lys	Pro	Gly	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Ser
		195					200					205			
Glu	Pro	Pro	Ser	Glu	Glu	Asn	Glu	Glu	Glu	Ser	Ile	Thr	Leu	Cys	Leu
	210					215					220				
Ser	Gly	Asp	Glu	Pro	Asp	Ala	Lys	Asp	Arg	Ala	Gly	Asp	Val	Glu	Met
225				230					235					240	
Asp	Arg	Lys	Gln	Pro	Ser	Pro	Ala	Pro	Thr	Pro	Thr	Ala	Pro	Ala	Gly
			245					250						255	
Ala	Ala	Cys	Leu	Glu	Arg	Ser	Arg	Ser	Val	Ala	Ser	Pro	Ser	Cys	Leu
		260					265						270		
Arg	Ser	Leu	Phe	Ser	Ile	Thr	Lys	Ser	Val	Glu	Leu	Ser	Gly	Leu	Pro

275	280	285
Ser Thr Ser Gln Gln His Phe Ala Arg Ser Pro Ala Cys Pro Phe Asp		
290	295	300
Lys Gly Ile Thr Gln Gly Asp Leu Lys Thr Asp Tyr Thr Pro Phe Thr		
305	310	315
Gly Asn Tyr Gly Gln Pro His Val Gly Gln Lys Glu Val Ser Asn Phe		
325	330	335
Thr Met Gly Ser Pro Leu Arg Gly Pro Gly Leu Glu Ala Leu Cys Lys		
340	345	350
Gln Glu Gly Glu Leu Asp Arg Arg Ser Val Ile Phe Ser Ser Ser Ala		
355	360	365
Cys Asp Gln Val Ser Thr Ser Val His Ser Tyr Ser Gly Val Ser Ser		
370	375	380
Leu Asp Lys Asp Leu Ser Glu Pro Val Pro Lys Gly Leu Trp Val Gly		
385	390	395
Ala Gly Gln Ser Leu Pro Ser Ser Gln Ala Tyr Ser His Gly Gly Leu		
405	410	415
Met Ala Asp His Leu Pro Gly Arg Met Arg Pro Asn		
420	425	

<210> 289

<211> 822

<212> DNA

<213> Homo sapiens

<400> 289

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120

agcaagtcca aggcgaagga cgagcgcact gccgatgaga tcaggcggga tattgcagcg
180

accctgtgctt gcctggcagc cggggtggag aacctcgtgg aggaggtgca tccggcaacc
240

ctcaagcgtg aagcatctga tcgtgcccgt gattttgtgc aggggtgagtt tgatcaggtc
300

aagagccagg tcaaagatga gaaatggtgg cgcgtgcagc ggatcgcgat ggccgcagga
360

gtgctcgctg ccggcgtcgt cagcattatt gtgctgcgcg cgatagtcgg tcgcgcaacg
420

ggcgctaccg ctgcgcgcaa gcttgagaag ctgcagcttt ctcaggcgaa gcgggttcga
480

aaagatgccca agcagcgtag taaggaagat gaaaaggcag ccaagaaaaa tgccaagctc
540

ggcaagaaga acgctaagaa gtacggcaag ctcgataccg atgactcgtc ggtaagcaac
600

cttgccgaga aaatgctcaa acaggccgcc gtgctgcgtg cacaggcggc tgccggggcg
660

tgagaacagt gccgcctagc aaacagcggc cacagcgcaa aacaggtttg gctccgaccc
720

atgggtggacc ggagccaaac tgtgttaccg catcatttga taccgccagc agccaggcct
780

gcgacaatgc gacgctggaa taccagcacc atgatgacta gt
822

<210> 290
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 290
 Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu
 1 5 10 15
 Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val
 20 25 30
 Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala
 35 40 45
 Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys
 50 55 60
 Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met
 65 70 75 80
 Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg
 85 90 95
 Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu
 100 105 110
 Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln
 115 120 125
 Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly
 130 135 140
 Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser
 145 150 155 160
 Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg
 165 170 175
 Ala Gln Ala Ala Ala Gly Ala
 180

<210> 291
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 291
 ctccacgccg acaagactta cgacgggcgt cgctgccggg ctgagtgcgc ggcccgcctcc
 60
 atcacccccc gcatcgctcg ccgcggcggtg gagaccagcg agcgcttggg ccggtatcgc
 120
 tgggtcgctg agcgcacctt cgcctggctc aaccgctttc ggcgccctcgc catccgctac
 180
 gagcggcggtg ctgacatcca cgaagccttc gtgacccctg gctgcgcctt catctgcctc
 240
 aaccagatca gacggttttg ttaggtgctg taaagggaga atggctgcag ctgggctatc
 300
 tgctccctcg tcaaccagaa acaggctgct catcctcact caacaacgcg t
 351

<210> 292
 <211> 87
 <212> PRT

<213> Homo sapiens

<400> 292

```

Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
 1           5           10           15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
          20           25           30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
          35           40           45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
          50           55           60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
65           70           75           80
Asn Gln Ile Arg Arg Phe Cys
          85

```

<210> 293

<211> 716

<212> DNA

<213> Homo sapiens

<400> 293

```

nncttcacca caccggccat caacgcacct cctcgtgata acttgacett ctgccgaacc
60
ggttaatcag tttagtggcg aggcattgaca cgttgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cggcatgttg ctgtcgggtca cgacccttat ggtgatcgct
180
gtgagaaccc gaacggcaga tgcgattctg gcggcactgg atctgaacag gtttaagggt
240
gcgaagactt tcgatgttcc agtgtgctgc atagctggtg ccgggacagg taaaactcgt
300
gctgtcactc atcgcattgc ctacgggtgca gcgacaggca agcttgatcc gcgtcgtacc
360
ctcgcgggtca cttttacgac taaggcagct ggcacgatga gaggtcgact cgccgatctg
420
gggggttggtg gtgtgcaggc tcgcactatt cattctgcgg cgttgcggca gatcaagttt
480
ttctggcctc gtgcatataa ctgtgagttg ccaccggtga gtgattctcg tttctcgatg
540
gtggcgggaga cgacccatcg cattggtctg ggcaatgaca aggcgctgct gcgcgacttg
600
tccgcccgaga tctcgtgggc gaaggtctca aatgtgccga ctgatcaata cgcacccctg
660
gctagggcgg aaggtcgggt ggtggcggga gtttcggcaa ctgacgtagg acgcgt
716

```

<210> 294

<211> 190

<212> PRT

<213> Homo sapiens

<400> 294

```

Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

```

```

      1           5           10           15
Thr Ala Asp Ala Ile Leu Ala Ala Leu Asp Leu Asn Arg Phe Lys Val
      20           25           30
Ala Lys Thr Phe Asp Val Pro Val Cys Val Ile Ala Gly Ala Gly Thr
      35           40           45
Gly Lys Thr Arg Ala Val Thr His Arg Ile Ala Tyr Gly Ala Ala Thr
      50           55           60
Gly Lys Leu Asp Pro Arg Arg Thr Leu Ala Val Thr Phe Thr Thr Lys
      65           70           75           80
Ala Ala Gly Thr Met Arg Gly Arg Leu Ala Asp Leu Gly Val Val Gly
      85           90           95
Val Gln Ala Arg Thr Ile His Ser Ala Ala Leu Arg Gln Ile Lys Phe
      100          105          110
Phe Trp Pro Arg Ala Tyr Asn Cys Glu Leu Pro Pro Val Ser Asp Ser
      115          120          125
Arg Phe Ser Met Val Ala Glu Thr Thr His Arg Ile Gly Leu Gly Asn
      130          135          140
Asp Lys Ala Leu Leu Arg Asp Leu Ser Ala Glu Ile Ser Trp Ala Lys
      145          150          155          160
Val Ser Asn Val Pro Thr Asp Gln Tyr Ala Ser Leu Ala Arg Ala Glu
      165          170          175
Gly Arg Val Val Ala Gly Val Ser Ala Thr Asp Val Gly Arg
      180          185          190

```

<210> 295
 <211> 417
 <212> DNA
 <213> Homo sapiens

```

<400> 295
ttcatatcag gcagtacccg agtccatgcg atcaacaacg tcagcgtatc tttcacccat
60
tctggagtgc accttctcat gggagaaagc ggatcaggaa aaagcaccct catcaatctc
120
ctagctggtc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
180
gatcagagcg aggcgagcag agcccaatct cgattacgcc acatcgccgt catcttccag
240
gacgacaacc tcatcgctga gttgaccaat accgagaata ttgcgctacc cctgtgggag
300
cagggcacat cgaagtccga tgccactgaa atcgcccacg aagccatgcg aaaactagga
360
atcgagtcac tgggcagacg ctaccccggc gaggtctcgg gtggccaacg gcaacgc
417

```

<210> 296
 <211> 139
 <212> PRT
 <213> Homo sapiens

```

<400> 296
Phe Ile Ser Gly Ser Thr Arg Val His Ala Ile Asn Asn Val Ser Val
1           5           10           15
Ser Phe Thr His Ser Gly Val His Leu Leu Met Gly Glu Ser Gly Ser

```

```

      20      25      30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
      35      40      45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
      50      55      60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
      65      70      75      80
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
      85      90      95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
      100      105      110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
      115      120      125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
      130      135

```

<210> 297
 <211> 378
 <212> DNA
 <213> Homo sapiens

```

<400> 297
tacaccatcg gtgaccagat tgtcgaagct ctgcaggtgc actcgaagat gtccgacaag
60
gacgcttggg cgcgtgccat cgagctgctc gacttggtgg ggattccgaa tcccagggtg
120
cgtgccaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgtcatcgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccttcgac
240
gtgaccatcc aggcccagat tctcgatttg ctgcgcgtag cccagcgtga aaccatgcg
300
ggcgtcgta tgatcaccca cgacctcggt gtggtagctg gtctggctga cagggttgcc
360
gtgatgtatg ccggacgc
378

```

<210> 298
 <211> 126
 <212> PRT
 <213> Homo sapiens

```

<400> 298
Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
1      5      10      15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
20      25      30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
35      40      45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
50      55      60
Asn Asp Pro Asp Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
65      70      75      80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Leu Arg Val Ala Gln Arg

```

```

      85              90              95
Glu Thr His Ala Gly Val Val Met Ile Thr His Asp Leu Gly Val Val
      100              105              110
Ala Gly Leu Ala Asp Arg Val Ala Val Met Tyr Ala Gly Arg
      115              120              125

```

<210> 299
 <211> 368
 <212> DNA
 <213> Homo sapiens

```

<400> 299
gtgcacgggtt tcgttggcat ggcgaatgac cgggagaact tgcgttttga tccgagactt
60
ccagcccaat ggacgtcgat caaacaccac atgttcattg gcgactctca catgctcggtt
120
ttcctggaac gtgacgcat tacgttccag attctgtcgg gccatgaccg cgacgtgaca
180
gtgcgcggtg agctctacca cattgggggtt gagccggtga gggtgccggt gtccgatcag
240
gggcccgttg gtcctagcct gcgcgttacc catccgatct cgggggttgcg tcgagctgac
300
ggttctctta tcaactgcaga agttcccggc agcattgctg agacgattgg gtcttctccg
360
atctcgac
368

```

<210> 300
 <211> 122
 <212> PRT
 <213> Homo sapiens

```

<400> 300
Val His Gly Phe Val Gly Met Arg Asn Asp Arg Glu Asn Leu Arg Phe
1      5      10      15
Asp Pro Arg Leu Pro Ala Gln Trp Thr Ser Ile Lys His His Met Leu
20      25      30
Ile Gly Asp Ser His Met Leu Val Phe Leu Glu Arg Asp Ala Ile Thr
35      40      45
Phe Gln Ile Leu Ser Gly His Asp Arg Asp Val Thr Val Arg Gly Glu
50      55      60
Leu Tyr His Ile Gly Val Glu Pro Val Arg Val Pro Leu Ser Asp Gln
65      70      75      80
Gly Pro Leu Arg Pro Ser Leu Arg Val Thr His Pro Ile Ser Gly Leu
85      90      95
Arg Arg Ala Asp Gly Ser Leu Ile Thr Ala Glu Val Pro Gly Ser Ile
100     105     110
Ala Glu Thr Ile Gly Ser Ser Pro Ile Ser
115     120

```

<210> 301
 <211> 456
 <212> DNA
 <213> Homo sapiens

<400> 301
 ggccgggtta ttgccgccc gtttgcggg gaaaccggc agaccttga gcgcaccggc
 60
 aaccggcgcg actatttcgt accgcccgc gaaccgacct tgctcgacag gcttacggac
 120
 gcggggccga cggatgatgc aatcggcaag attggtgata tctacgcga caaaggcgtg
 180
 tctcaggtgc gtaaggcaat ggcaatattg gccttggtcg atgaaacact cattgccatg
 240
 gacgacgcgc aggacggcga tctggtcttc accaacttcg tggatttcga catgctctac
 300
 gggcatcgca gggatgtgcc cggctatgcc gccgcgctcg aggccttcga ccggaggctg
 360
 ccggaagcca tggcgaaatt gcggacgggc gatcttctga tctcgacagc cgatcatggc
 420
 tgcgaccga ccctcaaggg aaccgaccac acgcgt
 456

<210> 302

<211> 152

<212> PRT

<213> Homo sapiens

<400> 302
 Gly Arg Val Ile Ala Arg Pro Phe Val Gly Glu Thr Arg Gln Thr Phe
 1 5 10 15
 Glu Arg Thr Gly Asn Arg Arg Asp Tyr Ser Val Pro Pro Pro Glu Pro
 20 25 30
 Thr Leu Leu Asp Arg Leu Thr Asp Ala Gly Arg Thr Val Ile Ala Ile
 35 40 45
 Gly Lys Ile Gly Asp Ile Tyr Ala His Lys Gly Val Ser Gln Val Arg
 50 55 60
 Lys Ala Met Ala Ile Leu Ala Leu Phe Asp Glu Thr Leu Ile Ala Met
 65 70 75 80
 Asp Asp Ala Gln Asp Gly Asp Leu Val Phe Thr Asn Phe Val Asp Phe
 85 90 95
 Asp Met Leu Tyr Gly His Arg Arg Asp Val Pro Gly Tyr Ala Ala Ala
 100 105 110
 Leu Glu Ala Phe Asp Arg Arg Leu Pro Glu Ala Met Ala Lys Leu Arg
 115 120 125
 Thr Gly Asp Leu Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro Thr
 130 135 140
 Leu Lys Gly Thr Asp His Thr Arg
 145 150

<210> 303

<211> 402

<212> DNA

<213> Homo sapiens

<400> 303
 nncgtgggca tcgaggagtt cctcgacatg aagtatcacg cgacgccgat tcatcgctgc
 60

tgacagcggg tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg
 120
 ggtgctcagc tgttcagtga cagcgagtac gagcagcgcc tgagacgtgt ccgtgagctc
 180
 atggaccgtc aggggtctgtc ggcgatcatc gtcaccgata cggccaacat cttctatctg
 240
 atcggttaca acgcctggtc gttctacacc ccgcagatgc tgttcgtgcc gatcgacgga
 300
 gagatgggtcc tctacgctcg cgagatggat cgcattggcg acatcngcac gacgtcgttg
 360
 cccgccgata agatcgtcgg ttaccgggag agttatgtgc ac
 402

<210> 304

<211> 97

<212> PRT

<213> Homo sapiens

<400> 304

Met	Tyr	Leu	Gly	Ala	Gln	Leu	Phe	Ser	Asp	Ser	Glu	Tyr	Glu	Gln	Arg
1				5					10					15	
Leu	Arg	Arg	Val	Arg	Glu	Leu	Met	Asp	Arg	Gln	Gly	Leu	Ser	Ala	Ile
			20					25					30		
Ile	Val	Thr	Asp	Pro	Ala	Asn	Ile	Phe	Tyr	Leu	Ile	Gly	Tyr	Asn	Ala
		35					40					45			
Trp	Ser	Phe	Tyr	Thr	Pro	Gln	Met	Leu	Phe	Val	Pro	Ile	Asp	Gly	Glu
	50					55					60				
Met	Val	Leu	Tyr	Ala	Arg	Glu	Met	Asp	Arg	Met	Ala	His	Ile	Xaa	Thr
65					70				75				80		
Thr	Ser	Leu	Pro	Ala	Asp	Gln	Ile	Val	Gly	Tyr	Pro	Glu	Ser	Tyr	Val
			85					90					95		

His

<210> 305

<211> 375

<212> DNA

<213> Homo sapiens

<400> 305

nnacgcgtcg gttccgcata gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc
 60
 gtgctgctct ggcaatatg ggcgatcagc cggtagctt cgggacgctc gctcacctcg
 120
 gccgccattt cggatgcgac acgcgcgcct gcgcgctcgg cctccagcaa ctcgtcgagc
 180
 gtcgccacca gcgcggcgcg atcttcatgc ggagtcagat cggcgcgggc gtcaggcccc
 240
 tcgccatgcy tcggaatcga catgcagcac cctcctgccg ggatcgatgg cgtaatacgt
 300
 gcgacgggtac acggcgcgty ttgcacgaac gtgcaaata gcgcgtgcct cgtgccatat
 360
 acgtcacata atatg
 375

<210> 306
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 306
 Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr
 1 5 10 15
 Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr
 20 25 30
 Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg
 35 40 45
 Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Ser Val Ala Thr Ser
 50 55 60
 Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro
 65 70 75 80
 Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp
 85 90 95
 Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln
 100 105 110
 Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met
 115 120 125

<210> 307
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 307
 actagttctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag
 60
 ggtaggaag gctattctct ttggccactc tcatacctaag acctatttgg agaacctctg
 120
 gggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatagc acctcgcaca
 180
 tttgatgtct cttcttctca ccactcacc ccaccctggg gggtggggca aaaaagtggc
 240
 tcaaagctgc gggtcagagt tccttgtaaa caaggctcct ccctcactgt cctcaccctg
 300
 ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccatgcttgt ttctaaccga
 360
 gcagaactgg acataatggg aacagggtct gaagacaatc aatccagggc tgcagtgggt
 420
 gctgagctct gggaagcctc cacctggagg ggcagctggg cagtggcagc tcccttgga
 480
 tggctcagcc tctggacatc accccaccca accagagccc tggctcttgc tggatgtcca
 540
 cagatgagt cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagaggtgat
 600
 gagggagtga gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggctctgaa
 660
 ttggtgctgc agcactggca cgcgt
 685

<210> 308
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 308
 Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser
 1 5 10 15
 Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala
 20 25 30
 Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu
 35 40 45
 Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly
 50 55 60
 Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly
 65 70 75 80
 Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro
 85 90 95
 Leu Ser Ser Ser
 100

<210> 309
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 309
 caggctcgta ctattcgat ccctgtgcat atggctcgagg tcatcaataa gctggctcgc
 60
 gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac
 120
 gaactcgata tgaccgcaga gaaggctcatt gaggtgcaga aatacggtcg cgagccgac
 180
 tcgctgcata cccactggg tgaggatggc gattctgagt tcggtgacct tattgaggat
 240
 tccgaggcca tcgtgccagc agacgccgtc aacttcaccc tgttcaggga gcagctgcat
 300
 gatgtcctcg ataccttgtc cgagcgagag gccggtgtcg tgtcgatgcg attcggcttg
 360
 accgacggac agcccaagac cctggatgag atcggaag tctacggtgt tactcgggag
 420
 cgcacccgac ag
 432

<210> 310
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 310
 Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn
 1 5 10 15
 Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu

	20		25		30										
Pro	Thr	Pro	Glu	Glu	Leu	Ala	Asn	Glu	Leu	Asp	Met	Thr	Ala	Glu	Lys
	35						40					45			
Val	Ile	Glu	Val	Gln	Lys	Tyr	Gly	Arg	Glu	Pro	Ile	Ser	Leu	His	Thr
	50					55					60				
Pro	Leu	Gly	Glu	Asp	Gly	Asp	Ser	Glu	Phe	Gly	Asp	Leu	Ile	Glu	Asp
65					70					75				80	
Ser	Glu	Ala	Ile	Val	Pro	Ala	Asp	Ala	Val	Asn	Phe	Thr	Leu	Leu	Gln
				85					90					95	
Glu	Gln	Leu	His	Asp	Val	Leu	Asp	Thr	Leu	Ser	Glu	Arg	Glu	Ala	Gly
			100					105					110		
Val	Val	Ser	Met	Arg	Phe	Gly	Leu	Thr	Asp	Gly	Gln	Pro	Lys	Thr	Leu
	115					120					125				
Asp	Glu	Ile	Gly	Lys	Val	Tyr	Gly	Val	Thr	Arg	Glu	Arg	Ile	Arg	Gln
	130					135					140				

<210> 311

<211> 358

<212> DNA

<213> Homo sapiens

<400> 311

acgcgtatcg aaaatatccc tccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gagtgggccc atgtgggtgt cattggctct
120
ggactgggac aacaagcgtg gggcaaaaaa gcgctacaaa aggtcgagaa ttgtcgtaaa
180
ccgatgctgt gggatgccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgaagccaca ccccggcgag gccgcgcggc tgcttagctg cagcgtcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

<210> 312

<211> 116

<212> PRT

<213> Homo sapiens

<400> 312

Thr	Arg	Ile	Glu	Asn	Ile	Pro	Pro	Ile	Ile	Thr	Ala	Arg	Pro	Glu	Leu
1			5					10					15		
Met	Ala	His	Glu	Leu	Thr	Pro	Glu	Ser	Leu	Asp	Ala	Ser	Leu	Glu	Trp
			20					25				30			
Ala	Asp	Val	Val	Val	Ile	Gly	Pro	Gly	Leu	Gly	Gln	Gln	Ala	Trp	Gly
	35					40					45				
Lys	Lys	Ala	Leu	Gln	Lys	Val	Glu	Asn	Cys	Arg	Lys	Pro	Met	Leu	Trp
	50				55					60					
Asp	Ala	Asp	Ala	Leu	Asn	Leu	Leu	Ala	Ile	Asn	Pro	Asp	Lys	Arg	His
65				70						75				80	
Asn	Arg	Ile	Leu	Thr	Pro	His	Pro	Gly	Glu	Ala	Ala	Arg	Leu	Leu	Ser
			85					90					95		
Cys	Ser	Val	Ala	Glu	Ile	Glu	Asn	Asp	Arg	Leu	Leu	Xaa	Cys	Ala	Arg

100
Leu Val Lys Arg
115

105

110

<210> 313
<211> 347
<212> DNA
<213> Homo sapiens

<400> 313
ncaactgaaa gcattgagat gagcgacgtg ctgtccccct tccacccac caaggccaac
60
accctggtg gcgaaccgag caccatccgc acctcgaacg cgcacatcat tgccgtcacc
120
agtggcaaaag gcggcgtggg caagaccttt gtctccgcca acctggccgc cgcgctgacc
180
cgctctggac tgcgctgtct ggtactggac gccgacctgg gcctggccaa cttggacgtg
240
gtgctgaacc tctaccccaa ggtgacgtg cagcatgtgt tcaccggcaa ggctctgctg
300
caagacgcgg tggtcacggc ccccggcggc ttccatgtgc tgctagc
347

<210> 314
<211> 115
<212> PRT
<213> Homo sapiens

<400> 314
Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro
1 5 10 15
Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser
20 25 30
Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys
35 40 45
Thr Phe Val Ser Ala Asn Leu Ala Ala Leu Thr Arg Leu Gly Leu
50 55 60
Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val
65 70 75 80
Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly
85 90 95
Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His
100 105 110
Val Leu Leu
115

<210> 315
<211> 544
<212> DNA
<213> Homo sapiens

<400> 315
nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggagggaac catgcttgcc
60

gaagatatct acgcgatcat gctgttttca tcgctcatcc tggctgtccc ggggccatcc
 120
 aacaccttgc tgctcagcgc ccgtttccat ttccggctcgc tgcgggcggc gcccttcac
 180
 ctgcttgagg cgttgggcta ctcgctatcc atttcggcat ggggctgggt attggcgcgc
 240
 ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg
 300
 gcgcttctgg cgggtgaagac ctggaatgcc ntcgatccgc agtgcggggc cggtaacttc
 360
 cgccatgggc ccctgcccct gttcgtggca accctgtcga acccgaaggc gctgatcttc
 420
 gccagcgtga tctttcccgg caaggcgttc ctcgacttct ggaacaacta cacgatctcg
 480
 ctgctggcct tcctggttgt gctggcgccc atcgggatgc tttgggtcgg gctggggggc
 540
 ggta
 544

<210> 316
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 316
 Ile Tyr Ala Ile Met Leu Phe Ser Ser Leu Ile Leu Val Val Pro Gly
 1 5 10 15
 Pro Ser Asn Thr Leu Leu Leu Ser Ala Arg Phe His Phe Gly Ser Leu
 20 25 30
 Arg Ala Ala Pro Phe Ile Leu Leu Glu Ala Leu Gly Tyr Ser Leu Ser
 35 40 45
 Ile Ser Ala Trp Gly Trp Val Leu Ala Arg Leu Ser Glu Ser Asn Pro
 50 55 60
 Trp Ile Ile Ser Leu Thr Lys Ala Leu Cys Ala Leu Tyr Val Ala Leu
 65 70 75 80
 Leu Ala Val Lys Thr Trp Asn Ala Xaa Asp Pro Gln Cys Gly Ala Gly
 85 90 95
 Asn Phe Arg His Gly Pro Leu Pro Leu Phe Val Ala Thr Leu Ser Asn
 100 105 110
 Pro Lys Ala Leu Ile Phe Ala Ser Val Ile Phe Pro Gly Lys Ala Phe
 115 120 125
 Leu Asp Phe Trp Asn Asn Tyr Thr Ile Ser Leu Leu Ala Phe Leu Val
 130 135 140
 Val Leu Ala Pro Ile Gly Met Leu Trp Val Gly Leu Gly Ala Gly
 145 150 155

<210> 317
 <211> 343
 <212> DNA
 <213> Homo sapiens

<400> 317
 nggtcagcct ctcgcccagg caattctctt aagatacatg agctgctatg agtaccaaag
 60

ccagaggttt gtccactgag agaagcacat tggaaaagggg ggcgtggggc tgggactgtg
 120
 tggcacttta tgcacggggg gggcctaagg gggnggtcc accaaccatg cactgngggg
 180
 ggggtgtggg taacatgccg tgcattttgg ggggtgtgcca tgagtggcac accatggggg
 240
 tggcatgtgg ggcattgtat catgtggtgt tggcgagca aactcagctc ttacctggct
 300
 ggggccagcc tctaaaactt ctcacattgg gctcccttct gac
 343

<210> 318

<211> 98

<212> PRT

<213> Homo sapiens

<400> 318

Met	Ser	Thr	Lys	Ala	Arg	Gly	Leu	Ser	Thr	Glu	Arg	Ser	Thr	Leu	Glu
1				5				10						15	
Arg	Gly	Ala	Trp	Ala	Trp	Asp	Cys	Val	Ala	Leu	Tyr	Ala	Arg	Gly	Gly
			20				25					30			
Pro	Lys	Gly	Gly	Gly	Pro	Pro	Thr	Met	His	Xaa	Gly	Trp	Gly	Val	Gly
		35					40					45			
Asn	Met	Pro	Cys	Ile	Leu	Gly	Val	Cys	His	Glu	Trp	His	Thr	Met	Gly
	50					55				60					
Val	Ala	Cys	Gly	Ala	Cys	Met	His	Val	Val	Leu	Ala	Gln	Gln	Thr	Gln
65					70					75				80	
Leu	Leu	Pro	Gly	Trp	Gly	Gln	Pro	Leu	Lys	Leu	Leu	Thr	Leu	Gly	Ser
			85					90						95	
Leu	Leu														

<210> 319

<211> 429

<212> DNA

<213> Homo sapiens

<400> 319

gaattctcga tgtaccccct cccggcagtc ctattctcga gctgagcggg cacagtggcc
 60
 ccgttaacag tgtggcttgg ggtccacca gccagagcac gttgcgaaat ggacctagta
 120
 agggcatgat atgtacagga ggcgacgatg ctacgtgcct cgtatatgat ctgactagct
 180
 caactcttcg aacagcatct gctcaaggac ggcgctctcg aaacagtcca tataaacaaa
 240
 gccattcacc gggaatagac ggatggcgtg tcggcgagca agtgccggtg ctgccttata
 300
 cggccccgtc tatggtcaac aatgctagct ggctcggcat gcctgcgcca tcaaaacgca
 360
 catcgctaca gagcaaacac cgcagccttt accgcagctt actcagttag tggacttagt
 420
 atacgtccn
 429

<210> 320
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 320
 Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu
 1 5 10 15
 Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg
 20 25 30
 Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg
 35 40 45
 Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val
 50 55 60
 Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser
 65 70 75 80
 Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp
 85 90 95
 Thr Glu Tyr Thr Ser
 100

<210> 321
 <211> 530
 <212> DNA
 <213> Homo sapiens

<400> 321
 ngtgcacgac gtgctcgcca agtcctcgcg gtcctctaata gcatcaacg tggttcacgc
 60
 caccgtcgat gcgttgacgc agctcgagga gcccgagag gtcgcccgtc gccgcggcaa
 120
 gtccgttgag gagatcgccc cagcagccat gctgcgtgcg cgcaaggagg ccgacgaggc
 180
 cgccgctgct gcccgcatgg aggaaaaggc ggggggtaac tgatgagcaa gctgaagatc
 240
 acccagatca agtctggcat cgctaccaag ccaaatacatc gtgagaccct gcgcagcctc
 300
 ggactgaagc gtattggtga caccgtcatc aaggaggacc gcccgaggtt ccgcggcatg
 360
 gtcgggaccg ttcgtcacct cgtcaccatg gaagaggtgg actgacatgg ctattgagct
 420
 ccatgacctc aagcccgctc ctgggtgcca caaggccaag acccggttg gtcgtggtga
 480
 gggttccaag ggtaagaccg ctggctcgcg taccaagggc accggtgcac
 530

<210> 322
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

```

      1           5           10           15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly
      20           25           30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg
      35           40           45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp
      50           55           60

```

<210> 323

<211> 468

<212> DNA

<213> Homo sapiens

<400> 323

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ntccggaccc gctgtggcca cgtattctgc cggttcctgta ttgctaccag tctaaagaac
60
aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaact
120
gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtga caccctgggt
180
tgccctcagt aaatgagggc acatattcgg acttgtcaga agtacataga taagtatgga
240
ccactacaag aacttgagga gacagcagca aggtgtgtat gtcccttttg tcagagggaa
300
ctgtatgaag acagcttgct ggatcattgt attactcatc acagatcgga acggaggcct
360
gtgttctgtc cactttgcca tttaatacc gatgagaatc caagcagctt cagtggcagt
420
ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
468

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<210> 324

<211> 156

<212> PRT

<213> Homo sapiens

<400> 324

```

Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr
      1           5           10           15
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu
      20           25           30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser
      35           40           45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu
      50           55           60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly
      65           70           75           80
Pro Leu Gln Glu Leu Glu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe
      85           90           95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr
      100          105          110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu
      115          120          125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His

```

130 135 140
 Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe
 145 150 155

<210> 325
 <211> 374
 <212> DNA
 <213> Homo sapiens

<400> 325
 acgcgtgaag ggaggacgag gaagtaacgg gaagcacaag gccgctgctg gggagatggc
 60
 actggagccc cctaggaagc atctcacagg ctgtggccct tggcacgggg atctggggcc
 120
 aggtcgagcg caggtctggg tatcatgcga gtgcgggctc gctggggcgg gaaagagttt
 180
 ggagctctgc tcccaggga tccccactcc cgcagatgac ttgcccgaga gagttctgct
 240
 ggtggatttt gatggaaatt ctatttgatc gcacccactt ggttcactgt gtgcttccgg
 300
 gtccccaggt tttaggtgct tcatgccttg ctgggaacga gacacgctcc tgccctcagt
 360
 gaatcttcag tcta
 374

<210> 326
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser
 1 5 10 15
 Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu
 20 25 30
 Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser
 35 40 45
 Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr
 50 55 60
 Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val
 65 70 75 80
 Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu
 85 90 95
 Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg
 100 105

<210> 327
 <211> 538
 <212> DNA
 <213> Homo sapiens

<400> 327
 cactataaaa tccagtttgg ggcccgtgtt ctttcctatt ggtctgtcag gtgaaaaact
 60

ccggctgggg gaaaagcgtc cggtggtttg ttggtaaaga gggcgctga tgggctctgg
 120
 ggaatggagg atggcgccacc ggctgtgggt ggactgtgga aacggggggg ggcagtgccg
 180
 gggtagttgt cctgctggtc tggttttggg atcctgggct ggagaaatgc gatccaaaag
 240
 agctcgggat gggctcagag cgaccacga aaataccagg ggccaagtaa aatgaacca
 300
 ccctttaaca gtgcacaaag cgctggcaca cggtcacgt ctggtgacgc aggctgcccg
 360
 aagcgctcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc
 420
 cgccccctgc ccactctggc cagccggagt tttcaccta cagaccaata ggaaagaaca
 480
 cgggccccaa actggatttt atagtctgag ctctcagcat ctaaggaatg atatgccc
 538

<210> 328

<211> 125

<212> PRT

<213> Homo sapiens

<400> 328

Met	Val	Gly	Ala	Leu	Arg	Ala	Ala	Cys	Val	Thr	Arg	Arg	Gly	Pro	Cys
1				5				10					15		
Ala	Ser	Ala	Leu	Cys	Thr	Val	Lys	Gly	Trp	Val	His	Phe	Thr	Trp	Pro
			20					25					30		
Leu	Val	Phe	Ser	Trp	Val	Ala	Leu	Ser	Pro	Ser	Arg	Ala	Leu	Leu	Asp
		35					40					45			
Arg	Ile	Ser	Pro	Ala	Gln	Asp	Pro	Lys	Thr	Arg	Pro	Ala	Gly	Gln	Leu
	50				55					60					
Pro	Arg	His	Cys	His	Pro	Pro	Phe	Pro	Gln	Ser	Thr	His	Ser	Arg	Cys
65				70					75					80	
Ala	Ile	Leu	His	Ser	Pro	Glu	Pro	Ile	Thr	His	Pro	Leu	Tyr	Gln	Gln
			85						90					95	
Thr	Thr	Gly	Arg	Phe	Ser	Pro	Ser	Arg	Ser	Phe	Ser	Pro	Asp	Arg	Pro
		100						105					110		
Ile	Gly	Lys	Asn	Thr	Gly	Pro	Lys	Leu	Asp	Phe	Ile	Val			
		115					120					125			

<210> 329

<211> 407

<212> DNA

<213> Homo sapiens

<400> 329

tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa
 60
 gctcttcagt ctttctgctc cactgagcag tggtttcctg atacccttgg taccctgccca
 120
 gcagcctcgt tatgactcct aactccattg ccctccatgg cccctgggag ctctctctct
 180
 ctttctctcc aggtagtaga gcactgcttc tggcttcttg tgcacagaag ggtttcccac
 240

agctgagagc tgggctccta ctgacatagt tatttccttt atatcctgcc ccaccttctt
 300
 ctggtagcac acagcaacct tgcatagttag ctggtatcat taccttccca atcaacaggc
 360
 cttgatttct tataggactt tttctctcag atttacattg cttcttt
 407

<210> 330
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 330
 Met Ile Pro Ala Thr Met Gln Gly Cys Cys Val Leu Pro Glu Glu Gly
 1 5 10 15
 Gly Ala Gly Tyr Lys Gly Asn Asn Tyr Val Ser Arg Ser Pro Ala Leu
 20 25 30
 Ser Cys Gly Lys Pro Phe Cys Ala Gln Glu Ala Arg Ser Ser Ala Leu
 35 40 45
 Leu Pro Gly Glu Lys Glu Arg Glu Ser Ala Gln Gly Pro Trp Arg Ala
 50 55 60
 Met Glu Leu Gly Val Ile Thr Arg Leu Leu Ala Gly Tyr Gln Gly Tyr
 65 70 75 80
 Gln Glu Asn Thr Ala Gln Trp Ser Arg Lys Thr Glu Glu Leu Gln Ala
 85 90 95
 Leu Phe Pro His Gly Phe Leu Glu Gly Ile Pro Gly Glu Gly Thr Leu
 100 105 110
 Arg

<210> 331
 <211> 523
 <212> DNA
 <213> Homo sapiens

<400> 331
 tgtaccgaac ctgctggtct cgagggcctt gctgggctcg tcgtacgcac agctgacgaa
 60
 tccaccggcc cccatcccg cgccactttc gctgaggcca tggagtcgat cggagccagc
 120
 tacgacggat cggcggggtt ggccggaagt cagctcggcg tcgatgtgcc cgtgacaagg
 180
 ttgcagcgag cggctgaact cttcgtcgaa ttgttgaaca ccacgagcct ggttgaagag
 240
 gacatcgccc gtcagatcga cgcggcgcca gcctccctgg cccagaccag ccagcgcgga
 300
 tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtggggtc acggctcgtcc
 360
 ctgcccacga tcggtaccct ctgctcgggtg gaaaagctca acgccgcagc cgcacgagaa
 420
 ttctgggccg cgcactggac gatctccgat gccgtgctgg tggttgccgg agagggagtc
 480
 gaggacctcg acttgtcaat attcaaggag tggacgacca gct
 523

<210> 332
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 332
 Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg
 1 5 10 15
 Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu
 20 25 30
 Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala
 35 40 45
 Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala
 50 55 60
 Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu
 65 70 75 80
 Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr
 85 90 95
 Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Ala Arg Ala Leu
 100 105 110
 Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser
 115 120 125
 Ser Val Glu Lys Leu Asn Ala Ala Ala Arg Glu Phe Trp Ala Ala
 130 135 140
 His Trp Thr Ile Ser Asp Ala Val Leu Val Val Ala Gly Glu Gly Val
 145 150 155 160
 Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser
 165 170

<210> 333
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 333
 nntgttcgtc gtgtcgaccc ggaactcaag gcccgagcga tgacgggtgaa ggtgccaacc
 60
 gatccccatc accgcccggg agttccattg aagtctgcga aggaccgtat ggacatcatt
 120
 tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgcgg caccacccac
 180
 aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccacccac cgggtggcaag
 240
 gaacggggccc gcaactacga tgcgggtggcc cagctcgtcg cgcagcgagt cgcgcgggtca
 300
 cacggccgga tcaactgcaa acggctgcta ccggtagcgc gagcggcagg atatgagggg
 360
 tcggcgcgga at
 372

<210> 334
 <211> 88
 <212> PRT

<213> Homo sapiens

<400> 334

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Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
 1           5           10           15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
      20           25           30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
      35           40           45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
      50           55           60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
      65           70           75           80
Gly Tyr Glu Gly Ser Ala Arg Asn
                        85

```

<210> 335

<211> 356

<212> DNA

<213> Homo sapiens

<400> 335

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gtgcacgcct tgctgggcga gggcgatgcg cctgcgcgca ccttcgtgga cggtagcttt
60
ggcaggggag ggcattcgcg gctcatcctg cagcgggttg ggccgcaagg ccgcctgggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgcttt
180
tccatcnggc accagggggt cagccatctc ggggaactgc ccgccgccag cgtgtccggt
240
gtgctgctgg acctgggcgt gagctccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgtttcg atgggtccgct ggacatgcgc atggacacca ctccgatgca tggatg
356

```

<210> 336

<211> 118

<212> PRT

<213> Homo sapiens

<400> 336

```

Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
 1           5           10           15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
      20           25           30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
      35           40           45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
      50           55           60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
      65           70           75           80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
      85           90           95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

```

100
Thr Thr Pro Met His Gly
115

105

110

<210> 337
<211> 447
<212> DNA
<213> Homo sapiens

<400> 337
cagcctctct cgcaccgcgc cgggtgtgaag cacgggcatg ccggtgtgca agtggcacca
60
cagccaaaac agcgagctca cacttcaaac tccttcaaag accccaggcc tctgtaagaa
120
ccgctcatct ctgtgcccac agtcccccg cttccatgtg acccagaaat ggaaccacgc
180
agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcaggc ttctgtgcaa
240
acaggcgcca tcatgtcagc cgggtgagcag gagcaacgtg cgtgggtcag ggggtggcca
300
cacgtccaac ttataagaa atgacagatt ccctgatggc catagggatc tgcagggcca
360
gcagcaggca taggacttcc ggtggccctg cgtcttcac aacactgagt attgtcaggg
420
tttctgtact gtttttacag ccaattg
447

<210> 338
<211> 111
<212> PRT
<213> Homo sapiens

<400> 338
Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu
1 5 10 15
Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu
20 25 30
Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala
35 40 45
Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg
50 55 60
Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn
65 70 75 80
Val Arg Gly Ser Gly Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp
85 90 95
Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Ala
100 105 110

<210> 339
<211> 588
<212> DNA
<213> Homo sapiens

<400> 339

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aagggcgta
 60
 gatcgtttat cctgcagttg ccattcatca gacaaatcca gtggaacca atggaagaca
 120
 ccgacctgca agcgctgatg gccagactcg aattgctaata tgatcgggtc gagcaactta
 180
 agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc
 240
 tcattgaaaa aaacgaaatc gcccggcgta aggtcgaatc gatgatttcg cgcctgaagg
 300
 ccctggagca agactatgag ttaagcaata gcgttacgtg cagatcctcg acaaagaata
 360
 ttgatcatc tgcccccagg aagaacgcag cacctggtga gtgctgcccg ctacctggaa
 420
 ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcac ggtgccgacc gcacgcccgt
 480
 gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca
 540
 ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt
 588

<210> 340
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 340
 Met Glu Asp Thr Asp Leu Gln Ala Leu Met Ala Arg Leu Glu Leu Leu
 1 5 10 15
 Ile Asp Arg Val Glu Gln Leu Lys Ser Gln Asn Gly Leu Leu Leu Ala
 20 25 30
 Gln Glu Lys Thr Trp Ala Arg Xaa Arg Ala His Leu Ile Glu Lys Asn
 35 40 45
 Glu Ile Ala Arg Arg Lys Val Glu Ser Met Ile Ser Arg Leu Lys Ala
 50 55 60
 Leu Glu Gln Asp Tyr Glu Leu Ser Asn Ser Val Thr Cys Arg Ser Ser
 65 70 75 80
 Thr Lys Asn Ile Arg Ser Ser Ala Pro Arg Lys Asn Ala Ala Pro Gly
 85 90 95
 Glu Cys Cys Pro Leu Pro Gly Arg Pro Lys Gly Val Lys Ser Ala Ala
 100 105 110
 Ala Ala Lys Ser Ser Val Pro Thr Ala Ser Pro
 115 120

<210> 341
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 341
 ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtgaccg ctcggccttt
 60
 gcaatgaacg acacgccgac agttgcgacc gcgcgcagcc tgatcctgcg tggcttcttg
 120

ctgaacattc ttaaccccaa gctgacaatt ttcttctctg ccttcctgcc tcaattcgta
 180
 acgccaggcg gcaccgcgcc ggccttgacg atgctggtac tgagcggcgt gttcatggcg
 240
 atgacgcttg cagtgtttgt gctgtatggc ctgttgccga atgtgtttcg tcgtgcagtg
 300
 gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgccggg
 360
 ctgggggtga acctggcggt tgcgcagcgc tgaggacgcg t
 401

<210> 342

<211> 130

<212> PRT

<213> Homo sapiens

<400> 342

Xaa	Arg	Ala	Ala	Tyr	Leu	Leu	Tyr	Leu	Ala	Tyr	Ala	Thr	Trp	Arg	Asp
1				5					10					15	
Arg	Ser	Ala	Phe	Ala	Met	Asn	Asp	Thr	Pro	Thr	Val	Ala	Thr	Ala	Arg
			20					25					30		
Ser	Leu	Ile	Leu	Arg	Gly	Phe	Leu	Leu	Asn	Ile	Leu	Asn	Pro	Lys	Leu
		35					40					45			
Thr	Ile	Phe	Phe	Leu	Ala	Phe	Leu	Pro	Gln	Phe	Val	Thr	Pro	Gly	Gly
	50					55					60				
Thr	Ala	Pro	Ala	Leu	Gln	Met	Leu	Val	Leu	Ser	Gly	Val	Phe	Met	Ala
65				70					75					80	
Met	Thr	Leu	Ala	Val	Phe	Val	Leu	Tyr	Gly	Leu	Leu	Ala	Asn	Val	Phe
			85					90					95		
Arg	Arg	Ala	Val	Val	Glu	Ser	Pro	Arg	Val	Gln	Asn	Trp	Leu	Arg	Arg
			100					105					110		
Ser	Phe	Ala	Thr	Ala	Phe	Ala	Gly	Leu	Gly	Leu	Asn	Leu	Ala	Phe	Ala
		115					120					125			
Gln	Arg														
	130														

<210> 343

<211> 389

<212> DNA

<213> Homo sapiens

<400> 343

gtgttgccga actacatggc gtccctgccg ttcagcgtgg tcgagtcggc gcgcacgcac
 60
 ggggtgctcca acttccagat cttctggaag ctgacgccc cgatggcgat gccggcgatg
 120
 gcggcgcttcg cgaccctgca gttcctgtgg gtgtggaacg acctgctcat cgccaagctc
 180
 ttccctacca acgacaaccc cacggtgatc gtcaagctcc aacagcttcc cnnngggcccc
 240
 aaggcccagg gtgcggagct gctgacggcg ggcgccttca tctccatcgt gctacccatg
 300
 atcgtcttct tcgtgctcca gaacttctg gtgcgcggta tgacgtcggg tgccgtcaag
 360

gggtgaccgc tcaactgcag tggcccggg
389

<210> 344
<211> 121
<212> PRT
<213> Homo sapiens

<400> 344
Val Leu Arg Asn Tyr Met Ala Ser Leu Pro Phe Ser Val Val Glu Ser
1 5 10 15
Ala Arg Ile Asp Gly Cys Ser Asn Phe Gln Ile Phe Trp Lys Leu Ile
20 25 30
Ala Pro Met Ala Met Pro Ala Met Ala Ala Phe Ala Thr Leu Gln Phe
35 40 45
Leu Trp Val Trp Asn Asp Leu Leu Ile Ala Lys Leu Phe Leu Thr Asn
50 55 60
Asp Asn Pro Thr Val Ile Val Lys Leu Gln Gln Leu Ser Xaa Gly Pro
65 70 75 80
Lys Ala Gln Gly Ala Glu Leu Leu Thr Ala Gly Ala Phe Ile Ser Ile
85 90 95
Val Leu Pro Met Ile Val Phe Phe Val Leu Gln Asn Phe Leu Val Arg
100 105 110
Gly Met Thr Ser Gly Ala Val Lys Gly
115 120

<210> 345
<211> 360
<212> DNA
<213> Homo sapiens

<400> 345
ctagtacttt atgctgatgg tgaacgtcgt tacatccttg ccctaaagg catggttgct
60
ggtgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg
120
cgtaatatcc cagttggtac aacagtacac gctgtagaaa tgaaacctgc taaaggtgca
180
caaattgcac gttctgctgg ttcttacagc caaattatag ctgctgatgg tgcttacgtt
240
actctacgtt tacgtagtgg tgaaatgcgt aaaatccctg ctgagtgtcg tgcaacaatc
300
ggtgaagttg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt
360

<210> 346
<211> 120
<212> PRT
<213> Homo sapiens

<400> 346
Leu Val Leu Tyr Ala Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys
1 5 10 15
Gly Met Val Ala Gly Asp Val Ile Gln Ser Gly Glu Asp Ala Ser Ile

```

      20      25      30
Lys Val Gly Asn Cys Leu Pro Met Arg Asn Ile Pro Val Gly Thr Thr
      35      40      45
Val His Ala Val Glu Met Lys Pro Ala Lys Gly Ala Gln Ile Ala Arg
      50      55      60
Ser Ala Gly Ser Tyr Ser Gln Ile Ile Ala Arg Asp Gly Ala Tyr Val
65      70      75      80
Thr Leu Arg Leu Arg Ser Gly Glu Met Arg Lys Ile Pro Ala Glu Cys
      85      90      95
Arg Ala Thr Ile Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Gln
      100      105      110
Leu Gly Lys Ala Gly Ala Thr Arg
      115      120

```

<210> 347

<211> 565

<212> DNA

<213> Homo sapiens

<400> 347

```

accggtgatg ccaaaggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgccg tcatcatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgtc gggatcctca cggatgcctt cttggtgcgg
180
atgaccctcg tcccggccgt gatggccctg ctaggtgaca aggcattggtg gttgcccggg
240
tggctggatc gacgcctacc ccgcctcgac atcgaggag aaggatcac ccacaggaa
300
aagctggccg cctggccac agcgatcac accgagccc tgcacgccga ggggatcggg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaac cgcgtcaggt gcaagccgtc
420
gtcggatcgc agaacagtgt ctgcccgtc ctgctggcga tccggggacg gctgcccttg
480
gatcacggcc ggatgaggtc gggaggattg ctgctaccgc agcgggcttc cagagtgcgt
540
cgggtgacgt ggttcctcga cgcgt
565

```

<210> 348

<211> 188

<212> PRT

<213> Homo sapiens

<400> 348

```

Thr Gly Asp Ala Lys Gly Ala Val Thr Arg Gly Phe Ile Gly Ser Gly
1      5      10      15
Lys Val Val Thr Ala Ala Ala Val Ile Met Ile Ser Val Phe Val Phe
      20      25      30
Phe Ile Pro Glu Gly Met Asn Ala Ile Lys Glu Ile Ala Leu Ala Leu
      35      40      45
Ala Val Gly Ile Leu Thr Asp Ala Phe Leu Val Arg Met Thr Leu Val

```



```

      50              55              60
Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly
65              70              75              80
Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile
      85              90              95
Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu
      100              105              110
Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu
      115              120              125
Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln
      130              135              140
Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Gly Arg Leu Pro Leu
145              150              155              160
Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala
      165              170              175
Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala
      180              185

```

<210> 349
 <211> 339
 <212> DNA
 <213> Homo sapiens

```

<400> 349
ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
60
gagctcgggtt cggctaccgc tcatacgttt gcggacaatt tgccgttcct tcttaaaactg
120
ctcgcggcag aagagccact atcgttgacg gctcatccca gtttggcgca agcacaggaa
180
gggtacgggc gggagaatcg caaaggggtg ccattagatg cccagaccg gaattaccac
240
gatcccaacc ataaaccgga gcttattgtt gggctgacgc gattccacgc actagccggc
300
ttccgtgaac cacaacgcac acttgagctt tttgacgcg
339

```

<210> 350
 <211> 113
 <212> PRT
 <213> Homo sapiens

```

<400> 350
Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala
1      5      10      15
Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp
      20      25      30
Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser
      35      40      45
Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg
      50      55      60
Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His
65      70      75      80
Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His

```

	85		90		95										
Ala	Leu	Ala	Gly	Phe	Arg	Glu	Pro	Gln	Arg	Thr	Leu	Glu	Leu	Phe	Asp
	100		105		110										
Ala															

<210> 351
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 351
 gcgcgcgccca gtgccgagac ccggggcttc aggagccggc cccgggagag aagagtgcgg
 60
 cggcgggacgg agaaaacaac tccaaagtgt gcgaaaggca ccgcccctac tcccgggctg
 120
 ccgcgcctc cccgccccca gccctggcat ccagagtacg ggtcgagccc gnggccatgg
 180
 agccccctg gggaggcggc accagggagc ctgggccccg gggctccgcc gcgacccat
 240
 cgggtagacc acagaagctc cgggaccctt ccggcacctc tggacagccc aggatgctgt
 300
 tggccaccn ntctcctcc tctccttgg aggcgtctg gcccatccag accg
 354

<210> 352
 <211> 118
 <212> PRT
 <213> Homo sapiens

Ala	Arg	Pro	Ser	Ala	Glu	Thr	Arg	Gly	Phe	Arg	Ser	Arg	Pro	Arg	Glu
1				5				10					15		
Arg	Arg	Val	Arg	Arg	Arg	Thr	Glu	Lys	Thr	Thr	Pro	Lys	Leu	Ala	Lys
		20					25					30			
Gly	Thr	Ala	Pro	Thr	Pro	Gly	Leu	Pro	Pro	Pro	Pro	Arg	Pro	Gln	Pro
	35					40					45				
Trp	His	Pro	Glu	Tyr	Gly	Ser	Ser	Pro	Xaa	Pro	Trp	Ser	Pro	Pro	Gly
	50				55					60					
Glu	Ala	Ala	Pro	Gly	Ser	Leu	Gly	Pro	Gly	Ala	Pro	Pro	Arg	Pro	His
65				70					75					80	
Arg	Val	Asp	His	Arg	Ser	Ser	Gly	Thr	Leu	Pro	Ala	Pro	Leu	Asp	Ser
			85				90					95			
Pro	Gly	Cys	Cys	Trp	Pro	Pro	Xaa	Pro	Pro	Pro	Pro	Pro	Trp	Arg	Arg
		100				105							110		
Ser	Gly	Pro	Ser	Arg	Pro										
		115													

<210> 353
 <211> 1469
 <212> DNA
 <213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggg tgacggcggt
60
attgagccgg tggacctcgt ggctggagat gtctctttta tctccttgac gatgatcctt
120
gaacccattt cagctgttgt cagccacac ggctcatgc tgttgctggg gaagcctcaa
180
tttgagggtg gttgcaaggc tttgggagcc catggcggtg tcacggacct ggccctgcgc
240
ttgcaggcca tcgcggtgt catggcagca gcggtagatt tgggttggcg tatgctgac
300
gagtgcgata gcccggtgcc cgggcaggat ggaaacgtt agcacttcgt cttgctggaa
360
cgtacgggtc ggtgacagac gtccgggcat atcatgggccc gctactgtgg tcttgtgaac
420
gacacgagcc ctctgagata cgttgctcgc gtcacccatg ccacgcggga cgacgctttt
480
gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattgggtg cgcgggtccg
540
gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttggga
600
gagttcgccc acgaggcgga ggtggtcgc gtctttggcg gcgacggcac gatcttgca
660
gctgctgaat ggtcattacc tcgccacgtt cccatgattg gcgtcaacct tggccatgct
720
ggttttctgg ctgagctgga gcgctccgat atggcggtac tagtgaacaa ggtgtgttcg
780
cgcgactaca ccgttgagga tcgcctcgtg cttaaaacca ccgtcaccga gcattccgga
840
caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaaaggc agccggcg
900
cgcgtgctgc acgttctggc gtctgtcgac gagttgccgg tgcaacgctg gagttgcgac
960
gggatcctgg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcgccccg
1020
gtcatgtggc ccgatctcga cgccatgctc atgggtgccg tgagcgctca cgctctcttt
1080
gtctgaccgc tggatcatgag cccagctgct cgagtggacc ttgacatcca gccagacggt
1140
tcagaatcgg cggttctgtg gtgcgacggg cgccgatcgt gcaccgtacg accgggggaa
1200
agaatcacgg tcgtccgcca tcccgaccgt ctgcgcattg ctggtctggc cgcgcagccc
1260
ttcacatcgc gtctgggtcaa gaagtttgag ctcccgtca gcgggtggcg tcagggtcgt
1320
gaccgtcatc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg
1380
tcatcgatga gacggtctc gaacctcat ccgcgctgac ggcagtcacc ggcgagaccg
1440
gcgcccggaaa gaccatggtg gtcaccggt
1469

<210> 354

<211> 318

<212> PRT

<213> Homo sapiens

<400> 354

```

Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1           5           10           15
Val Val Val Val Thr His Ala Thr Arg Asp Asp Ala Phe Asp Ala Ala
      20           25           30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
      35           40           45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
      50           55           60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
65           70           75           80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
      85           90           95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
      100          105          110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
      115          120          125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
      130          135          140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
145          150          155          160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
      165          170          175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
      180          185          190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
      195          200          205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
      210          215          220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
225          230          235          240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
      245          250          255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
      260          265          270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
      275          280          285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
      290          295          300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Glu Thr Ser
305          310          315

```

<210> 355

<211> 558

<212> DNA

<213> Homo sapiens

<400> 355

```

nggatccac ctctggaat ggaaaccac ataccagttc tcttctcga tttgaatgcg
60
gatgacctca gtgccaatga gcagcttggt ggccccatg catcggcgt gaactccatc
120

```

ctgccaagg agcatggcag ccagtttttc tacctgcccc tcataaagca cagtgatgat
 180
 gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca cttgaatggg
 240
 gtcacaccac agaatgaaag gatttaccta attgtgaaaa ccacagttca actcagccac
 300
 cctgtgcta tggagttagt attacgaaaa cgaattgcag ccaatattta caacaaacag
 360
 agtttcacgc agagtttgaa gaggagaata tccctgaaaa atatatttta ttctgtgggt
 420
 gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa
 480
 acgctggctc tcctggcagc aaggagttaa aacgaaggca catcagatgg gaagacgtac
 540
 attgagaagt acactcga
 558

<210> 356
 <211> 186
 <212> PRT
 <213> Homo sapiens

<400> 356
 Xaa Ile Pro Pro Gly Met Glu Thr His Ile Pro Val Leu Phe Leu
 1 5 10 15
 Asp Leu Asn Ala Asp Asp Leu Ser Ala Asn Glu Gln Leu Val Gly Pro
 20 25 30
 His Ala Ser Gly Val Asn Ser Ile Leu Pro Lys Glu His Gly Ser Gln
 35 40 45
 Phe Phe Tyr Leu Pro Ile Ile Lys His Ser Asp Asp Glu Val Ser Ala
 50 55 60
 Thr Ala Ser Trp Asp Ser Ser Val His Asp Ser Val His Leu Asn Gly
 65 70 75 80
 Val Thr Pro Gln Asn Glu Arg Ile Tyr Leu Ile Val Lys Thr Thr Val
 85 90 95
 Gln Leu Ser His Pro Ala Ala Met Glu Leu Val Leu Arg Lys Arg Ile
 100 105 110
 Ala Ala Asn Ile Tyr Asn Lys Gln Ser Phe Thr Gln Ser Leu Lys Arg
 115 120 125
 Arg Ile Ser Leu Lys Asn Ile Phe Tyr Ser Cys Gly Val Thr Tyr Glu
 130 135 140
 Ile Val Ser Asn Ile Pro Lys Ala Thr Glu Glu Ile Glu Asp Arg Glu
 145 150 155 160
 Thr Leu Ala Leu Leu Ala Ala Arg Ser Glu Asn Glu Gly Thr Ser Asp
 165 170 175
 Gly Lys Thr Tyr Ile Glu Lys Tyr Thr Arg
 180 185

<210> 357
 <211> 323
 <212> DNA
 <213> Homo sapiens

<400> 357

acgcgtgcgt gtgttggtgt agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg
 60
 gtacgatcag gctgaaggct gatcaggcac aaggctctgg gggagagccc tggttccagc
 120
 cctgggggtca gagcagcagg ggccagaaag acggcagggg tgagcactgc acccgctggg
 180
 cagggcaggg ccacagaagg cagggcatgg aggccacgtg aagggttga cagagtggat
 240
 ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg
 300
 gtcaccatgg gtcagcgagg atn
 323

<210> 358
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 358
 Met Val Thr Leu Thr His Ala Ser Leu Ile Leu Leu Thr Gly Pro Arg
 1 5 10 15
 Arg Cys Phe Arg Arg His Pro Ser Thr Leu Ser Ser Pro Ser Arg Gly
 20 25 30
 Leu His Ala Leu Pro Ser Val Ala Leu Pro Cys Pro Ala Gly Ala Val
 35 40 45
 Leu Thr Pro Ala Val Phe Leu Ala Pro Ala Ala Leu Thr Pro Gly Leu
 50 55 60
 Glu Pro Gly Leu Ser Pro Arg Ala Leu Cys Leu Ile Ser Leu Gln Pro
 65 70 75 80
 Asp Arg Thr Pro Pro Ala Ala His Pro His Ala Cys Thr His Pro Thr
 85 90 95
 His Thr Thr His Ala Arg
 100

<210> 359
 <211> 265
 <212> DNA
 <213> Homo sapiens

<400> 359
 acgcgtaccg acaagcgcgc ggtgatggcc gaccttcgcg aatcgggcgc aatcgagcag
 60
 gatgcggaca tgatcgtctt catctaccgc gacgattact acaacaagga aaattcgccg
 120
 gacaaggggc tggccgagat catcatcggc aagcatcggg ggggccccac cggctcgtgc
 180
 aagctgaagt tcttcggcga gtacaccgct ttcgacaacc tggcccacaa ctcggttggt
 240
 tcgttcgaat aacggatgat tccgg
 265

<210> 360
 <211> 83
 <212> PRT

<213> Homo sapiens

<400> 360

```

Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
 1           5           10           15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
      20           25           30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
      35           40           45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
      50           55           60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
65           70           75           80
Ser Phe Glu

```

<210> 361

<211> 453

<212> DNA

<213> Homo sapiens

<400> 361

```

gctttgcagg aggaaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccctg gctacaaatc tgtcctgagg atcagcctca cccacccgac catccccttc
120
aacctcatga aggtgcacct catggtagcg gtggagggcc gcctcttcag gaagtggttc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aaggtgtttg ggctttcaga agcctttggt tccgtggggt atgaatatga atcctgcccc
300
gatctaattc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttgagg gatggagcct agacaaacat catgcctca acattcaaag tggcatcctg
420
cacaagggga atgngagaa ccagtttgtg tct
453

```

<210> 362

<211> 151

<212> PRT

<213> Homo sapiens

<400> 362

```

Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
 1           5           10           15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
      20           25           30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
      35           40           45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
      50           55           60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

```

```

65          70          75          80
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
          85          90          95
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
          100          105          110
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
          115          120          125
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
          130          135          140
Gly Glu Asn Gln Phe Val Ser
145          150

```

<210> 363
 <211> 502
 <212> DNA
 <213> Homo sapiens

```

<400> 363
gggtacaaaaa aagtttgcca cagtattcac actccaggtc tccataaacc ttccagatcc
60
gctcacacaa gctggtgttc atttgcttct tctgtaaact gttcaggacc ttcataaaaag
120
cggtgatgcc tgaccggtgc tcaggggagc ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggagggagga ggtctgaggc ctcagctggg tttgacctga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgttctgc cttcccccta
300
gggggctctg ggcgccatgg ctttcctgat ctgaccagc actctgggccc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgaggagg aggtatcatt tttcaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

```

<210> 364
 <211> 136
 <212> PRT
 <213> Homo sapiens

```

<400> 364
Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
1          5          10          15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
          20          25          30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
          35          40          45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
          50          55          60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65          70          75          80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```


	85		90		95										
Ala	Phe	Met	Lys	Val	Leu	Asn	Ser	Leu	Gln	Lys	Lys	Gln	Met	Asn	Thr
		100					105					110			
Ser	Leu	Cys	Glu	Arg	Ile	Trp	Lys	Val	Tyr	Gly	Asp	Leu	Glu	Cys	Glu
	115					120						125			
Tyr	Cys	Gly	Lys	Leu	Phe	Trp	Tyr								
	130					135									

<210> 365
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 365
 atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgctcaca
 60
 ccactgatcg ttgggattct atttgggggt gagaccctct ctggagtcct tgctgggtgcc
 120
 cttgtctctg gtgttcagat tgccatttct gcatccaaca ctgggtgggtgc ctgggacaac
 180
 gccaagaagt acattgaggc tggagtttca gagcatgccca ggacccttgg cccaaaaggt
 240
 tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg
 300
 tctggccctt ccctcaacat cctcatcaag ctt
 333

<210> 366
 <211> 111
 <212> PRT
 <213> Homo sapiens

Ile	Ser	Thr	Asp	Ala	Ser	Ile	Lys	Glu	Met	Ile	Pro	Pro	Gly	Ala	Leu
1				5				10					15		
Val	Met	Leu	Thr	Pro	Leu	Ile	Val	Gly	Ile	Leu	Phe	Gly	Val	Glu	Thr
		20					25					30			
Leu	Ser	Gly	Val	Leu	Ala	Gly	Ala	Leu	Val	Ser	Gly	Val	Gln	Ile	Ala
	35				40					45					
Ile	Ser	Ala	Ser	Asn	Thr	Gly	Gly	Ala	Trp	Asp	Asn	Ala	Lys	Lys	Tyr
	50			55				60							
Ile	Glu	Ala	Gly	Val	Ser	Glu	His	Ala	Arg	Thr	Leu	Gly	Pro	Lys	Gly
65			70				75					80			
Ser	Asp	Pro	His	Lys	Ala	Ala	Val	Ile	Gly	Asp	Thr	Ile	Gly	Asp	Pro
			85			90				95					
Leu	Lys	Asp	Thr	Ser	Gly	Pro	Ser	Leu	Asn	Ile	Leu	Ile	Lys	Leu	
	100					105					110				

<210> 367
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 367

gcgttcgtcg cactaccggg cggcggcgga acccttgacg agctactcga agcatggaca
 60
 tggcagcagc tcggtgtaca cagcaaaccg gtgngccttg tacgactcga cnncttctgg
 120
 gcaccgctga ccgcgctact caaccacatg accatcgaaa gcttcattcg ccctgaggac
 180
 cgcgcctcgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg
 240
 accccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca
 300
 ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct
 360
 cngttcaggt ggcccgaat g
 381

<210> 368

<211> 89

<212> PRT

<213> Homo sapiens

<400> 368

Ala	Phe	Val	Ala	Leu	Pro	Gly	Gly	Gly	Gly	Thr	Leu	Asp	Glu	Leu	Leu
1				5				10					15		
Glu	Ala	Trp	Thr	Trp	Gln	Gln	Leu	Gly	Val	His	Ser	Lys	Pro	Val	Xaa
			20					25					30		
Leu	Val	Arg	Leu	Asp	Xaa	Phe	Trp	Ala	Pro	Leu	Thr	Ala	Leu	Leu	Asn
			35				40					45			
His	Met	Thr	Ile	Glu	Ser	Phe	Ile	Arg	Pro	Glu	Asp	Arg	Ala	Ser	Leu
	50					55				60					
Val	Ile	Ala	Asp	Thr	Ile	His	Gln	Leu	Met	Ala	Asp	Leu	Glu	Gly	Trp
65				70					75					80	
Thr	Pro	Pro	Pro	Pro	Lys	Trp	Arg	Ser							
				85											

<210> 369

<211> 313

<212> DNA

<213> Homo sapiens

<400> 369

gatacatgat cctctcatat cgcacacaca ccgctcccct ctgccgcaat tcgcagacaa
 60
 acttgcgagc gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc
 120
 gtacgcgagt tctcggacat caacgccaac gtcgggcaag atactgtcaa cgccatctac
 180
 acattctacg agcagcaagc gaccagtttc cttcgccagc tgaacgacct cccacccgaa
 240
 gagcttcccg acgtcatoga ggacttcttc cgcctgtcca ctgatgtcct tctttaccat
 300
 ttccagcaag ctt
 313

<210> 370

<211> 101
 <212> PRT
 <213> Homo sapiens

<400> 370
 Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg
 1 5 10 15
 Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp
 20 25 30
 Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val
 35 40 45
 Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala
 50 55 60
 Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Pro Glu Glu Leu Pro
 65 70 75 80
 Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Leu Tyr
 85 90 95
 His Phe Gln Gln Ala
 100

<210> 371
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 371
 atgacgggtc acgtcatcct ggcgattcca caggtggtga cgatcatggat cggcctcatc
 60
 tgcacgcaca ttggcacggg ctttatcaag ccgaacctct ccacgggtgt aggaggtctt
 120
 tacgatgacg gtgacccccg ccgcgatcag ggtttcctgt acttctacat gtcgatcagt
 180
 attggatctc tcttcgcgcc gatcgtcacc ggcctcctca aggaccatta cggctaccac
 240
 gtaggtttca ttgccgctgc taccggtatg gctctgggtc tgatcgctt cttccacggt
 300
 cgttccaaac tgcgtgagct cgccttcgac atcccgaatc cgctggcccc cggcgagggt
 360
 cgccggatgg tgctccgcgg
 380

<210> 372
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 372
 Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp
 1 5 10 15
 Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn
 20 25 30
 Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg
 35 40 45
 Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

```

      50              55              60
Phe Ala Pro Ile Val Thr Gly Leu Leu Lys Asp His Tyr Gly Tyr His
65              70              75              80
Val Gly Phe Ile Ala Ala Ile Gly Met Ala Leu Gly Leu Ile Ala
      85              90              95
Phe Phe His Gly Arg Ser Lys Leu Arg Glu Leu Ala Phe Asp Ile Pro
      100              105              110
Asn Pro Leu Ala Pro Gly Glu Gly Arg Arg Met Val Leu Arg
      115              120              125

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<210> 373
 <211> 475
 <212> DNA
 <213> Homo sapiens

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<400> 373
acatgttgga aaaattgcct cccactctgg tgctacaggt atgaatctca gccacagtga
60
tgactgtggc agctacaggc ctgatgaaca cccaccaag aaaaggagca tcatgtgcct
120
gcttctctct ggttcctaaa tcctttggcc aaacattttc cccacaaccc tccactccag
180
ttggctggtc actgcctctc agaaagaagt cccagggtccc tgtcagcccc agagcgctcg
240
catggactct gccactgtc cttttccaac acggaggccc ccaattctgg ggaccctac
300
accctaccct gtaccaccac atccccatgc ctgctccaga cagcactaac ctcccatgac
360
agtgggacca aagcagttct taaaggcca atccactcag ttcttaaatg aaaaacagtt
420
gcccatgagt ccccccaaa gacgtccgca catatgccaa acattcggtg tgcac
475

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<210> 374
 <211> 109
 <212> PRT
 <213> Homo sapiens

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<400> 374
Met Gly Met Trp Trp Tyr Arg Val Gly Cys Arg Gly Pro Gln Asn Trp
1      5      10      15
Gly Pro Pro Cys Trp Lys Gly Thr Val Gly Arg Val His Ala Gly Ala
      20      25      30
Leu Gly Leu Thr Gly Thr Trp Asp Phe Phe Leu Arg Gly Ser Asp Gln
      35      40      45
Pro Thr Gly Val Glu Gly Cys Gly Glu Asn Val Trp Pro Lys Asp Leu
      50      55      60
Gly Thr Arg Glu Lys Gln Ala His Asp Ala Pro Phe Leu Gly Gly Val
65      70      75      80
Phe Ile Arg Pro Val Ala Ala Thr Val Ile Thr Val Ala Glu Ile His
      85      90      95
Thr Cys Ser Thr Arg Val Gly Gly Asn Phe Ser Asn Met
      100      105

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<210> 375
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 375
 nnacgcgtcg cctccacctc gaaacccgcc ggcggtcggt ttttcaccat ggccgaccgc
 60
 aaggcccaag ttgcgacggt cacggacacg ctgtatttca cgccgtcgca atgggatgga
 120
 tgcattggcac ggatgcgtgg ggataagata tcagcactga agtggaatca gatgcagatg
 180
 gcggcatgct ccttcatagc ggcagtgggt gcgaagctgg gctgcccgc ggcactatg
 240
 ggcacggcgc agctgctgta ccagcgtttc catctatttc atgcgccgac tgagttttcg
 300
 ttacatgagg tggctttgac gtgtctcttc ac
 332

<210> 376
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 376
 Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr
 1 5 10 15
 Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr
 20 25 30
 Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp
 35 40 45
 Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser
 50 55 60
 Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met
 65 70 75 80
 Gly Thr Ala Gln Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro
 85 90 95
 Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe
 100 105 110

<210> 377
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 377
 cgcggtgccag gtatgtcaac tgatctgtcg gatatttccg aggttgagta ccgtcaactg
 60
 aggctggaac gagggtgct gtgttcggtg tggactcagg gaactgccgc agacccgag
 120
 aacgctatgg cggagctgaa agcccttgct gaaacggcgg gatctcaggt actcgaagct
 180
 gtcattgcaac gtcggactac cccggatccg gcgacgtaca ttggttcggg caaggtggct
 240

gagcttgccg aggtggtgcg ggcgactggt gccgatactg tcatttgtga cggatgaactt
 300
 gacgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagttgt ggaccggtcg
 360
 gtctgattc
 369

<210> 378
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 378
 Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu
 1 5 10 15
 Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr
 20 25 30
 Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala
 35 40 45
 Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg
 50 55 60
 Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala
 65 70 75 80
 Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys
 85 90 95
 Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val
 100 105 110
 Lys Xaa Lys Val Val Asp Arg Ser Val
 115 120

<210> 379
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 379
 acgcgttact taaacttata tgtaaataat aaattcatta tttctagttg gtttaggtact
 60
 atgggctgtg gtttaccagg tgctatggca gctaaaattg cttatccaaa ccgtcaagca
 120
 gtagctatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctgtt
 180
 caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcattaaa
 240
 tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat
 300
 gctaaatttg ctgaagctgc tgggtggtaaa ggctatgttg tgagagatgt aagtcgtctt
 360
 gacgacatcg ttgaagaggc aatgggtcaa gatgttccaa caatcggt
 408

<210> 380
 <211> 136
 <212> PRT

<213> Homo sapiens

<400> 380

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Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
 1           5           10           15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
      20           25           30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
      35           40           45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
      50           55           60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
      65           70           75           80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
      85           90           95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
      100          105          110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
      115          120          125
Ala Gln Asp Val Pro Thr Ile Val
      130          135

```

<210> 381

<211> 613

<212> DNA

<213> Homo sapiens

<400> 381

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naccggtcat aggcgggccc agtgaagac caccgaaca cagttggtg agatccgct
60
tgagggaag gtctgcgcg tcccgcaaa tctggtcaag gcctaccact ctgggctgat
120
cgacgtcgag gactgaaccc tgggagcctg ggcggtccag catgactgct caggctcatt
180
acaaaaacgc gtcgatcccg taggggtgtc gtcatgagca agcccgaagt gaccctgccc
240
gattccgccc ccgacgacct cgtcgttgag gacatcacca tcggcgacgg cctgaagcg
300
tccgctggca acctcgtcga agtgactac gtcggcgtgg ccttaagcaa tggctcgtgag
360
ttcgattctt cctggaaccg cggggagccg ctgaccttcc aactaggggc tggccagggtg
420
atccccgagt gggatgaagg tgtccaaggt atgaaggctg gtggacgacg caaactcgtc
480
atccccacc accttgctta cgggccgcaa ggaatctccg gtgtgatcgc tggcggtgag
540
acgctggtct tcgtctgcga ccttgtaaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

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<210> 382

<211> 137

<212> PRT

<213> Homo sapiens

<400> 382

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Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
 1           5           10           15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
      20           25           30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
      35           40           45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
      50           55           60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
65           70           75           80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
      85           90           95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
      100          105          110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
      115          120          125
Phe Val Cys Asp Leu Val Asn Ile Ile
      130          135

```

<210> 383

<211> 352

<212> DNA

<213> Homo sapiens

<400> 383

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nggagcaaca cctggtcctt gggaatgaag tgtaggagtt gcatttgctg aggttggtgt
60
ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcac gttcaaaacc
120
cagttttctg tttttcacac ctgaacatac acccccctgc agttgggtgg ctccccggtt
180
accagctggg ctctatctac agagagagca atggcttccc ttcccttgaa ggaagtctca
240
ccctcacaag gacacttgat ccgctgcaaa gcagaaagtg tgcggaccct ttgggaaggg
300
cgttcttttc ttgttttagaa cctaggattc tgtttttccc aaacaggatc an
352

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<210> 384

<211> 93

<212> PRT

<213> Homo sapiens

<400> 384

```

Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
 1           5           10           15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
      20           25           30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
      35           40           45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```


50 55 60
 Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser
 65 70 75 80
 Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile
 85 90

<210> 385
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 385
 gccggcgcca cgaaatgcaa aatgcgccct tcaccggacg ccagggtgat cgagccgcca
 60
 gcacctcggg caatgtcctg ggcctgactg gcacacgcaa tcaaagcgag caacaacaca
 120
 caaaaacgca tcatgaggca gacgccaggg aagtgcagaga agccgcagca ggcgcgcggc
 180
 gattggaaat atcggtgagg ctaatggtca ccagcgcttg caggttgat tcggtggcca
 240
 attcgcggaa cgacagcacc gccagttcca gctcgccgcg cagcaccagg cgacgcaagc
 300
 tgcggcgcaa ctccgggtgc accaacaaca ccgcactgtt ca
 342

<210> 386
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 386
 Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser
 1 5 10 15
 Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu
 20 25 30
 Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr
 35 40 45
 Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met
 50 55 60
 Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp
 65 70 75 80
 Ser Thr Ala Ser Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu
 85 90 95
 Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe
 100 105

<210> 387
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 387
 acgcgtgacg cgccggcatc ggaagcgttg actgcagaga agaccgcgca cgtggctgtg
 60

ggacgtgctg gcacgtctga catggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc
 120
 atgcaagagg agcttgacaa tgtgcgtgat ctgcgccatg cgcggcagca agcgctcgat
 180
 gctgttcggt ccgagctgct cgaagcgcag caagcatgtg cctcgtgccca gctgcagctg
 240
 cagcatgtgc cagatgatcg tgtgcgagcg catcccatat accaggcgct ccatgcggac
 300
 gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct
 360
 gagaatgcga gcctgcgcg
 379

<210> 388

<211> 114

<212> PRT

<213> Homo sapiens

<400> 388

Met	Arg	Leu	Val	Arg	Asp	Gln	Val	Leu	Ala	Ala	Cys	Lys	Gln	Arg	Pro
1				5					10					15	
His	Gly	Ala	Pro	Gly	Ile	Trp	Asp	Ala	Leu	Ala	His	Asp	His	Leu	Ala
		20						25					30		
His	Ala	Ala	Ala	Ala	Ala	Gly	Thr	Arg	His	Met	Leu	Ala	Ala	Leu	Arg
		35					40					45			
Ala	Ala	Arg	Asn	Glu	Gln	His	Arg	Ala	Leu	Ala	Ala	Ala	His	Gly	Arg
	50					55					60				
Asp	His	Ala	His	Cys	Gln	Ala	Pro	Leu	Ala	Trp	His	Ala	Gln	Ala	Lys
65					70					75				80	
Arg	Arg	Arg	Val	His	Ala	Pro	Cys	Gln	Thr	Cys	Gln	His	Val	Pro	Gln
			85						90					95	
Pro	Arg	Ala	Arg	Ser	Ser	Leu	Gln	Ser	Thr	Leu	Pro	Met	Pro	Ala	Arg
			100					105						110	
His	Ala														

<210> 389

<211> 382

<212> DNA

<213> Homo sapiens

<400> 389

ngatggccga ctgtcccaact gtcagtagcg gaagctcgcc gtcgagtcgg tccacgtccg
 60
 ggcctcccaac gtgctccgca accctccgaa gcgatgacct ggcccggggg cggcaacgag
 120
 gtattgcgtt tggagacgct tgggggtcaat tacggccagg tgcgcgccgt cgatgccttg
 180
 acgaccaccg tagagcgcgg caccatcacc tgctcatgg gtcgaaatgg atcaggcaag
 240
 tcgtctctga tgtgggcat ccaaggggca acaaagtcct caggagggtt actggtcaac
 300
 cagcagggtt cttgggctga ccccgcaaaa gccgacgccg cgaccgctcg acgaatggtg
 360

agcttagtcc cgcagtcagc cn
382

<210> 390
<211> 127
<212> PRT
<213> Homo sapiens

<400> 390
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val
1 5 10 15
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met
20 25 30
Thr Trp Pro Gly Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly
35 40 45
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val
50 55 60
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys
65 70 75 80
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg
85 90 95
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp
100 105 110
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala
115 120 125

<210> 391
<211> 456
<212> DNA
<213> Homo sapiens

<400> 391
nnacgcgttg ccgctctgtg aggcgcctat cacggtgaca ctctcggtgc tatgagcgtg
60
tgcgacccta tcggtggcat gcacgccttg ttcagegact ctattcccca gcagatcttc
120
ctgcccgcgc cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga
180
ggccgatgaa tcctggacac ccaccgcgac gacctggccg ggatcattgt cgagcccatc
240
ttgcaaggag ccggaggcat gtggccgtgg tctccgtcct gtctgaagca cctgcgccgt
300
cgtgctgatg aacttgacct agttcttata gccgacgagg tcgctactgg atttgggcgg
360
actggcacaac ttttcgcatg cgagtgggccc gatatcggtc ctgacatcat ggtgggtggg
420
aaatccatga ctggcggata cctgacccag tcggcc
456

<210> 392
<211> 55
<212> PRT
<213> Homo sapiens

<400> 392

Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro
 1 5 10 15
 Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Gln Ile
 20 25 30
 Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Arg Gly Arg Arg Gly
 35 40 45
 Asp Val Val Gln Arg Gly Arg
 50 55

<210> 393

<211> 371

<212> DNA

<213> Homo sapiens

<400> 393

nacgcgttgc tcgtcattgg tggctactcg gcctacgaag gtatctacac catgatgact
 60
 gagecgggacc ggtacccggc tttccgtatt ccgacgggtg gcaccccggc ttctatcgac
 120
 aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgtcatcgtc
 180
 gaggcgatgg acaagattaa ggagtcgggt atcgcggtcca gacgctgctt cgtcgtcgag
 240
 acgatgggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgcagc tggcgctgag
 300
 cggatctata ccaacgagga cggtatctcc ctggacgac tagccaacga cgtccattgg
 360
 ttgcgggagt c
 371

<210> 394

<211> 123

<212> PRT

<213> Homo sapiens.

<400> 394

Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr
 1 5 10 15
 Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr
 20 25 30
 Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu
 35 40 45
 Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp
 50 55 60
 Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu
 65 70 75 80
 Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala
 85 90 95
 Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp
 100 105 110
 Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu
 115 120

<210> 395
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 395
 gaattctagt tgggagattc attgaccaga cttttggaat aaacactagt catcatgcta
 60
 gcgacagggtg gtcttgtgca tggtagaaag gcagtccaag cctatgtctc tgaaacctgc
 120
 tctcatttct gttttctact ttacgattta tgttatctca tactcccat gttgcctggt
 180
 ctccagtttt tttacttgtg ttatttccat tcttctatc ctgctcaatt tctgcctcag
 240
 ggcagaattg tgtccaacag ctcttaaatg cagcgagaa actgtgatgt taaaaacatc
 300
 ttgttatccg gcccacaaac atgttgcct tggtaactct tactggttg t
 351

<210> 396
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 396
 Met Val Glu Arg Gln Ser Lys Pro Met Ser Leu Lys Pro Ala Leu Ile
 1 5 10 15
 Ser Val Phe Tyr Phe Thr Ile Tyr Val Ile Ser Tyr Ser Pro Cys Cys
 20 25 30
 Leu Phe Ser Ser Phe Phe Thr Cys Val Ile Ser Ile Leu Leu Phe Leu
 35 40 45
 Leu Asn Phe Cys Leu Arg Ala Glu Leu Cys Pro Thr Ala Leu Lys Cys
 50 55 60
 Ser Ala Glu Thr Val Met Leu Lys Thr Ser Cys Tyr Pro Ala Pro Lys
 65 70 75 80
 His Val Val Leu Gly Asn Ser Tyr Trp Phe
 85 90

<210> 397
 <211> 483
 <212> DNA
 <213> Homo sapiens

<400> 397
 gccgtcatta aagagatcac ccctctctc caacctgggtg atgtcctcgt cgacggtggt
 60
 aatgcttatt ttggtgatac ccgccgccgt gaggaggaaa tacgtccac cggcattcac
 120
 tatgttggtg ctggcatctc cggtggggga gtcggggccc tgagggtccc atcaattatg
 180
 cctggcgggg ttaaggaatc ttacgaaatc atcggaccgg tcttagaaaa aatctccgcc
 240
 cacgtcgacg gtgaacctg ctgcgcatgg atgggtactg acggcgccgg acacttcgtc
 300

aagatggtcc ataatggcat cgagtacgcc gatatgcagt tcattggcga ggcgcccttc
 360
 ctttttgcn tgcccgcgg tttgaccaat gctgaggccg ccgatgcctt cgagtcgtgg
 420
 aaccatggcg acctcaattc ctacctgctc gaaatcactt ctcgggtact gcgtgccaag
 480
 gat
 483

<210> 398
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 398
 Ala Val Ile Lys Glu Ile Thr Pro Leu Leu Gln Pro Gly Asp Val Leu
 1 5 10 15
 Val Asp Gly Gly Asn Ala Tyr Phe Gly Asp Thr Arg Arg Arg Glu Glu
 20 25 30
 Glu Ile Arg Pro Thr Gly Ile His Tyr Val Gly Thr Gly Ile Ser Gly
 35 40 45
 Gly Gly Val Gly Ala Leu Arg Val Pro Ser Ile Met Pro Gly Gly Val
 50 55 60
 Lys Glu Ser Tyr Glu Ile Ile Gly Pro Val Leu Glu Lys Ile Ser Ala
 65 70 75 80
 His Val Asp Gly Glu Pro Cys Cys Ala Trp Met Gly Thr Asp Gly Ala
 85 90 95
 Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp Met
 100 105 110
 Gln Phe Ile Gly Glu Ala Pro Phe Leu Phe Ala Xaa Pro Ala Gly Leu
 115 120 125
 Thr Asn Ala Glu Ala Ala Asp Ala Phe Glu Ser Trp Asn His Gly Asp
 130 135 140
 Leu Asn Ser Tyr Leu Val Glu Ile Thr Ser Arg Val Leu Arg Ala Lys
 145 150 155 160
 Asp

<210> 399
 <211> 314
 <212> DNA
 <213> Homo sapiens

<400> 399
 nngggaatga agaccaccca gcccttcctt tcctcaaacc ttctccaggc ttctgtgcat
 60
 gggtcatcca cccatccact cattcaccca tctatccatc cactcatcca cccatccagt
 120
 cattcactca ttgtccatc cactcatgta cccatccact cattcgccca ttatccatc
 180
 cactcaacca tccactcatc caccatcca nctcatcatc cgtccagtca cccatctatc
 240
 caccatgta tccatccact catccaccca tccactcatc tgtccatcca cttatccacc
 300

catctactca ccca

314

<210> 400

<211> 104

<212> PRT

<213> Homo sapiens

<400> 400

Xaa Gly Met Lys Thr Thr Gln Pro Phe Leu Ser Ser Asn Leu Leu Gln
 1 5 10 15
 Ala Ser Val His Gly Ser Ser Thr His Pro Leu Ile His Pro Ser Ile
 20 25 30
 His Pro Leu Ile His Pro Ser Ser His Ser Leu Ile Cys Pro Ser Thr
 35 40 45
 His Val Pro Ile His Ser Phe Ala His Leu Ser Ile His Ser Thr Ile
 50 55 60
 His Ser Ser Thr His Pro Xaa His His Pro Ser Ser His Pro Ser Ile
 65 70 75 80
 His Pro Cys Ile His Pro Leu Ile His Pro Ser Thr His Leu Ser Ile
 85 90 95
 His Leu Ser Thr His Leu Leu Thr
 100

<210> 401

<211> 2165

<212> DNA

<213> Homo sapiens

<400> 401

gagaaaatgg aactacctgt atataaatta ggtgagcaaa cagtgatata ggtagtttta
 60
 agaagcaaat atatacagtc aatttaacag tgtttacttc tctggattgt ttaatgggtg
 120
 caaaatgaaa gatctattga agtttactta tacattgcat tgattgaacc ttggagagtt
 180
 ttatgaaaaa gaggggcatc ccttgccatc tgtttgccag tcttccttgc cccttccttt
 240
 gaaatgcctg cctctttttt gccagattg tttcctgacc atccgaactc agatgggggc
 300
 ctctaagtgc ttctgggata ttcacaaatc ccttcacaag gccacagtgc gaagtgaatg
 360
 atctggaggt gcctgggcat ctgtgttgga agggagtcaa gactcaccag ccagtcagtt
 420
 tgtgggttac agttgtccca caaaaatcag gcatgttcac ctccccctctg ggccccctaca
 480
 gctgggactg atcatagcct cagattagaa gaaatactga cttctaactc tataagccag
 540
 cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc
 600
 tgagcctaca gttttgtact ggggtgcacg gatgacagct gggaagatgg aaaggcagct
 660
 tgaggattta tagcagctaa agggtaaagt ctgttatgca aaagggtccc atatgaactt
 720

cctacaggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggatgatga
780
aaaattcctc tttgcatcac aagcgagtgg aaagccaggg gctgcatgag tggagaaagc
840
acagtctggt ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagtgt
900
aggcccaggt tacacaggct cccggaatac agacctggga agatagggga ggagagggga
960
agcttgtggc cttttgatcc gcccccgaa tgcccaccgt gcgctgcttt gctgccttca
1020
tctcctgctc agaggccttc tccttcccag agacctcctt ggatgggtct aaggagaca
1080
ctgcccgggc ctttttcctt gcaatcacia ggtccaaatc ctccaggctg cgcttgatcg
1140
gccgcgcgc cccaatgttc tacgggtca ttttccgggt caggattggg tggaccatgc
1200
cttccatctt cctgaaatc tccagtctca catggtgagg ttttctgat cttgaaagcg
1260
attcagggtg ttttttaggg cctgacatgg tcatgggtga taccgacag gctttggggt
1320
gacagtctcg actctggctg cctaagacct ggaactggga gatgcctttg ctctcctggg
1380
gccctgtggt ggaatgagcc agggccagga ccttgccggg aggtttgtgc gggttcttgg
1440
gaaggctcag atctgtaggc tgatcatccg taggggcttc tgctgccgcc gactttttgt
1500
cttgaggtg cagggacgtg agataattta catggagctt ttcttgggtg ctgtgggaag
1560
gaaaagaact gttttccgat tcctgtaca tgccttga agggattttg gatgtctgtt
1620
cattatgaag atggtgctcg gtgtgtctgt agaggctatg gagatgaggg gacgagtaga
1680
agtcagccag gaagctaggc atgtgggaat gggggagggc ctttttctct aagagtttat
1740
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaagggg ttaagtgat
1800
gcttgagaa gctgcagcgg tgggatctg atcgactcag tttctcatgc ttaaagatgt
1860
cattgatggt ctttctctct tccgagggtc tgcttctgaa actctggacg tgctgaatca
1920
ctgatggccg gctgaccgcc atatggtcag tgctttggcc atggtgggtc tgggacaaac
1980
tggaacacaa gtcatcccta gcaatcagtt tctttttgct gatcaaaggg ggtggggagc
2040
cataagggtg gctgctggag aggtggccc cactcacttg ggacaaaagc ttttcttgg
2100
ccagtggga catcatgcct gggttgcccc tagagtagag caggggcgtg taattaagtc
2160
catgg
2165

<210> 402

<211> 87

<212> PRT

<213> Homo sapiens

<400> 402

```

Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu
 1           5           10           15
Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Glu Arg Gly Ser Leu Trp
          20           25           30
Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro
          35           40           45
Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met
          50           55           60
Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly
65           70           75           80
Pro Asn Pro Pro Gly Cys Ala
          85

```

<210> 403

<211> 369

<212> DNA

<213> Homo sapiens

<400> 403

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cccatgggtg tgtcccagga cggcgatcatg aagcgatcagg taaatgacaa ggaaacgggc
60
ggcacttgt tcgaatacac gacgcaagtg tctgtcgact cgacgccgca actcgtccag
120
ccttcgcccc cgtcgcacga caacctcgtg cctgtccaga tgatcttttg cttcaagcag
180
cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcatgcta
240
cagcccgaca tggtcgtctt ggtggacgtc ggcacgaagc ccggccacct cgcctatac
300
catctatggc aggcattcta tcaccgacct accttgggcg gtgcttgagg cgaaattcat
360
gctatgatc
369

```

<210> 404

<211> 123

<212> PRT

<213> Homo sapiens

<400> 404

```

Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp
 1           5           10           15
Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val
          20           25           30
Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn
          35           40           45
Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys
          50           55           60
Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu
65           70           75           80
Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His

```

85 90 95
 Leu Ala Leu Tyr His Leu Trp Gln Ala Phe Tyr His Arg Pro Thr Leu
 100 105 110
 Gly Gly Ala Cys Gly Glu Ile His Ala Met Ile
 115 120

<210> 405
 <211> 840
 <212> DNA
 <213> Homo sapiens

<400> 405
 gaattcccg gcaccagctc gaagctggag cactttgtgt ctatcctgct gaagtgtctc
 60
 gactcgccct ggaccacgag ggcctgtcg gagacagtgg tggaggagag cgacccaag
 120
 ccggccttca gcaagatgaa tgggtccatg gacaaaaagt catcgaccgt cagtgaggac
 180
 gtggaggcca ccgtgcccat gctgcagcgg accaagtcac ggatcgagca gggatcgtg
 240
 gaccgctcag agacgggctg gctggacaag aaggaggggg agcaagccaa ggcgctgttt
 300
 gagaaggatga agaagttccg gacccatgtg gaggaggggg acattgtgta ccgctctac
 360
 atgcggcaga ccatcatcaa ggtgatcaag ttcacctca tcatctgcta caccgtctac
 420
 tacgtgcaca acatcaagtt cgacgtggac tgcaccgtgg acattgagag cctgacgggc
 480
 taccgcacct accgctgtgc ccacccctg gccacactct tcaagatcct ggcgtccttc
 540
 tacatcagcc tagtcatctt ctacggctc atctgcatgt atacactgtg gtggatgcta
 600
 cggcgctccc tcaagaagta ctggttgag tcgatccgtg aggagagcag ctacagcgac
 660
 atccccgacg tcaagaacga ctgcgcttc atgctgcacc tcattgacca atacgaccg
 720
 ctctactcca agcgcttcgc cgtcttctg tcggaggtga gtgagaacaa gctgcggcag
 780
 ctgaacctca acaacgagtg gacgctggac aagctccggt acggagagaa gacaacgcgt
 840

<210> 406
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 406
 Leu Ile Cys Met Tyr Thr Leu Trp Trp Met Leu Arg Arg Ser Leu Lys
 1 5 10 15
 Lys Tyr Ser Phe Glu Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile
 20 25 30
 Pro Asp Val Lys Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln
 35 40 45
 Tyr Asp Pro Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val

50 55 60
 Ser Glu Asn Lys Leu Arg Gln Leu Asn Leu Asn Glu Trp Thr Leu
 65 70 75 80
 Asp Lys Leu Arg Tyr Gly Glu Lys Thr Thr Arg
 85 90

<210> 407
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 407
 gcctattgta ccagctctcc agggctgggg acttgctaga gcagggttcc cagtgcccc
 60
 aggtcttact ttgctctgcc tggctctcagg gtgtagggga tggagagctg gacttccagc
 120
 ctgcttcttg gctgtctagg ggccaggggc tcgggacaca gagctcctgg aggccgagca
 180
 caagccttgg gcagaggtga ggcagagctc tgactgtttc attcgactac gttgccaagg
 240
 agatgctcgc tcggagtggg tgcctctggc ctgggattcc aaaccaagct gccttctctg
 300
 atgtggcctt agtgcctctg gcggtatgtac cttggctctg cctggaccct ctctctcttc
 360
 caggcctctg tcccaccagg atgatgccta tccagagctc attgtcctct cccacttctt
 420
 ccccgagctt cccattccgt gtctctctgg agggcccatc atcatcctgg tggaggtgtt
 480
 gcaactgagga ccacagcagc cctcgcatc ccacgggcaa aggggtatgt gtagg
 535

<210> 408
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 408
 Met Leu Ala Arg Ser Gly Cys Ser Gly Ser Gly Ile Pro Asn Gln Ala
 1 5 10 15
 Ala Phe Ser Asp Val Ala Leu Val Leu Trp Ala Asp Val Pro Trp Leu
 20 25 30
 Cys Leu Asp Pro Leu Ser Leu Pro Gly Leu Cys Pro Thr Arg Met Met
 35 40 45
 Pro Ile Gln Ser Ser Leu Ser Ser Pro Thr Ser Ser Pro Ser Phe Pro
 50 55 60
 Phe Arg Val Ser Leu Glu Gly Pro Ser Ser Ser Trp Trp Arg Cys Cys
 65 70 75 80
 Thr Glu Asp His Ser Ser Pro Arg Ile Pro Thr Gly Lys Gly Val Cys
 85 90 95
 Val

<210> 409
 <211> 375

<212> DNA

<213> Homo sapiens

<400> 409

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ngtgtcatgg gtgtctatac cagcgatgag gccaaagactg ccaagacttt tggatttggt
60
ggacttccga ttacgactaa tatttctctt gccacaact tcaatatgga tgaaatttct
120
gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct
180
agaaaattga ccgaaattgc tggctctcag caaggggagt atcaggtgtc agatgcgact
240
gcagccttcc aagaagtgc acaattgttc ggctttataa ctacgattat tagtgccatt
300
gcaggaattt ccctttttgt tggagggact ggtgttatga acatcatgct ggtttcggtg
360
acggagcgta cgcgt
375

```

<210> 410

<211> 125

<212> PRT

<213> Homo sapiens

<400> 410

```

Xaa Val Met Gly Val Tyr Thr Ser Asp Glu Ala Lys Thr Ala Lys Thr
1      5      10      15
Phe Gly Ile Gly Leu Pro Ile Thr Thr Asn Ile Ser Leu Ala Asn
20     25     30
Asn Phe Asn Met Asp Glu Ile Ser Asp Ile Val Phe Arg Val Asn Asp
35     40     45
Thr Ser Leu Thr Pro Thr Val Gly Pro Glu Leu Ala Arg Lys Leu Thr
50     55     60
Glu Ile Ala Gly Leu Gln Gln Gly Glu Tyr Gln Val Ser Asp Ala Thr
65     70     75     80
Ala Ala Phe Gln Glu Val Gln Gln Leu Phe Gly Phe Ile Thr Thr Ile
85     90     95
Ile Ser Ala Ile Ala Gly Ile Ser Leu Phe Val Gly Gly Thr Gly Val
100    105    110
Met Asn Ile Met Leu Val Ser Val Thr Glu Arg Thr Arg
115    120    125

```

<210> 411

<211> 409

<212> DNA

<213> Homo sapiens

<400> 411

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ccacatactt caccctctc acccctcca cctactccac cacctggcag tcgccatcga
60
ggatgggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca
120
gcacgcggtc ggggccctt gagctcgaag gcgcggcgca tcgggcagtg ctgcgcggcc
180

```

tggtcgcagg gcacgtcgta ctggtgagac acgcggaagc acttgtggcc gatgtaggcg
 240
 cgatcggtcg tcccgaactg gcgctgatag gccgtgtaca caacacaaac tgttgtactc
 300
 ccggtccacc acgatcatgg gctgggactc gtgttccagg tggggggcca gggcttgggc
 360
 ctgcggtgag cgcgtggggg ggatggggca tagcgtcggg gaggaggtg
 409

<210> 412
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 412
 Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro
 1 5 10 15
 Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Gly Pro Gly Val
 20 25 30
 Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln
 35 40 45
 Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser
 50 55 60
 Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala
 65 70 75 80
 Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr
 85 90 95
 Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp
 100 105 110
 Gly Asp Cys Gln Val Val Glu
 115

<210> 413
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 413
 ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggt agggactcca
 60
 gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag
 120
 gcaccacctc catatcccgg cccacatcca gctggacccc ctgtcataca gcagccaaca
 180
 acacccatgt ttgtagctcc cccccaaag acccagcggc ttcttctactc agaggcctac
 240
 ctgaaatata ttgaaggact cagtgcggag tccaacagca ttagcaagtg ggatcagaca
 300
 ctggcagctc ggagacgcga cgtccatttg tcgaaagaac aggagagccg cctaccc
 357

<210> 414
 <211> 119
 <212> PRT

<213> Homo sapiens

<400> 414

```

Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
 1           5           10           15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
      20           25           30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
      35           40           45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
      50           55           60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
      65           70           75           80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
      85           90           95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Asp Val His Leu Ser Lys
      100          105          110
Glu Gln Glu Ser Arg Leu Pro
      115

```

<210> 415

<211> 332

<212> DNA

<213> Homo sapiens

<400> 415

```

tctagagcca acttggttat cgtaatgaat agagagacta catctatatc aattattacg
60
ctctatagta atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg gcgacttact aaaagaaaaa gaccatttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccgtccattg tcagaattca aggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

```

<210> 416

<211> 102

<212> PRT

<213> Homo sapiens

<400> 416

```

Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
 1           5           10           15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
      20           25           30
Gln Glu Tyr Gly Asp Leu Leu Lys Lys Asp His Leu Gln Asp Met
      35           40           45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
      50           55           60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

```

```

<400> 418
Glu Phe Leu Ala Val Ser Glu Val Gly Glu Asp Thr Phe Val Arg Ser
 1             5             10             15
Thr Glu Gly Asp Tyr Ala Ala Asn Val Glu Ala Val Val Thr Pro Ala
          20             25             30
Pro Ala Glu Lys Asp Ile Glu Gly Gln Pro Glu Ala Gln Glu His Asp
          35             40             45
Thr Pro Gly Thr Glu Thr Ile Glu Lys Leu Val Glu Trp Ala Gln Gly
          50             55             60
Ala Gly Ile Thr Val Asn Pro Arg Val Val Cys Tyr Tyr Thr Leu Lys
65             70             75             80
Cys Met Met Ile Lys Leu His His Pro Ala Ala Glu Ser Glu Glu Arg
          85             90             95
Glu Ser Glu Leu Ala Ala Val Leu Ile Pro Gly Asp Arg Glu Leu Asp
          100            105            110
Glu Lys Arg Leu Glu Ala Ala Leu Glu Pro Val Glu Phe Glu Leu Ala
          115            120            125
Gly Asp Lys Asp Phe Ala Asp Asn Asp Phe Leu Val Lys Gly Tyr Val

```

130	135	140
Gly Pro Arg Ala Leu Asn Ala Asn Gly Ile Lys Val Leu Ala Asp Pro		
145	150	155
Arg		160

<210> 419
 <211> 797
 <212> DNA
 <213> Homo sapiens

<400> 419
 atttcacccc aggaaaacca gtaaggacca atgattaagc ccaagggttg gtaccgagtt
 60
 cggatccata agtaccggcc gccaggggtg ctggaatttg ggctcccccc ggtgaaaata
 120
 tccatgcagc cgcgttgtct taggtagaaa agggagactg ggggtgggtg ggctgagctc
 180
 aagcccctgc ctacatactt tagtagtaac gactcccgat ctgcatccaa cacatttacc
 240
 gaacttctag taagcgcccc ccgctgcaag cgaaagcact cccctgccaa gaaacagatc
 300
 ttttcactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta
 360
 catgatctga agggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg
 420
 aaaatccttg acgttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa
 480
 ttccagtgtg gcagtgcacg cagattcttc attggtgtta gtgtatttcc atacggtatg
 540
 tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt
 600
 tttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggtctcat
 660
 aatttacaga gcaatcacag ccttctttga aacggagaaa ttagattcta tgaaattttg
 720
 tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaaa agatgaggct
 780
 tgaatgatgg ctggcca
 797

<210> 420
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu
 1 5 10 15
 Arg Cys Leu Lys Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys
 20 25 30
 Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn
 35 40 45
 Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg


```

      50              55              60
Thr Leu Ser His Thr Asn Val Leu Ser Pro Glu Asn Val Lys Asp Phe
65              70              75              80
His Gln Pro Leu Pro Asp Ser Pro Asn Leu Glu Asn Val Met Ser Thr
      85              90              95
Leu Gln Ile Met Tyr Thr Leu Phe Val Gln
      100              105

```

<210> 421
 <211> 406
 <212> DNA
 <213> Homo sapiens

```

<400> 421
ggatccacca tgatggagcc caccacacca tcctcagtc acctgctgca gcttctccat
60
aaccacaacac aggtcaatct tgtctcccta aacacaccat gtgctctcat gctgccatgg
120
tttgcttggg gccctctcta cctcctctgc tttctggaga acccttgac tctcccaag
180
ccttcaagtt ggaaagtga cagtcagcat atgtctctag ctcagccctt actgcgtgga
240
ttcatgaaga ttggttcaact gtcagccctt gaccagaacg tgtgttttag gaaagcagga
300
accaagtctt accaatgtct gtagtccag cctccaccct ggcatacagt aggtgctcat
360
tgaatgtggg agggaaagag gagacacatg gaagggaatg tcattc
406

```

<210> 422
 <211> 104
 <212> PRT
 <213> Homo sapiens

```

<400> 422
Met Met Glu Pro Thr His Pro Ser Ser Val His Leu Leu Gln Leu Leu
1              5              10              15
His Asn Pro Thr Gln Val Asn Leu Val Ser Leu Asn Thr Pro Cys Ala
      20              25              30
Leu Met Leu Pro Trp Phe Ala Trp Gly Pro Leu Tyr Leu Leu Cys Phe
      35              40              45
Leu Glu Asn Pro Cys Thr Pro Pro Lys Pro Ser Ser Trp Lys Val Asn
      50              55              60
Ser Gln His Met Ser Leu Ala Gln Pro Leu Leu Arg Gly Phe Met Lys
65              70              75              80
Ile Gly Ser Leu Ser Ala Pro Asp Gln Asn Val Cys Phe Arg Lys Ala
      85              90              95
Gly Thr Lys Ser Tyr Gln Cys Leu
      100

```

<210> 423
 <211> 628
 <212> DNA
 <213> Homo sapiens

<400> 423

ngccacccta cgcctcgctt gcaatggcaa cttcagatcc ccggtggcac cgtagtctta
 60
 gagccaccgg ttctgagcgg ggaggacgac ggggttgggg cggaggaagg agagggagaa
 120
 ggagatgggg atttctgac gcagacccaa gcccacacgc cgactccagc acccgcttgg
 180
 ccggcgcccc cagccacacc gcgcttcttg gccctcgcaa atggctccct gttggtgccc
 240
 ctcttgagtg ccaaggaggc gggcgtctac acttgccgtg cacacaatga gctgggcgcc
 300
 aactctacgt caatacgcgt ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc
 360
 gccgggggag aaccgcacgg acaggccccg acctctgagc gcaagtccac agccaagggc
 420
 cggggcaaca gcgtcctgcc ttccaaaccc gagggcaaaa tcaaaggcca aggcctggcc
 480
 aaggtcagca ttctcgggga gaccgagacg gagccggagg aggacacaag tgagggagag
 540
 gaggccgaag accagatcct cgcggaccgc gcggaggagc agcgctgtgg caacggggac
 600
 ccctctcggt acgtttctaa ccacgcgt
 628

<210> 424

<211> 209

<212> PRT

<213> Homo sapiens

<400> 424

Xaa	His	Pro	Thr	Pro	Arg	Leu	Gln	Trp	Gln	Leu	Gln	Ile	Pro	Gly	Gly
1				5				10						15	
Thr	Val	Val	Leu	Glu	Pro	Pro	Val	Leu	Ser	Gly	Glu	Asp	Asp	Gly	Val
			20					25					30		
Gly	Ala	Glu	Gly	Glu	Gly	Gly	Glu	Gly	Asp	Gly	Asp	Leu	Leu	Thr	Gln
			35				40					45			
Thr	Gln	Ala	Gln	Thr	Pro	Thr	Pro	Ala	Pro	Ala	Trp	Pro	Ala	Pro	Pro
			50				55				60				
Ala	Thr	Pro	Arg	Phe	Leu	Ala	Leu	Ala	Asn	Gly	Ser	Leu	Leu	Val	Pro
65				70					75					80	
Leu	Leu	Ser	Ala	Lys	Glu	Ala	Gly	Val	Tyr	Thr	Cys	Arg	Ala	His	Asn
				85					90					95	
Glu	Leu	Gly	Ala	Asn	Ser	Thr	Ser	Ile	Arg	Val	Ala	Val	Ala	Ala	Thr
			100					105					110		
Gly	Pro	Pro	Lys	His	Ala	Pro	Gly	Ala	Gly	Gly	Glu	Pro	Asp	Gly	Gln
			115				120					125			
Ala	Pro	Thr	Ser	Glu	Arg	Lys	Ser	Thr	Ala	Lys	Gly	Arg	Gly	Asn	Ser
			130				135				140				
Val	Leu	Pro	Ser	Lys	Pro	Glu	Gly	Lys	Ile	Lys	Gly	Gln	Gly	Leu	Ala
145				150					155					160	
Lys	Val	Ser	Ile	Leu	Gly	Glu	Thr	Glu	Thr	Glu	Pro	Glu	Glu	Asp	Thr
				165				170						175	
Ser	Glu	Gly	Glu	Glu	Ala	Glu	Asp	Gln	Ile	Leu	Ala	Asp	Pro	Ala	Glu

180 185 190
 Glu Gln Arg Cys Gly Asn Gly Asp Pro Ser Arg Tyr Val Ser Asn His
 195 200 205
 Ala

<210> 425
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 425
 ccggccgctcg aagactttga ggacgatgta gctcgcagcg cagcgttacg agccctggag
 60
 tacgtggatt tgaccccagg cactnaagtg cgcgtcatcg ccattgacac cgtgttccta
 120
 ggatcgtgca cgaatggccg tgaggactta cggctggctg ctgagggtcc caaaggacga
 180
 catatcgcag cgggcacccg gatgctcgtc gccctggat ctgctcgtgt ccgtctgcag
 240
 gctatggagg aaggcctcga cgagatcggg tcccggtttg ctgacatctt tcgcaataac
 300
 tctgcgaaca atggcttggt actggctcag gttgaccccg aggtcgtcga agagttgtgg
 360
 gactttgccg agcagcatcc tggtagcag ctcaccgtct ccctcgagaa tcggacgatc
 420
 aaccttcggt gtcgcacgac ctaccgttc catattgatg acgtcacgcg t
 471

<210> 426
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 426
 Pro Ala Val Glu Asp Phe Glu Asp Asp Val Ala Arg Ser Ala Ala Leu
 1 5 10 15
 Arg Ala Leu Glu Tyr Val Asp Leu Thr Pro Gly Thr Xaa Val Arg Val
 20 25 30
 Ile Ala Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Glu
 35 40 45
 Asp Leu Arg Leu Ala Ala Glu Val Pro Lys Gly Arg His Ile Ala Ala
 50 55 60
 Gly Thr Arg Met Leu Val Ala Pro Gly Ser Ala Arg Val Arg Leu Gln
 65 70 75 80
 Ala Met Glu Glu Gly Leu Asp Glu Ile Gly Ser Arg Phe Ala Asp Ile
 85 90 95
 Phe Arg Asn Asn Ser Ala Asn Asn Gly Leu Leu Leu Ala Gln Val Asp
 100 105 110
 Pro Glu Val Val Glu Glu Leu Trp Asp Phe Ala Glu Gln His Pro Gly
 115 120 125
 Glu Gln Leu Thr Val Ser Leu Glu Asn Arg Thr Ile Asn Leu Pro Gly
 130 135 140
 Arg Thr Thr Tyr Pro Phe His Ile Asp Asp Val Thr Arg

145 150 155

<210> 427
 <211> 546
 <212> DNA
 <213> Homo sapiens

<400> 427
 ctagcggtag tagaaggat gcagtttgat cgcggtact tgtctccgta tttcatcaac
 60
 aatcaagaaa caatgaatgc agagctagaa aaccatttta ttcttcttgt tgataagaaa
 120
 atttctaata tccgtgactt gctaccaatt ttggaagggt ttgctaaagc atcgcgccca
 180
 ttgttgatca ttgcggaaga cggtgaaggc gaagcggtgg caaccttggt tgtaaacact
 240
 atgcgcggca tcgtaaaaagt agcggcagcg aaagcgccag gttttggtga tcgccgtaaa
 300
 gcaatgcttc aagacattgc tgtgctaacg ggttcaactg ttatttcaga agaaattggc
 360
 attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgcggt tacattgaca
 420
 aaagaaagta caacgattgt tgatggtgcg ggtgttgacg ctaatattac tggtcgtggt
 480
 gagcaaattc gtgcagaaat tgctaactct tcttctggct acgataaaga gaaattgcaa
 540
 gaacgc
 546

<210> 428
 <211> 182
 <212> PRT
 <213> Homo sapiens

<400> 428
 Leu Ala Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro
 1 5 10 15
 Tyr Phe Ile Asn Asn Gln Glu Thr Met Asn Ala Glu Leu Glu Asn Pro
 20 25 30
 Phe Ile Leu Leu Val Asp Lys Lys Ile Ser Asn Ile Arg Asp Leu Leu
 35 40 45
 Pro Ile Leu Glu Gly Val Ala Lys Ala Ser Arg Pro Leu Leu Ile Ile
 50 55 60
 Ala Glu Asp Val Glu Gly Glu Ala Leu Ala Thr Leu Val Val Asn Thr
 65 70 75 80
 Met Arg Gly Ile Val Lys Val Ala Ala Ala Lys Ala Pro Gly Phe Gly
 85 90 95
 Asp Arg Arg Lys Ala Met Leu Gln Asp Ile Ala Val Leu Thr Gly Ser
 100 105 110
 Thr Val Ile Ser Glu Glu Ile Gly Ile Lys Leu Glu Glu Ala Thr Ile
 115 120 125
 Glu Gln Leu Gly Thr Ala Lys Arg Val Thr Leu Thr Lys Glu Ser Thr
 130 135 140
 Thr Ile Val Asp Gly Ala Gly Val Ala Ala Asn Ile Thr Gly Arg Val

145 150 155 160
 Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys
 165 170 175
 Glu Lys Leu Gln Glu Arg
 180

<210> 429
 <211> 425
 <212> DNA
 <213> Homo sapiens

<400> 429
 gctagcagcc cttacaggag acgggctaataataatgcag cagtggctcc gacaacttgc
 60
 ccgttgacgc cggtcacgga tccatttgct tttagtagac aggcgctcca aagtacacca
 120
 ctgggcagtt cgtccaaaag cagtccacct gtcttgcaag gccagcccc cgcagggttt
 180
 tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcaggggacc
 240
 ctgtgagccc ctgcctggac ctctgacaca gccagagca catgccagtc cgttttctgg
 300
 tgcattgaca ccttcagcac ctctggggcc tgagatgaac aggagtgcag aggtcgggtcc
 360
 cagttcagag cctgaagtgc agactctgcc atatcttcct cactacattc caggagtgga
 420
 tctctg
 425

<210> 430
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 430
 Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile
 1 5 10 15
 His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val
 20 25 30
 Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly
 35 40 45
 Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn
 50 55 60
 Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro
 65 70 75 80
 Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro
 85 90 95
 Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu
 100 105 110
 Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val
 115 120 125
 Asp Pro
 130

<210> 431
 <211> 192
 <212> DNA
 <213> Homo sapiens

<400> 431
 cttagccatcc accagcgtac acacacggga gagaggccct acactggcct cgggtgcaac
 60
 cgccgcttcc gccagcgcac ggccctcgtc atccaccagc gcatccacac gggcgagaag
 120
 cctnaccgt gcccgactg cgagcggcgc ttctctcct cctctcgcct ggtcagtcac
 180
 cgcggtgtgc ac
 192

<210> 432
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 432
 Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly
 1 5 10 15
 Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His
 20 25 30
 Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu
 35 40 45
 Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His
 50 55 60

<210> 433
 <211> 635
 <212> DNA
 <213> Homo sapiens

<400> 433
 nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtgagta tctttggtac
 60
 ctcattggagg agcgtggcgc gtatgcggag gccgcgcgc tcatgccgct gctgctccgg
 120
 accgaccgag gcgcgtggga cacgtttgtg tgctgctacc tcgagcggca ccaaaggat
 180
 gcgatactcc cgcacattcc gacgcaggac cccagctga gtgagatggt gtacgatctc
 240
 gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg
 300
 ccgagtcaca tctactcgaa gcaggcgggtg gctgcggcga tcggcgatca cgcacgaacc
 360
 agccgcacgc tgctcgagtg cctcgcacag ctgtacatgg ccgcacatca gcccggaag
 420
 gctctgacat actacatgcy cctgcgtgat ccatgcgtgt ttgatctcat tcgcgagtac
 480
 gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcaggaatgc
 540

gccgggtccca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atataccac
 600
 tcgattccca tccagcgcgc catggcgcag ctcga
 635

<210> 434
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 434
 Xaa Pro Ala Ala Leu Gly Tyr Asp Val Ala Ala Ile Gly Arg Glu
 1 5 10 15
 Tyr Leu Trp Tyr Leu Met Glu Glu Arg Gly Ala Tyr Ala Glu Ala Ala
 20 25 30
 Ala Leu Met Pro Leu Leu Leu Arg Thr Asp Arg Gly Ala Trp Asp Thr
 35 40 45
 Phe Val Cys Cys Tyr Leu Glu Arg His Gln Arg Asp Ala Ile Leu Pro
 50 55 60
 His Ile Pro Thr Gln Asp Pro Gln Leu Ser Glu Met Val Tyr Asp Leu
 65 70 75 80
 Val Leu Val His Leu Leu Gln His Asp Pro Thr Gln Leu Leu Ala Thr
 85 90 95
 Leu Arg Ala Trp Pro Ser His Ile Tyr Ser Lys Gln Ala Val Ala Ala
 100 105 110
 Ala Ile Gly Asp His Ala Arg Thr Ser Arg Thr Leu Leu Glu Cys Leu
 115 120 125
 Ala Gln Leu Tyr Met Ala Ala His Gln Pro Gly Lys Ala Leu Thr Tyr
 130 135 140
 Tyr Met Arg Leu Arg Asp Pro Cys Val Phe Asp Leu Ile Arg Glu Tyr
 145 150 155 160
 Asp Leu Leu Ile Asp Val Gln His His Ile Gly Thr Leu Val Glu Leu
 165 170 175
 Asp Gln Glu Cys Ala Gly Ser Thr Glu Pro Arg Ser Ser Ala Leu Met
 180 185 190
 Pro Leu Leu Val Pro Tyr Thr His Ser Ile Pro Ile Gln Arg Ala Met
 195 200 205
 Ala Gln Leu
 210

<210> 435
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 435
 nncgtacgtt cgcgtatttt ccgcgcccgg gaagctatcg ataataaagt tcaaccgctg
 60
 atccagcgtt agcaatggcg ggcacaggaa gggacttag gcatgcagaa agaaaagctt
 120
 tccgctctga tggatggtga atcgttcgac agcgagctgt tgagttctct gtcgcaagat
 180
 cgaacgcttc aacaaagctg gcagggctat cacctgatac gtgacacact gcgaggtgat
 240

gtcgggcaag tgatgcatct cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa
 300
 cccgccccgc tgggtgccttc cgccgttcag gaatctcagc cgcagcctca cacctggcag
 360
 aaaatgccgt tctgggacaa agtgcgtccc tgggagagcc agattacgca aatcgggtatg
 420
 gcggcctgcg tgtcgctggc ggtgatcgtc ggcgtgcagc agtacaacca gccttctgcg
 480
 ccatcgaacg cgt
 493

<210> 436

<211> 130

<212> PRT

<213> Homo sapiens

<400> 436

Met	Gln	Lys	Glu	Lys	Leu	Ser	Ala	Leu	Met	Asp	Gly	Glu	Ser	Phe	Asp
1				5					10					15	
Ser	Glu	Leu	Leu	Ser	Ser	Leu	Ser	Gln	Asp	Arg	Thr	Leu	Gln	Gln	Ser
		20						25					30		
Trp	Gln	Gly	Tyr	His	Leu	Ile	Arg	Asp	Thr	Leu	Arg	Gly	Asp	Val	Gly
		35					40					45			
Gln	Val	Met	His	Leu	Asp	Ile	Ala	Asp	Arg	Val	Ala	Ala	Ala	Leu	Glu
	50					55				60					
Lys	Glu	Pro	Ala	Arg	Leu	Val	Pro	Ser	Ala	Val	Gln	Glu	Ser	Gln	Pro
65					70					75				80	
Gln	Pro	His	Thr	Trp	Gln	Lys	Met	Pro	Phe	Trp	Asp	Lys	Val	Arg	Pro
		85							90					95	
Trp	Ala	Ser	Gln	Ile	Thr	Gln	Ile	Gly	Met	Ala	Ala	Cys	Val	Ser	Leu
		100						105					110		
Ala	Val	Ile	Val	Gly	Val	Gln	Gln	Tyr	Asn	Gln	Pro	Ser	Ala	Pro	Ser
		115					120						125		
Asn	Ala														
	130														

<210> 437

<211> 447

<212> DNA

<213> Homo sapiens

<400> 437

ntggtaaccg gtgtccctga tatggaccct gctgtgtag agcgtaaatt atttatttta
 60
 cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caacttttac
 120
 attaatacat tctcatacaa aacaatcggt tataaagggt agttaaccac tgaacaagtg
 180
 ccacaatatt tcttagatgt acaaaatcca agtatggtaa cggcattagc gcttggtcat
 240
 tcacgtttct caacaaatac atttcctcgt tggcgtttag cacaaccatt ccgttacatc
 300
 gtcataatg gcgaaatcaa tacggttcgc ggtaatatca attggatgaa agcacgtgaa
 360

gcgttacttg aagctgaatt tttcactcgc tcagaattag atatgttaat gccaatctgt
 420
 acggatggta tgtctgactc ggcaagg
 447

<210> 438
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 438
 Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys
 1 5 10 15
 Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val
 20 25 30
 Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr
 35 40 45
 Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe
 50 55 60
 Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His
 65 70 75 80
 Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro
 85 90 95
 Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn
 100 105 110
 Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe
 115 120 125
 Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met
 130 135 140
 Ser Asp Ser Ala Arg
 145

<210> 439
 <211> 395
 <212> DNA
 <213> Homo sapiens

<400> 439
 nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tcctgcagca gctgcaccag
 60
 cttcccaggg gccggtgga cctggccacg caaagcctga cggtggagac ctgcagggcc
 120
 ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggctctgag tgactgcatg
 180
 ctcagcgagg aaggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc
 240
 tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc
 300
 ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg
 360
 gacgatgcct tcgccacctt ctgcgggggc ctggc
 395

<210> 440

<211> 128
 <212> PRT
 <213> Homo sapiens

<400> 440
 Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His
 1 5 10 15
 Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val
 20 25 30
 Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys
 35 40 45
 Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr
 50 55 60
 Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp
 65 70 75 80
 Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys
 85 90 95
 Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn
 100 105 110
 Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu
 115 120 125

<210> 441
 <211> 364
 <212> DNA
 <213> Homo sapiens

<400> 441
 gcccagtact acgtgaacat gttc gatgcc gagcagggct tcttcgacag gcgcagcccg
 60
 ggcggcgagt tccaagccgg cttggatccg gaatcctggg gcggtctggt cactgagacc
 120
 gacggttgga acttcgcctt ccacgctcca caggacggcc gggggctggc cgcgctctac
 180
 ggcggtccga aaggcttgga gaacaagctc gatgcctttt tcgcgacgcc ggaaaacgcg
 240
 gacaagccgg cgtacggcgg aatccacgaa atggtcgagg ccagagcggg ccggatgggc
 300
 caattgggca tgtccaacga gccctgcgac catattccct acatctacaa ctatgccggc
 360
 gcgc
 364

<210> 442
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 442
 Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp
 1 5 10 15
 Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser
 20 25 30
 Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His

```

      35              40              45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys
   50              55              60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala
65              70              75              80
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala
      85              90              95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile
      100              105              110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala
      115              120

```

<210> 443

<211> 430

<212> DNA

<213> Homo sapiens

<400> 443

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accgggttacg gctcagtgca acaagagatg ttcgccaaca acctcgtgcg gatgccgctg
60
ctcatgggtgc tggcaatccc cttcgccaag atcctctcga cgacctgtc catcggatcg
120
ggcgggtccgg cggcgtcttc cggccctggc atggtcacgc gcggagccac tggcgcgga
180
ctgtggcgcc tcctcgaggg gctgccaggt atcccatcct caccgatgag ttctgtcatt
240
gtcggcatga tcgcctgctt cggtgcggtt gcccatgcc cactcggcgt gctgctcatg
300
gttgccgaga tgaccggaaa cctgtcgctg ctcgctcctg gcatgatcgc cgtcgccgc
360
gctggccgag ttgtcgggga cacttcgatc tacacctctc agctcaagga tcgcctggag
420
ggcgacgcgt
430

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<210> 444

<211> 143

<212> PRT

<213> Homo sapiens

<400> 444

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Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val
 1              5              10              15
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu
      20              25              30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly
      35              40              45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu
      50              55              60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile
65              70              75              80
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly
      85              90              95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala

```

	100		105		110
Pro Gly Met Ile Ala Val Ala Val Ala Gly Arg Val Val Gly Asp Thr					
	115		120		125
Ser Ile Tyr Thr Ser Gln Leu Lys Asp Arg Leu Glu Gly Asp Ala					
	130		135		140

<210> 445
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 445
 ccattggggct gcttagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt
 60
 tcttgcttta ttgctcacc tgtccagggt tcctctgtt tgtgaggag ctgctgccac
 120
 cttgggtcca ggaagcatga agctccgcag gtcagcctcc tgggtggagg acttttcctt
 180
 agttttcttt gctcttctgc tctgagtcga gccctggctg gacctttgat cccttctctc
 240
 tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc
 300
 caagtgggaa caagccatga aggagctgca ccccgaaag tctgagggtg ggacacgcgt
 360

<210> 446
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 446
 Met Ala Cys Ser His Leu Glu Met Ala Ser Gln Ile Leu Lys Arg Gln
 1 5 10 15
 Lys Lys Lys Val Arg Lys Phe Pro Asp Lys Glu Arg Arg Asp Gln Arg
 20 25 30
 Ser Ser Gln Gly Trp Thr Gln Ser Arg Arg Ala Lys Lys Thr Lys Glu
 35 40 45
 Lys Ser Ser His Gln Glu Ala Asp Leu Arg Ser Phe Met Leu Pro Gly
 50 55 60
 Pro Lys Val Ala Ala Ala Pro Ser Gln Thr Glu Gly Thr Leu Asp Arg
 65 70 75 80
 Val Ser Asn Lys Ala Arg Asn Leu Pro Cys Trp Cys His Gln Leu Arg
 85 90 95
 Gly Leu Pro Arg Gly
 100

<210> 447
 <211> 487
 <212> DNA
 <213> Homo sapiens

<400> 447
 acgcgtgaag ggggaaattg ctcgtgccac ctgaggatta atcattaccc tggaaccctt
 60

cccaaggcca tcaaggaaca cgcacccctt accagacctt ccagctgctg ggggctctcc
 120
 gaggtaggct gaggtcatgg agaaggggaat ggggggcccc catggccagc tggacctgat
 180
 cactgcctcc cactcagcc acagccctca gggccctgtg ccagtccaga agcccattca
 240
 gggacacctt tggccaatgt tctgtttcat ctgcgaggca accttccccca gtgccccaac
 300
 catagcgttt tcccccaaac accctcagga aggagggacc actacctgtg cagggggggc
 360
 caggagcctc ctgagagcct catatgggga ggaagtggta ccatctcacc cccattgcct
 420
 ttctctecta ctccacctg gccagcttcc ctcagtggcc ctectgcctc agtgccccctt
 480
 cagcgt
 487

<210> 448
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 448
 Met Glu Lys Gly Met Gly Gly Pro His Gly Gln Leu Asp Leu Ile Thr
 1 5 10 15
 Ala Ser Pro Leu Ser His Ser Pro Gln Gly Pro Val Pro Val Gln Lys
 20 25 30
 Pro Ile Gln Gly His Leu Trp Pro Met Phe Cys Phe Ile Cys Glu Ala
 35 40 45
 Thr Phe Pro Ser Ala Pro Thr Ile Ala Phe Ser Pro Lys His Pro Gln
 50 55 60
 Glu Gly Gly Thr Thr Thr Cys Ala Gly Gly Ala Arg Ser Leu Leu Arg
 65 70 75 80
 Ala Ser Tyr Gly Glu Glu Val Val Pro Ser His Pro His Cys Leu Ser
 85 90 95
 Leu Leu Leu Pro Pro Gly Gln Leu Pro Ser Val Pro Leu Leu Pro Gln
 100 105 110
 Cys Pro Phe Thr Arg
 115

<210> 449
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 449
 gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttgga gcaggccaag
 60
 ggaagggggg agcgggcaga gaagctggag agggagctac agcgactcca ggaggagaac
 120
 gggaggctgg ccaggaaggt gacctccctg gagacagcca ccgagaaagt cgaggccctg
 180
 gagcatgaga gccaggcct gcagctggag aaccggactc tgaggaagtc tctggacacc
 240

ttgcagaacg tgccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca
 300
 gagaacctgg agctgcgcag gctggtggag accatgcgga gacgacaacg cgt
 353

<210> 450
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 450
 Glu Leu Ser Gln Leu Glu Phe Glu Lys Arg Gln Leu His Arg Asp Leu
 1 5 10 15
 Glu Gln Ala Lys Glu Lys Gly Glu Arg Ala Glu Lys Leu Glu Arg Glu
 20 25 30
 Leu Gln Arg Leu Gln Glu Glu Asn Gly Arg Leu Ala Arg Lys Val Thr
 35 40 45
 Ser Leu Glu Thr Ala Thr Glu Lys Val Glu Ala Leu Glu His Glu Ser
 50 55 60
 Gln Gly Leu Gln Leu Glu Asn Arg Thr Leu Arg Lys Ser Leu Asp Thr
 65 70 75 80
 Leu Gln Asn Val Ser Leu Gln Leu Glu Gly Leu Glu Arg Asp Asn Lys
 85 90 95
 Gln Leu Asp Ala Glu Asn Leu Glu Leu Arg Arg Leu Val Glu Thr Met
 100 105 110
 Arg Arg Arg Gln Arg
 115

<210> 451
 <211> 444
 <212> DNA
 <213> Homo sapiens

<400> 451
 gtgatgcggc tgactaagcc tactttatcc accaatatcc cagtaacatg tgaagagaaa
 60
 gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cgттаатggt
 120
 gcagaagttt таатgттggg agaaatgctg actttaccac agaattttgg gaatatattt
 180
 ttgggagaga ctttttccag ttatatcagc gttcataatg atagcaatca agttgtaaaa
 240
 gacatattag таааagctga tcttcagaca agttctcagc gtttaaatct ttcagcctcc
 300
 аатgctgcag tggctgaact тааассggat tgттgtattg atgatgtcat аатсатgaa
 360
 gtcaaagaaa ttggaacaca catcttggtg tgtgctgtga gttatacaac tcaggctgga
 420
 gaaaaaatgt atttcagaaa attt
 444

<210> 452
 <211> 148
 <212> PRT

<213> Homo sapiens

<400> 452

```

Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
 1           5           10           15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
      20           25           30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
      35           40           45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
      50           55           60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
65           70           75           80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
      85           90           95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
      100          105          110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
      115          120          125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
      130          135          140
Phe Arg Lys Phe
145

```

<210> 453

<211> 373

<212> DNA

<213> Homo sapiens

<400> 453

```

gctagctctg accccacctt tgccaagtgg cactaggggtg gccaatgggg actaggggtg
60
tataattgga aaatacagtc tccctgttg tccaagaaag gcccagatg acctggggct
120
tgaaaggcac tcccgctggg tgcttcctgg gagcaggtgg ggggcagcgg ggcggcgggg
180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggctctgag cccactggt
240
gcgttttggg atgggctggc ctgcgcggct gtcgtttcag agcacacaga agagaccctg
300
ccacaggagg agtgggagga gaagctgttg atgttcctgc gagacaccct ggccatcatt
360
tctgacaacg cgt
373

```

<210> 454

<211> 108

<212> PRT

<213> Homo sapiens

<400> 454

```

Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
 1           5           10           15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```

20 25 30
 Gln Ala Ser Pro Ser Gln Asn Ala Pro Val Gly Leu Arg Ala Gln His
 35 40 45
 Leu Pro Trp Ser Trp Gly Cys Ser Ala Gln Thr Gly Pro Ala Ala Pro
 50 55 60
 Leu Pro Pro Thr Cys Ser Gln Glu Ala Pro Ser Gly Ser Ala Phe Gln
 65 70 75 80
 Ala Pro Gly His Leu Gly Pro Phe Leu Asp Asn Arg Gly Asp Cys Ile
 85 90 95
 Phe Gln Leu Tyr Asn Pro Ser Pro His Trp Pro Pro
 100 105

<210> 455

<211> 602

<212> DNA

<213> Homo sapiens

<400> 455

cctaggcaaa gcatgcccac cctacctccc cttaccctta cccttcattt tcccctaagc
 60
 acccatcacc accgatgtta ctgtatgtgt ttgcttacgc tgacagccca ccaccacac
 120
 tggaaatgcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
 180
 gagcttttga ggggtgttggg cacagagtgg agtgggtact taataagtat ctgtggaatg
 240
 aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
 300
 cttgccactt actaagtcct ttttctctcg cccctctca ctgacctggg tttgatgccca
 360
 gacagcacag atgggctagg gaggcagggtg gggaagcaga gatctgcgtc tcttgagct
 420
 ggagctgggt ggtggggctc cttcctgggt ctgaggagc tcattgggga ggtggcagcg
 480
 acccctcag gagcctctgt cgctgcact cagatctgtg cctttccaca gcgcccggag
 540
 gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggctcacgc
 600
 gt
 602

<210> 456

<211> 100

<212> PRT

<213> Homo sapiens

<400> 456

Met Pro Thr Leu Pro Pro Leu Thr Leu Thr Leu His Phe Pro Leu Ser
 1 5 10 15
 Thr His His His Arg Cys Tyr Cys Met Cys Leu Leu Thr Leu Thr Ala
 20 25 30
 His His Pro His Trp Asn Val Arg Thr Thr Lys Ala Gly Leu Leu Ala
 35 40 45
 Ala Leu Ala Thr Ala Gly Ser Pro Glu Leu Cys Arg Val Leu Gly Thr


```

      50              55              60
Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg
65              70              75              80
Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe
      85              90              95
Leu Ala Thr Tyr
      100

```

<210> 457
 <211> 324
 <212> DNA
 <213> Homo sapiens

```

<400> 457
acgcgtcatg tggatattcc tgggaggttc ccaggaacgt ttctggacgg gcccccgacc
60
agaggtcagg gaacttttct tattattctg cactgcccc gggatagtca aaccaggtct
120
tcccccttctg ctggccgcaa cagccagcc gccgccacga ccgcacgctg aattcatgac
180
ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcatcgaaga
240
tcgttttctg tccactggcc agcgccacta tgatcaggtg gggatatccgc ccggcgggcg
300
gagcaccggg acgccggggc gccg
324

```

<210> 458
 <211> 105
 <212> PRT
 <213> Homo sapiens

```

<400> 458
Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro
1      5      10      15
Arg Pro Glu Val Arg Glu Leu Phe Leu Leu Phe Cys Thr Cys Pro Gly
      20      25      30
Ile Val Lys Pro Gly Leu Pro Leu Leu Leu Ala Ala Thr Arg Gln Pro
      35      40      45
Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln
      50      55      60
Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe
65      70      75      80
Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly
      85      90      95
Gly Gly Ser Thr Gly Thr Pro Gly Arg
      100      105

```

<210> 459
 <211> 415
 <212> DNA
 <213> Homo sapiens

<400> 459

acgcgttcat tggcatctg cttccatgga tttcctgcgg ggaggcgcgg ccgagagtgc
 60
 ggggtgctgaa cagcagactt cagtgatcgt ttcaaccacc ggccgagatg ggtcctgacg
 120
 ctgggcttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccgggtggtt
 180
 tatgctgccg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaaggg
 240
 agaggcctca cccgacagct gggcatcgga tttacgaagc ccacgacgaa tcttcctcgc
 300
 ctctcaaaag ccgatcatcg gcatgccagg tttgtggttg aatgcttcga tcaacacact
 360
 aggatcggtg ggggccacca catacaccga gcggcaatcg agcggatacg acctc
 415

<210> 460

<211> 105

<212> PRT

<213> Homo sapiens

<400> 460

Met	Pro	Met	Ile	Gly	Phe	Glu	Glu	Ala	Arg	Lys	Ile	Arg	Arg	Gly	Leu
1				5					10					15	
Arg	Lys	Ser	Asp	Ala	Gln	Leu	Ser	Gly	Glu	Ala	Ser	Pro	Phe	Lys	His
		20						25				30			
Val	Gln	Ile	Pro	Arg	Glu	Gly	Arg	Ala	Gln	Ser	Ser	Ala	Gly	Ser	Ile
		35					40					45			
Asn	His	Arg	Asn	Arg	Ala	Ala	Arg	Asp	Gln	Glu	Arg	Glu	Arg	Lys	Arg
	50					55				60					
Leu	Glu	Ala	Gln	Arg	Gln	Asp	Pro	Ser	Arg	Pro	Val	Val	Glu	Thr	Ile
65				70					75					80	
Thr	Glu	Val	Ser	Cys	Ser	Thr	Pro	Ala	Leu	Ser	Ala	Ala	Pro	Pro	Arg
			85						90					95	
Arg	Lys	Ser	Met	Glu	Ala	Asp	Ala	Glu							
			100					105							

<210> 461

<211> 357

<212> DNA

<213> Homo sapiens

<400> 461

acgcgttcga ggtcggctaa atttatcatg cgcacgacaa agagagtagt ggctcacaac
 60
 cgggtcacat gcatgatgac aaaaactggc agaataagagt tgatgtcatc ccgtctacca
 120
 gctcctagaa ccagctcaga gagtcccggt gtcgggtaccg tcgagactca gtacacaact
 180
 gtcgcgatac cggacgaccc tcttcatctg gttgcagatg ggcgctctcaa tcacgtcact
 240
 gtcgcttacg aaacctacgg gaagctcaat acgtccagcg acaatgcggt ctatacctgt
 300
 catgcgctta ctggtgatgc ccatgcagcc ggatttcacc ccggtgtagt ccgtccg
 357

<210> 462
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 462
 Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val
 1 5 10 15
 Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile
 20 25 30
 Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser
 35 40 45
 Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro
 50 55 60
 Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr
 65 70 75 80
 Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala
 85 90 95
 Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe
 100 105 110
 His Pro Gly Val Val Arg Pro
 115

<210> 463
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 463
 gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac
 60
 gaggcagctg gtgacgatga agtggtgcga tgcgaggaat gcgacgtat cctggtgcgt
 120
 accggagagt ccatctgagc ccttcttggtg gcggtgatgc cgggatatcc gtagaattag
 180
 cggtcggacg agccatccgg gtgatcgagg cagcggtagg ttgtcgagga aagtcggggc
 240
 tccatagagc aggggtggtg gtaacgccc cccggggtga cccgcgggaa agtgccacag
 300
 agaacagact gccggtttcg agccggtgag ggtgaaacgg tggagtaagt gccaccgcg
 360
 tcatcggtga cggtgacggc atggcaaacc ccacctggag caaggccaag aagaccgtga
 420
 ggtcgcggaac gcgt
 434

<210> 464
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```

      1           5           10           15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
      20           25           30
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
      35           40           45
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
      50           55           60
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
      65           70           75           80
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
      85           90           95
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
      100          105          110
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
      115          120          125

```

<210> 465
 <211> 438
 <212> DNA
 <213> Homo sapiens

```

<400> 465
gatcatttag aatttatgga agaagctgat gtgaaagcta tggtaaatac tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgtc agtacggagt agacattgct atttogacgg atgctaatac agggacgtcg
180
ccagcgttat cattacggtt aatgatgaat atggcatgta ccttgtttgg tatgacacct
240
gaaaccgccc ttgcaggggt aacaattcat gcggcaaaag cgttggggat tagcgattct
300
catggcactt tagaagttgg caaggtagct gattttgtct gctgggatgt ggaaagcccc
360
ggtgaacttt gttattggtt aggagagcag ttagtaaagc aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

```

<210> 466
 <211> 143
 <212> PRT
 <213> Homo sapiens

```

<400> 466
Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
      1           5           10           15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
      20           25           30
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
      35           40           45
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
      50           55           60
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro

```

```

65          70          75          80
Glu Thr Ala Leu Ala Gly Val Thr Ile His Ala Ala Lys Ala Leu Gly
          85          90          95
Ile Ser Asp Ser His Gly Thr Leu Glu Val Gly Lys Val Ala Asp Phe
          100          105          110
Val Cys Trp Asp Val Glu Ser Pro Gly Glu Leu Cys Tyr Trp Leu Gly
          115          120          125
Glu Gln Leu Val Lys Gln Arg Ile Gln His Gly Val Ser His Glu
          130          135          140

```

<210> 467
 <211> 460
 <212> DNA
 <213> Homo sapiens

```

<400> 467
ntttccctgg ctattggcca tgtgggacac aacgttccgc ctaccccaga gcggttaagc
60
tgcacccctg caccttcttc tcccaccgct tcaaagccac agtgaggaac ttcggagctt
120
ctcgcagtga agatggcggt ggaggaatgg atgccctggc tagaagaggc ggaatatctg
180
ttgattgtgt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
240
tccaggcaag caagaagggc ccagctgttt acctggttcc acttttccct ctcctaccgg
300
ccgggggtcca agaacatcag gctggatgcc ctttcttgcc actttatggg catggggcca
360
ttctccagg cttgcctgtc acccgggctc ccgtcaaacc ctggccttcg tgcgacaaca
420
ctcttggtgc cttctatggt tctgtatggt gccgcaattg
460

```

<210> 468
 <211> 118
 <212> PRT
 <213> Homo sapiens

```

<400> 468
Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
1      5      10      15
Pro Trp Leu Glu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
20     25     30
Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
35     40     45
Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
50     55     60
Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
65     70     75     80
Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
85     90     95
Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
100    105    110
Leu Tyr Val Ala Ala Ile

```

115

<210> 469
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 469
 cttgtgcaca cgttattttt ccaatacaaa tagtttaaaa agtaaactcc aaatacctat
 60
 aagccccctc aaagcacctt ccaaatatga accttggtta tgcccaagggt ccagaggggt
 120
 cccccagaaa ggcccaggag cctggggcat gggaaagctg tcgggggtccc catgctgact
 180
 ccctggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct
 240
 tgacccaaaa tccattcggc cctggatact ggagaggcag aggcctctgc tgatgagaag
 300
 ccctgagttc ctggctagct gtgggtaacc acaaaaaatg cgggggggtga tgattttcga
 360
 agtccatcgg caaagaaaga c
 381

<210> 470
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 470
 Met Asp Phe Glu Asn His His Pro Pro His Phe Leu Trp Leu Thr Thr
 1 5 10 15
 Ala Ser Gln Glu Leu Arg Ala Ser His Gln Gln Arg Pro Leu Pro Leu
 20 25 30
 Gln Tyr Pro Gly Pro Asn Gly Phe Trp Val Lys Ala Ser Leu Pro Gln
 35 40 45
 Pro Gly Gly Pro Gly Phe Met Glu Tyr Arg Leu Glu Ser Arg Glu Ser
 50 55 60
 Ala Trp Gly Pro Arg Gln Leu Ser His Ala Pro Gly Ser Trp Ala Phe
 65 70 75 80
 Leu Gly Asp Pro Ser Gly Pro Trp Ala Leu Thr Arg Phe Ile Phe Gly
 85 90 95
 Arg Cys Phe Glu Gly Ala Tyr Arg Tyr Leu Glu Phe Thr Phe
 100 105 110

<210> 471
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 471
 accggtgact acctgcagca ctggattgac atgggtaaaa agggcggcga ccgcatgcc
 60
 gaggtcttcc tgggtaactg gttccgccgc ggcgacgatg gccgcttcct gtggccgngg
 120

cttggcgaaa acttccccgt cctanagtgg atcatcgacc gcattgaagg caacgtagag
 180
 gccgaggaca cggtaggtcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt
 240
 gacttcgatg tcgacgacgt tcgcgcgcga ctgcgcgttg acccgaagga atgggaaggc
 300
 gatatgcaag acaacgccga gtacctgaac ttcttgggct cccgcgtgcc cgaggaagtg
 360
 tggaaccagt tccgcgcc
 378

<210> 472

<211> 126

<212> PRT

<213> Homo sapiens

<400> 472

Thr	Gly	Asp	Tyr	Leu	Gln	His	Trp	Ile	Asp	Met	Gly	Lys	Lys	Gly	Gly
1				5				10						15	
Asp	Arg	Met	Pro	Glu	Val	Phe	Leu	Val	Asn	Trp	Phe	Arg	Arg	Gly	Asp
		20					25					30			
Asp	Gly	Arg	Phe	Leu	Trp	Pro	Xaa	Leu	Gly	Glu	Asn	Phe	Pro	Val	Leu
	35					40					45				
Xaa	Trp	Ile	Ile	Asp	Arg	Ile	Glu	Gly	Asn	Val	Glu	Ala	Glu	Asp	Thr
50					55					60					
Val	Val	Gly	Arg	Thr	Ala	Arg	Ala	Glu	Asp	Ile	Asp	Leu	Gln	Gly	Leu
65			70				75						80		
Asp	Phe	Asp	Val	Asp	Asp	Val	Arg	Ala	Ala	Leu	Ala	Val	Asp	Pro	Lys
		85					90					95			
Glu	Trp	Glu	Gly	Asp	Met	Gln	Asp	Asn	Ala	Glu	Tyr	Leu	Asn	Phe	Leu
		100				105						110			
Gly	Ser	Arg	Val	Pro	Glu	Glu	Val	Trp	Asn	Gln	Phe	Arg	Ala		
	115					120						125			

<210> 473

<211> 339

<212> DNA

<213> Homo sapiens

<400> 473

accggttggt gggggaaggg acccatccca tgccacctgt cctagaaaat gtttcccctt
 60
 gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa
 120
 aggcaccaag taaaagaagg gggaagctgc caaaaccccc cctgcaaaa ctctcccacc
 180
 ctgcttccat ttcctctcc agggaacagg tgtacctccc ctctccctg tcctctcag
 240
 atgccccagg ggtctcttac ttcattctg ccgacctgc caggagtggc ctcaggggta
 300
 gaggctccta gttggagaat ttgcttgac gaaggtgaa
 339

<210> 474

<211> 97
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu
 1 5 10 15
 Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly
 20 25 30
 Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe
 35 40 45
 Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Pro Cys Pro Pro Gln
 50 55 60
 Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val
 65 70 75 80
 Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly
 85 90 95
 Glu

<210> 475
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 475
 acgcgtgaag ggtccctcc aaactctgag cctccttcca agccttgctg ggagctcccc
 60
 agcgctgcc ggagaggcct ctctccagg cgggcttccc gcgccgatgt gaaggagagg
 120
 ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtccacacagc cataatcccc
 180
 aatgctggga ctcttcagta aaggaagaga tggttttttc gttcatctgc ctttctgaaa
 240
 ggtaaaatat ctccagatcc gggctctctg ggcgactgcg tatgtggggg tccctgaagc
 300
 ctttgatgga tcttggttaga agtgggttgt tcatcttggg gtttt
 345

<210> 476
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 476
 Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro
 1 5 10 15
 His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu
 20 25 30
 Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu
 35 40 45
 Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr
 50 55 60
 Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys


```

65          70          75          80
Pro Ala Trp Arg Arg Gly Leu Ser Gly Arg Arg Trp Gly Ala Pro Ser
          85          90          95
Lys Ala Trp Lys Glu Ala Gln Ser Leu Glu Gly Thr Leu His Ala
          100          105          110

```

<210> 477
 <211> 422
 <212> DNA
 <213> Homo sapiens

```

<400> 477
acgcgtggcc gagccagcgt gctcaaggaa atggtcaacg gcactcttat taacggctgg
60
gactctcccg aggtggaacg ggcactggac ctgtgcatgg cgtgcaaagg gtgcgcccga
120
gattgccccca ccggaatcga catggccagc taccgcagca cggttcttga cgaaaaatac
180
cgtcaccgtc tccgccctcg ctcccacctg acgatggggc tgctgcccac gtgggaacgt
240
ttgctcaatc ggaccccagg agcgccgtcg ctggctaacg cagtgttttc gatgccggtc
300
ttcgcacgtc ttgctagatg gacagccggg gtggatcagc gtcgtcccct ccccgattc
360
cagccctcgg ccagattggc cagtccgcag gccgcccggg ttaaggagat tgtggcggat
420
cc
422

```

<210> 478
 <211> 140
 <212> PRT
 <213> Homo sapiens

```

<400> 478
Thr Arg Gly Arg Ala Ser Val Leu Lys Glu Met Val Asn Gly Thr Leu
1          5          10          15
Ile Asn Gly Trp Asp Ser Pro Glu Val Glu Arg Ala Leu Asp Leu Cys
          20          25          30
Met Ala Cys Lys Gly Cys Ala Arg Asp Cys Pro Thr Gly Ile Asp Met
          35          40          45
Ala Ser Tyr Arg Ser Thr Val Leu Asp Glu Lys Tyr Arg His Arg Leu
          50          55          60
Arg Pro Arg Ser His Leu Thr Met Gly Leu Leu Pro Met Trp Glu Arg
65          70          75          80
Leu Leu Asn Arg Thr Pro Gly Ala Pro Ser Leu Ala Asn Ala Val Leu
          85          90          95
Ser Met Pro Val Phe Ala Arg Leu Ala Arg Trp Thr Ala Gly Val Asp
          100          105          110
Gln Arg Arg Pro Leu Pro Arg Phe Gln Pro Ser Ala Arg Leu Ala Ser
          115          120          125
Pro Gln Ala Ala Pro Val Lys Glu Ile Val Ala Asp
          130          135          140

```

<210> 479
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 479
 cgcgtaggcca ttggccgggc gctggtgcgg caccgcgcac tggtagattgc cgatgagccg
 60
 atctcggcgt tggacatgac catccagaag cagattcttg agctgttcga gcgcctgcag
 120
 gcgcagtacg gctttgcctg cctgttcacg tcccacgacc tggcagcggg ggaacgcacg
 180
 gcccaccggg tggcgggtgat gagcgagggc aggggtgggtg aaatgggtgc ccgcgacgag
 240
 atcttcgacc gcccgcagca cccctacacc cgcaagctgc tggccgcgcg cagccccctg
 300
 gagaaaacttg aaaacgggtg ctaccgcacg cgccagggcc ccgtaccg
 348

<210> 480
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile
 1 5 10 15
 Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile
 20 25 30
 Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu
 35 40 45
 Phe Ile Ser His Asp Leu Ala Ala Val Glu Arg Ile Ala His Arg Val
 50 55 60
 Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu
 65 70 75 80
 Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala
 85 90 95
 Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln
 100 105 110
 Gly Pro Val Pro
 115

<210> 481
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 481
 aagcttctga ctgtggcatt ctccctgctt aatatgtcct caatatcccc tacttactgg
 60
 gcaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tggtagccttc
 120
 cctgccctgc cggcttgccg tggcttctct agtgtagga ttaccatcac attgcatcat
 180

gagagcagaa gaccatctcc atgtgactgc tgcccctgct cccagcaggg cccacaanca
 240
 cccagtccag gacctggctc acgctgggtg gcggatgccc aggaatgggg ctctggatct
 300
 gcctcttctc ctgcaggacc aggaaaccgc tgcccctgtcc ctgccccagg aaaccctcag
 360
 taaatcccca gtcatttgag tttccctca gcgccagaga ccaataacac atctccacca
 420
 acctgaaaaa ccttcacgcg t
 441

<210> 482

<211> 120

<212> PRT

<213> Homo sapiens

<400> 482

Lys	Leu	Leu	Thr	Val	Ala	Phe	Ser	Leu	Leu	Asn	Met	Ser	Ser	Ile	Ser
1				5					10					15	
Pro	Thr	Tyr	Trp	Ala	Lys	Ser	Cys	Leu	Cys	Phe	Gly	Thr	Ser	Ser	Lys
			20					25					30		
Thr	Thr	Pro	Leu	Asp	Gly	Ala	Phe	Pro	Ala	Leu	Pro	Ala	Cys	Ala	Gly
			35				40						45		
Phe	Leu	Ser	Val	Arg	Ile	Thr	Ile	Thr	Leu	His	His	Glu	Ser	Arg	Arg
	50					55				60					
Pro	Ser	Pro	Cys	Asp	Cys	Cys	Pro	Cys	Ser	Gln	Gln	Gly	Pro	Gln	Xaa
65					70				75					80	
Pro	Ser	Pro	Gly	Pro	Gly	Ser	Arg	Trp	Val	Ala	Asp	Ala	Gln	Glu	Trp
			85					90					95		
Gly	Ser	Gly	Ser	Ala	Ser	Ser	Pro	Ala	Gly	Pro	Gly	Asn	Arg	Cys	Pro
			100					105					110		
Val	Pro	Ala	Pro	Gly	Asn	Pro	Gln								
			115				120								

<210> 483

<211> 330

<212> DNA

<213> Homo sapiens

<400> 483

acgcgttcac tccctgatgg ccacgcacga gctaacggag ggatggggcg aagggaaggc
 60
 caagggttgc tcgaagacca aggagtgtgc agggcaggac ctcgttttaa aggaatatcc
 120
 tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccaggctccg
 180
 agcgtctgcc cagcccagca tccctgtccc cagccaggaa tatgtcttcg tggcatagag
 240
 ggagctcttg gagccacacc tgcgtgtgca catgtgtcac cccactgctg ggaggggctc
 300
 tcccgggacc ctgcagcgtg ggctgggccc
 330

<210> 484

<211> 96
 <212> PRT
 <213> Homo sapiens

<400> 484
 Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys
 1 5 10 15
 Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala
 20 25 30
 Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val
 35 40 45
 Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly
 50 55 60
 Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro
 65 70 75 80
 His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro
 85 90 95

<210> 485
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 485
 acgcgtgctc ggcgcggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtagcc
 60
 gccaggttcg gcgatcgccg cattcggccg gccggaatcg agaaggaatg cgtggacgta
 120
 cgggggatac caaaggaatc ttgtcgaggg cttcgcgggc ctcgacgtgg atcacctgta
 180
 cccgacggac gtggggaagc cgtcccgcga gctcacggga ctccgcgaca tcgatgtgcg
 240
 atacgatttg caccgtcgtc ggctgcgtgc gcgacacatg ctccgcgacg gcctcagcgg
 300
 tgggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtcgcc gttatgtcgg
 360
 cattcccatt cctcggg
 377

<210> 486
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 486
 Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro
 1 5 10 15
 Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu
 20 25 30
 Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp
 35 40 45
 Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg
 50 55 60
 Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

```

65          70          75          80
Pro Arg Ser Pro Gln Arg Trp Phe Pro Thr Ser Ala Gly Thr Trp Arg
          85          90          95
Arg Val Ala Trp Arg Ser Pro Leu Cys Arg His Ser His Ser Ser
          100          105          110

```

<210> 487
 <211> 459
 <212> DNA
 <213> Homo sapiens

```

<400> 487
nnacgcgtaa gatcgattgt ggatcagcac cgatgctggt ccccccgcac ttgttgttgg
60
cggtgttgt tgtaaggagt gtgtgtgatg cgtgttggtg ttctactga ggtaagaat
120
agtgatttc gtgtggctgt gacgccggcg ggtgttcattg cgttggttgg tcgtggtcat
180
gaggtgttgg ttcaggctgg tgctggtgtg gggtcgggta ttccgattc ggattttgtg
240
ggtgctggtg cgcgggttgt gggatgatgt gagtcggtgt ggggtgatgc tgatttggtg
300
ttgaaggtga aggagcctgt tgcggaggag tatgggcggt tgcattgaggg tttggttctt
360
tttacctatc ttcatttggc tgctgatgag gcgttgactc gtgagctttt ggggcgtggg
420
gtgacgtcga ttgcgtatga gacggtggag ttggccgat
459

```

<210> 488
 <211> 124
 <212> PRT
 <213> Homo sapiens

```

<400> 488
Met Arg Val Gly Val Pro Thr Glu Val Lys Asn Ser Glu Phe Arg Val
1          5          10          15
Ala Val Thr Pro Ala Gly Val His Ala Leu Val Gly Arg Gly His Glu
          20          25          30
Val Leu Val Gln Ala Gly Ala Gly Val Gly Ser Gly Ile Pro Asp Ser
          35          40          45
Asp Phe Val Gly Ala Gly Ala Arg Val Val Gly Asp Val Glu Ser Val
          50          55          60
Trp Gly Asp Ala Asp Leu Val Leu Lys Val Lys Glu Pro Val Ala Glu
65          70          75          80
Glu Tyr Gly Arg Leu His Glu Gly Leu Val Leu Phe Thr Tyr Leu His
          85          90          95
Leu Ala Ala Asp Glu Ala Leu Thr Arg Glu Leu Leu Gly Arg Gly Val
          100          105          110
Thr Ser Ile Ala Tyr Glu Thr Val Glu Leu Ala Asp
          115          120

```

<210> 489
 <211> 542

<212> DNA

<213> Homo sapiens

<400> 489

nacgcgtttg gcgtactgag tgcggtggtg gatggcgacg acagtggcaa gccgctgctc
 60
 aaccagcacg gttgctacaa agtgcgcttt ccatttacct gcgatcaaaa gcccagcact
 120
 cgggggttcgg catggctgcg caggggtgctg ttgtctgccg gttccagcca tggcatgcac
 180
 tttccgctgc tcaaaggcag tgaagtgttg gtgtcatttc tggggggcga ccccgaccgg
 240
 ccgattatcg ttggtgcgt accaaactcg gaaaccccgga gcatggctcg tgagcgtaac
 300
 gccaccaga gcggcttctc caccggccgga gggcacttcc tggcgatgga agaccacccc
 360
 ggggctgccc atctgaagct ggggtgcgct ggcggaaca gcgtcttcac actgggcaat
 420
 ggcaaagtcg ccggcgcgca actgcgcacc aacgccccac atgcaattga catcgtcttc
 480
 gctcaaacac gaagtgcgag gcgtgtactc attgtcgatg ggcaccgggg acccgcgggc
 540
 cg
 542

<210> 490

<211> 180

<212> PRT

<213> Homo sapiens

<400> 490

Xaa Ala Phe Gly Val Leu Ser Ala Val Val Asp Gly Asp Asp Ser Gly
 1 5 10 15
 Lys Pro Leu Leu Asn Gln His Gly Cys Tyr Lys Val Arg Phe Pro Phe
 20 25 30
 Thr Arg Asp Gln Lys Pro Ser Thr Arg Gly Ser Ala Trp Leu Arg Arg
 35 40 45
 Val Ser Leu Ser Ala Gly Ser Ser His Gly Met His Phe Pro Leu Leu
 50 55 60
 Lys Gly Ser Glu Val Leu Val Ser Phe Leu Gly Gly Asp Pro Asp Arg
 65 70 75 80
 Pro Ile Ile Val Gly Cys Val Pro Asn Ser Glu Thr Pro Ser Met Val
 85 90 95
 Val Glu Arg Asn Ala Thr Gln Ser Gly Phe Ser Thr Ala Gly Gly His
 100 105 110
 Phe Leu Ala Met Glu Asp His Pro Gly Ala Ala His Leu Lys Leu Gly
 115 120 125
 Ala Pro Gly Gly Asn Ser Val Phe Thr Leu Gly Asn Gly Lys Val Ala
 130 135 140
 Gly Ala Gln Leu Arg Thr Asn Ala Pro His Ala Ile Asp Ile Val Phe
 145 150 155 160
 Ala Gln Thr Arg Ser Ala Arg Arg Val Leu Ile Val Asp Gly His Arg
 165 170 175
 Gly Pro Gly Gly

180

<210> 491
 <211> 825
 <212> DNA
 <213> Homo sapiens

<400> 491
 nacgcgtcga ggcgacggtc ggcccgctca tggcgactgt tctcgagggc acatgggaac
 60
 gcatcgggtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg
 120
 tgggcggccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg
 180
 aactcatcgg cgggcccgtc ggcgcggttg ccgcgatgca cggagggtca atcgaattgg
 240
 tcgacgtgtc ggtcgggtgac gaagagcgca gactcgacgt caccatgaag ggagcatgcc
 300
 gaggttgccc ggagccatc agaccctaca tcagcgcttg gaacatcaac tgagtctgcg
 360
 nattgcgcga gccggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg
 420
 acgagcacct ccacgacgag gccaaagccac tcgtagacgc attcctctctc ggcaccaat
 480
 tcctcccggg ccgcccggagc gacttcgtcg gcagtaacct ggtcgatgat ccctagcctg
 540
 gcggccatca tgccacgcag cgcattgaca gtacgaagcc aacgttgctg catcacaggg
 600
 ttcatggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcg
 660
 tcttcccagc gcgcccgac atcctcggcg tcatggtcga catggaattg cgcgtcagct
 720
 gactcgctgt cacgataggc gctgggcagg atcaatcgac gcacctcgtc gtcctcctgg
 780
 agtccagaaa actggtctct ccaaaaagcg aacgggtccc cctcc
 825

<210> 492
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 492
 Met Asn Gly Trp Ala Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg
 1 5 10 15
 His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg
 20 25 30
 Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser
 35 40 45
 Val Thr Lys Ser Ala Glu Ser Thr Ser Pro
 50 55

<210> 493
 <211> 863

<212> DNA

<213> Homo sapiens

<400> 493

nacgcgttcc aacctcgtca aaacggctat cgcaggaaat gaccccaact ggggtcgcac
 60
 cctcgcggcg atcggatgtg ttcctgagaa tatagctccc ttcgatcccg accaggtgga
 120
 tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct
 180
 cgctgatatg aggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga
 240
 agctgcggta tggactaatg atctgacca ccaatacgtc gaagagaata gcgcgtatac
 300
 atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa
 360
 tctgaggtcc tggtagaagc gctgccttgg atcaggcggg ttcagggccg cactgtcgtc
 420
 gtgaaatag ggggcaacgc gatggttgat cccggtctgc agcaggcctt cgccgacgac
 480
 attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacgggtg tggccctcag
 540
 atcaatgcc a tgcttctga atccgctacc ccggtggagt tccgtaatgg tttgcgggtg
 600
 acatctccgg aggtcatgga ggttgtccgg atggtgctcg tcgggcaggg gggccgtcag
 660
 ctcgtaacc gaatcaacgc ctatgcgccg ctagcagctg gcatgtcagg cgaggacttt
 720
 ggcctttttt cggcccgga gtcgcgggta attgttgatg gcgagcaa at agacatgggt
 780
 ttagtgggag acatcgttga cgtcaacatc gatctcgta tctctatgct tgatcgcggg
 840
 cagattccgg tcattgcacc ggt
 863

<210> 494

<211> 186

<212> PRT

<213> Homo sapiens

<400> 494

Met Thr Leu Ala Leu Asp Ile Pro Leu Asn Asp Ser Gln Phe Ser Ala
 1 5 10 15
 Gln Arg Lys Ser Glu Val Leu Val Glu Ala Leu Pro Trp Ile Arg Arg
 20 25 30
 Phe Gln Gly Arg Thr Val Val Val Lys Tyr Gly Gly Asn Ala Met Val
 35 40 45
 Asp Pro Gly Leu Gln Gln Ala Phe Ala Asp Asp Ile Val Phe Met Ala
 50 55 60
 Ser Val Gly Ile Arg Pro Ile Val Val His Gly Gly Gly Pro Gln Ile
 65 70 75 80
 Asn Ala Met Leu Ala Glu Ser Ala Thr Pro Val Glu Phe Arg Asn Gly
 85 90 95
 Leu Arg Val Thr Ser Pro Glu Val Met Glu Val Val Arg Met Val Leu


```

      100      105      110
Val Gly Gln Val Gly Arg Gln Leu Val Asn Arg Ile Asn Ala Tyr Ala
      115      120      125
Pro Leu Ala Ala Gly Met Ser Gly Glu Asp Phe Gly Leu Phe Ser Ala
      130      135      140
Arg Lys Ser Arg Val Ile Val Asp Gly Glu Gln Ile Asp Met Gly Leu
145      150      155      160
Val Gly Asp Ile Val Asp Val Asn Ile Asp Leu Val Ile Ser Met Leu
      165      170      175
Asp Arg Gly Gln Ile Pro Val Ile Ala Pro
      180      185

```

<210> 495
 <211> 514
 <212> DNA
 <213> Homo sapiens

```

<400> 495
gcgcgcgaca ccggtgcccc gattagcgtg ccagtgggtg acgtcactaa gggtcacgtc
60
tggaatgtga caggtgacgt tcttaacgcc ngatccctcc acaatcgagg tgacnntgag
120
cgttggccga tccaccggga tccccgggcc ttgatgacc ttgagcccgga gaccgagatg
180
ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cggcaagatt
240
ggcctctttg gcggcgctgg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
300
atcgcccaca acttcggcgg tacttcggtt ttccgccgtg tcggtgagcg taccgcgag
360
ggtaacgacc tcatcaacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
420
ttcggccaga tggacgagcc cccgggcacg cggtacgagc tgtcgcgctg gcagccctgc
480
ggcccatgcc tggtaactg ctgtgggacc ttgg
514

```

<210> 496
 <211> 171
 <212> PRT
 <213> Homo sapiens

```

<400> 496
Ala Arg Asp Thr Gly Ala Pro Ile Ser Val Pro Val Gly Asp Val Thr
1      5      10      15
Lys Gly His Val Trp Asn Val Thr Gly Asp Val Leu Asn Ala Xaa Ser
      20      25      30
Leu His Asn Arg Gly Asp Xaa Glu Arg Trp Pro Ile His Arg Asp Pro
      35      40      45
Pro Ala Phe Asp Asp Leu Glu Pro Glu Thr Glu Met Leu Glu Thr Gly
      50      55      60
Ile Lys Val Leu Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
65      70      75      80
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu

```

```

      85              90              95
Met Ile Tyr Arg Ile Ala His Asn Phe Gly Gly Thr Ser Val Phe Ala
      100              105              110
Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Leu Ile Asn Glu Met
      115              120              125
Asp Glu Ala Gly Val Leu Lys Asp Thr Ala Leu Val Phe Gly Gln Met
      130              135              140
Asp Glu Pro Pro Gly Thr Arg Tyr Glu Leu Ser Arg Trp Gln Pro Cys
145              150              155              160
Gly Pro Cys Leu Val Asn Cys Cys Gly Thr Leu
      165              170

```

<210> 497

<211> 662

<212> DNA

<213> Homo sapiens

<400> 497

```

acgcgtcctg ggatctcaac cccagcagtc tggcttggtt ctcattccca caatttcctg
60
ggttcacca agcagcgaaa actgccagga tgaatgagga aaaaaccag cccacaaaac
120
gagacacacg ctggcgggga gagacgcagc agagctcctt cctgtctgtg gactcggagc
180
aaagacgtgg ggccccatct tttgtgtttt cctcaagcgg ggaaagaatg gactgtttgc
240
atgcttcgtg ccacacgccc gcggtgatcc cagccagggc cccgagcgca gaggcggagc
300
tgtgtctcagc acaggcctgg gacctcccc ggagggcacc tgtgggggggt gcagcccccg
360
ggaaggaggc aactgcctca cttaacatcc tccgctgcaa ggtgggtggcg ccgagaggcg
420
tgtctgtgaa gacaggtacc aggatggcag gaccgcacg cctcttccca cacctgtcag
480
cttcggaagc atctctcgag gactctggtc ccaggatgtc tcccaggaca agccagtctg
540
cctcttcctc ctacttctgc ttagcctgg gaccagacct ggccaaggtc agccagcggg
600
gagggccgag gtctgagetc tcgtcctgcc gtggcccccg cgatggcttg gggtgcaagc
660
tt
662

```

<210> 498

<211> 191

<212> PRT

<213> Homo sapiens

<400> 498

```

Met Asn Glu Glu Lys Thr Gln Pro His Lys Arg Asp Thr Arg Trp Arg
  1              5              10              15
Gly Glu Thr Gln Gln Ser Ser Phe Leu Ser Val Asp Ser Glu Gln Arg
      20              25              30
Arg Gly Ala Pro Ser Phe Val Phe Ser Ser Ser Gly Glu Arg Met Asp

```

<400> 500															
Met	Thr	Val	Thr	Ala	Leu	Leu	Cys	Gln	Ala	Phe	Pro	Pro	Ser	Ile	Asp
1				5					10					15	
Glu	Glu	Gly	Leu	Leu	Leu	Pro	His	Phe	Ala	Asp	Lys	Glu	Ile	Glu	Val
			20					25					30		
Leu	Arg	Ser	Glu	Val	Thr	Ser	Ser	Asn	Pro	Pro	Val	Glu	Asp	Leu	Asn

```

      35          40          45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe
   50          55          60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu
65          70          75          80
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr
      85          90          95
Gln Leu Asn Thr Ala His Pro Ser Arg
      100          105

```

<210> 501
 <211> 800
 <212> DNA
 <213> Homo sapiens

```

<400> 501
agatctgac cgagaagtgg ctgctcaggg aaatgactac tccatgggtt tcttaactca
60
ggtactcctt attcaatgag aggcctgagg tgagaccgc catgcggcgc gtggatcgca
120
tggtgttagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
180
gacctgttac tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
240
gaagtttatt ctcccatgga tgatgctggc ttcccggtca aagctgagga gtttgtggtg
300
ctttctcagg aaccttctgt cacggaaacc attgcacca aaattgcaag acctttcata
360
gaggccctca agagtattga gtatctggag gaggatgcc agaagtccgc acaggagggg
420
gtgctgggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
480
gaaccatccc aattagagga gctagctgac ttcattggagc agcttacacc aattgaaaaa
540
tatgctttaa attacctgga atcttgaggc agggcctgag agagcacgct gcgccgtact
600
tccagcagct gcggcagacc acggctccac gcctgtgca gttccctgag ctgaggctgg
660
tgcagttcga ctcaggtagt cggcagttgg gggcgtggcc cgtgcgggag ctgcactggc
720
cctggatgat gaggcgctct tgatgtgatt cgtttcccag ggaagttgga agcttttagct
780
atcttgcttc agaaactgaa
800

```

<210> 502
 <211> 103
 <212> PRT
 <213> Homo sapiens

```

<400> 502
Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
 1          5          10          15
Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```

```

      20      25      30
Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala
      35      40      45
Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu
      50      55      60
Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu
65      70      75      80
Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr
      85      90      95
Ala Leu Asn Tyr Leu Glu Ser
      100

```

<210> 503

<211> 538

<212> DNA

<213> Homo sapiens

<400> 503

```

nnacgcgttg tcgtctctcc gatcattgat tttgttgat tctgcaatga tgtaaaggaa
60
gatgatgaca cggagaagtt taaagaagcc attgtgaaat ttcataggct gtttgggatg
120
ccagaggaag agaaactcgt caactattac tcttgcagct attggaaggg gaagggtcccc
180
cgtcagggtt ggatgtacct cagcattaac cacctttgct tttattcttt tcttatggga
240
agggaagcga aactgggtcat ccggtgggta gacatcactc agcttgagaa gaatgcccc
300
ctgcttctgc ctgatgtgat caaagtgagc acacggtcca gtgagcattt cttctctgta
360
ttcctcaaca tcaacgagac cttcaagtta atggagcagc ttgccaacat agccatgagg
420
caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaact caaaaggaaa
480
tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctgggccct tcacgcgt
538

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<210> 504

<211> 179

<212> PRT

<213> Homo sapiens

<400> 504

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Xaa Arg Val Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn
  1      5      10      15
Asp Val Lys Glu Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val
      20      25      30
Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn
      35      40      45
Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp
      50      55      60
Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly
65      70      75      80
Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu

```

```

      85          90          95
Lys Asn Ala Pro Leu Leu Leu Pro Asp Val Ile Lys Val Ser Thr Arg
      100          105          110
Ser Ser Glu His Phe Phe Ser Val Phe Leu Asn Ile Asn Glu Thr Phe
      115          120          125
Lys Leu Met Glu Gln Leu Ala Asn Ile Ala Met Arg Gln Leu Leu Asp
      130          135          140
Asn Glu Gly Phe Glu Gln Asp Arg Ser Leu Pro Lys Leu Lys Arg Lys
      145          150          155          160
Ser Pro Lys Lys Val Ser Ala Leu Lys Arg Asp Leu Asp Ala Trp Ala
      165          170          175
Leu His Ala

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<210> 505
 <211> 381
 <212> DNA
 <213> Homo sapiens

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<400> 505
gtgcacgaca ccgaacggta cgaacgtatc tcccaggcac gtcgagagga acagcaggcc
60
atgctcggct acgaacgtc aagaacctgt cgcattgacct tgctcaccgg gcagctggac
120
gacccctcca cgactccttg cggacgctgc gacgtctgtg ctggcccgtg gtactcagtc
180
gaggtcgatc agtcagccgc tgtgagagcc gtccaatccc tcaaccgggt gggagttccg
240
gtggaaccac ggcgcgcctg gcccgagggt atggacgccc tccaggttgc gctcaagggt
300
cgcatcagtg ccgaggagat cgctgcagag ggccgcgtca tcgccagact ctccgatctg
360
ggttggggag gggcgctgcg c
381

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<210> 506
 <211> 127
 <212> PRT
 <213> Homo sapiens

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<400> 506
Val His Asp Thr Glu Arg Tyr Glu Arg Ile Ser Gln Ala Arg Arg Glu
1      5      10      15
Glu Gln Gln Ala Met Leu Gly Tyr Asp Xaa Ser Arg Thr Cys Arg Met
20      25      30
Thr Leu Leu Thr Gly Gln Leu Asp Asp Pro Ser Thr Thr Pro Cys Gly
35      40      45
Arg Cys Asp Val Cys Ala Gly Pro Trp Tyr Ser Val Glu Val Asp Gln
50      55      60
Ser Ala Ala Val Arg Ala Val Gln Ser Leu Asn Arg Val Gly Val Pro
65      70      75      80
Val Glu Pro Arg Ala Ala Trp Pro Ala Gly Met Asp Ala Leu Gln Val
85      90      95
Ala Leu Lys Gly Arg Ile Ser Ala Glu Glu Ile Ala Ala Glu Gly Arg

```

100 105 110
 Val Ile Ala Arg Leu Ser Asp Leu Gly Trp Gly Gly Ala Leu Arg
 115 120 125

<210> 507
 <211> 499
 <212> DNA
 <213> Homo sapiens

<400> 507
 gccggcgtgt tcaacctcat ggtgtgggcc ttcattaccg acgtcatcga tgcccaggag
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 gtcattgtccg gggagcgtga agacggtgtc atctatggcg tgaactcctt cgcccgcaaa
 120
 cttgccccagg ccattgccgg tggaatcggc ggagccatgc tgacgatgat cggctaccag
 180
 tctctctccc aaggtggtgc cgttcagtcg gagtccgtcg tcaatcacct gtacacgctc
 240
 gccaccgcca tcccgacgat ctgctgcctc ggcgctgccc tgctcatgct gggctacccg
 300
 ctcacccgcg acaaggtggt cgccaacgcc gacgagttgg ctgctcgcca cgcagtacag
 360
 gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgctca tgcggatcac
 420
 cgaccacttg acaacctcgc cgggtatcca attgaaaatt gacaagcgat ggggtgcctc
 480
 cgtcacattt gtgacgcgt
 499

<210> 508
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 508
 Ala Gly Val Phe Asn Leu Met Val Trp Ala Phe Ile Thr Asp Val Ile
 1 5 10 15
 Asp Ala Gln Glu Val Met Ser Gly Glu Arg Glu Asp Gly Val Ile Tyr
 20 25 30
 Gly Val Asn Ser Phe Ala Arg Lys Leu Ala Gln Ala Ile Ala Gly Gly
 35 40 45
 Ile Gly Gly Ala Met Leu Thr Met Ile Gly Tyr Gln Ser Ser Ser Gln
 50 55 60
 Gly Gly Ala Val Gln Ser Glu Ser Val Val Asn His Leu Tyr Thr Leu
 65 70 75 80
 Ala Thr Ala Ile Pro Thr Ile Cys Cys Leu Gly Ala Ala Leu Leu Met
 85 90 95
 Leu Gly Tyr Pro Leu Thr Arg Asp Lys Val Val Ala Asn Ala Asp Glu
 100 105 110
 Leu Ala Arg Arg His Ala Val Gln Ala Glu Gln Asn Ser
 115 120 125

<210> 509
 <211> 360

<212> DNA

<213> Homo sapiens

<400> 509

ttggccatgg atttggtctg caagttcagt cccaaagatg tcacgctcta tctaattggac
 60
 ttcgggacca atgggtgtggc accactaggc caattaccac aggtggccga caccttgctt
 120
 ttggatcata cggagaagat tgccaagttt gtacgcatca tggagcggga gctcaaccgg
 180
 cgtaagaagc tcttgtccga ctacggtgtt ggtacactag agctctaccg tcaggctagc
 240
 ggtcagcaag agccggccat cgtcatcctg ctggacagtt atgagtccat gaaggaagag
 300
 gcctatgaag cggagctctt cagcgtcttg gtgcggatct cccgggaagg tctcagcatc
 360

<210> 510

<211> 120

<212> PRT

<213> Homo sapiens

<400> 510

Leu	Ala	Met	Asp	Leu	Ala	Arg	Lys	Phe	Ser	Pro	Lys	Asp	Val	Thr	Leu
1			5					10					15		
Tyr	Leu	Met	Asp	Phe	Gly	Thr	Asn	Gly	Val	Ala	Pro	Leu	Gly	Gln	Leu
			20				25					30			
Pro	Gln	Val	Ala	Asp	Thr	Leu	Leu	Leu	Asp	His	Thr	Glu	Lys	Ile	Ala
		35				40					45				
Lys	Phe	Val	Arg	Ile	Met	Glu	Arg	Glu	Leu	Asn	Arg	Arg	Lys	Lys	Leu
	50				55				60						
Leu	Ser	Asp	Tyr	Gly	Val	Gly	Thr	Leu	Glu	Leu	Tyr	Arg	Gln	Ala	Ser
65				70					75					80	
Gly	Gln	Gln	Glu	Pro	Ala	Ile	Val	Ile	Leu	Leu	Asp	Ser	Tyr	Glu	Ser
			85				90						95		
Met	Lys	Glu	Glu	Ala	Tyr	Glu	Ala	Glu	Leu	Phe	Thr	Leu	Leu	Val	Arg
		100					105					110			
Ile	Ser	Arg	Glu	Gly	Leu	Ser	Ile								
		115				120									

<210> 511

<211> 361

<212> DNA

<213> Homo sapiens

<400> 511

ntcgcgaacc gcggctatgc ggtgctccag cccaatttcc gcggatcggg cggttatggc
 60
 actgcgttcg gcgatgccgg catcggccag atcgggcgca agatgcagga cgatctcgac
 120
 gacgggatgg actggctggt caaggagggc atcgtcgaca agggccgggt gtgcatcgtc
 180
 ggggcctcct atggcggcta tgccgcatg tggggcgaga tccgcaatcc cgaacgctat
 240

cgctgcgcgg cgagcctggc ggggggttgcc gattaaggcc atgctcaaat ataaccggcg
 300
 ctatctcgac aaggaggcgg gcaagcgctg gccgccccgn tcaaccggcg aaccggaatt
 360
 c
 361

<210> 512
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 512
 Xaa Ala Asn Arg Gly Tyr Ala Val Leu Gln Pro Asn Phe Arg Gly Ser
 1 5 10 15
 Gly Gly Tyr Gly Thr Ala Phe Gly Asp Ala Gly Ile Gly Gln Ile Gly
 20 25 30
 Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys
 35 40 45
 Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr
 50 55 60
 Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr
 65 70 75 80
 Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp
 85 90

<210> 513
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 513
 nnatgcagac tagaagatgg catgacgggt ttggctggcg gtttcgggct atgcggcatt
 60
 ccagaaaatc tgattcaaga gatcaaacga cgccagactt gtgatttgac catagtgtca
 120
 aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc
 180
 aaaatggtgt cttcttatgt gggtgaaaat gcactgtttg agaagcaatt attacaaggt
 240
 gagttggaag tcgagctcac tcctcaaggc actcttgccg aaaaactacg cgctggcggc
 300
 gcgggaattc ctgccttttt cacagcaacg ggtgtaggta cacctattgg tgagggtaaa
 360
 gacacgcgt
 369

<210> 514
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 514
 Xaa Cys Arg Leu Glu Asp Gly Met Thr Val Leu Ala Gly Gly Phe Gly

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      1             5             10             15
Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
      20             25             30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
      35             40             45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
      50             55             60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
      65             70             75             80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
      85             90             95
Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
      100            105            110
Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
      115            120

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<210> 515
 <211> 387
 <212> DNA
 <213> Homo sapiens

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<400> 515
gcgtagggacg agaaggccgc cggcaactgc gcgatcgact acgggttcca ccagatcctc
60
tccgacgtgc aggactcgtc gctgaccgcg atggacgagc tgatcaccga gggcgtgaca
120
tccttcaagc tcttcgtggc ctacaagggc gtcttcctct cggacgacgg gcagatcctg
180
cgggcggttc agaagggcgc cgacaacggc gcgatgatga tgatgcacgc cgagaacggc
240
gcatcatcg acgtgctcgt gcagcaggcg ctcgaggccg ggaagaccac cccgtactac
300
cacggcatca gccggccgtg gcaggccgag gaggaggcca cccaccgccc gatcatgatc
360
gccgacctga ccggtgcgcc gttgtac
387

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<210> 516
 <211> 129
 <212> PRT
 <213> Homo sapiens

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<400> 516
Ala Trp Asp Glu Lys Ala Ala Gly Asn Cys Ala Ile Asp Tyr Gly Phe
1             5             10             15
His Gln Ile Leu Ser Asp Val Gln Asp Ser Ser Leu Thr Ala Met Asp
      20             25             30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
      35             40             45
Lys Gly Val Phe Leu Ser Asp Asp Gly Gln Ile Leu Arg Ala Phe Gln
      50             55             60
Lys Gly Ala Asp Asn Gly Ala Met Met Met Met His Ala Glu Asn Gly
      65             70             75             80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr

```

```

      85              90              95
Thr Pro Tyr Tyr His Gly Ile Ser Arg Pro Trp Gln Ala Glu Glu Glu
      100              105              110
Ala Thr His Arg Ala Ile Met Ile Ala Asp Leu Thr Gly Ala Pro Leu
      115              120              125
Tyr

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<210> 517
 <211> 377
 <212> DNA
 <213> Homo sapiens

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<400> 517
acgcgtgaag ggctggtggg caggccttgc gccccctctg gggacagctc tcctccaccc
60
agacccttc gggccaacag tggggagggg ctgccgtctg agccactgtt ccgacagggg
120
attcgcgagt tccgggggag ctggggactg agctgcgggc ctctctgggct ggggctcttc
180
tccgaggttg gaggcagctt tagaaacttg agacccttag ctggagaggg cagaaggggt
240
ccctgagctt cccagggaga agggggggcca atttgagct tgcttttcac ctgagatgag
300
gaatgggggt ggccaggccg agagcccagt ggggcatccc cagcacccat gaacatgcta
360
aggaagggga ggggccc
377

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<210> 518
 <211> 118
 <212> PRT
 <213> Homo sapiens

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<400> 518
Met Phe Met Gly Ala Gly Asp Ala Pro Leu Gly Ser Arg Pro Gly His
1      5      10      15
Pro His Ser Ser Ser Gln Val Lys Ser Lys Leu Gln Ile Gly Pro Pro
20     25     30
Ser Pro Gly Glu Ala Gln Gly Pro Leu Leu Pro Ser Pro Ala Arg Gly
35     40     45
Leu Lys Phe Leu Lys Leu Pro Thr Ser Glu Lys Ser Pro Ser Pro
50     55     60
Gly Gly Pro Gln Leu Ser Pro Gln Leu Pro Arg Asn Ser Arg Ile Pro
65     70     75     80
Cys Arg Asn Ser Gly Ser Asp Gly Ser Pro Ser Pro Leu Leu Ala Arg
85     90     95
Arg Gly Leu Gly Gly Gly Glu Leu Ser Pro Glu Gly Ala Gln Gly Leu
100    105    110
Pro Thr Ser Pro Ser Arg
115

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<210> 519
 <211> 311

<212> DNA

<213> Homo sapiens

<400> 519

g c g c g c c a g g g g g a a g g g a g a g a a a c a c a g a a a a t g a g g g g a a a t a c c a g a t a c t g a
 60
 a g a a t t t a a a t t a t t a t a a a g g a a c c t t t t c t g c a a c t c t g a a a a t g t t a g a a t a t c c a
 120
 a a g a a a t t g a t a a t t t t c t a g g a a a c a t g a c t t a c c a a a a t t a a c t c t a g a a a g a a t c
 180
 g a t a c a c a t c a g t a a c a a c a g a a g t t g a g a a g t a g t t a a c a t a t t g c c a a a c c t g g a a t
 240
 t c a t g a t t g a a t t c t t t g a g a t c t a c t g t g a g t a c a t a c t c t g c c t c t g t c a g e t g t t c
 300
 c a g a a c t t a a g
 311

<210> 520

<211> 92

<212> PRT

<213> Homo sapiens

<400> 520

Met	Arg	Gly	Lys	Tyr	Gln	Ile	Leu	Lys	Asn	Leu	Asn	Tyr	Tyr	Lys	Gly
1			5					10						15	
Thr	Phe	Ser	Ala	Thr	Leu	Lys	Asn	Val	Arg	Ile	Ser	Lys	Glu	Ile	Asp
		20					25					30			
Asn	Phe	Leu	Gly	Lys	His	Asp	Leu	Pro	Lys	Leu	Thr	Leu	Glu	Lys	Asn
		35				40					45				
Arg	Tyr	Thr	Ser	Val	Thr	Thr	Glu	Val	Glu	Lys	Val	Val	Asn	Ile	Leu
	50				55					60					
Pro	Asn	Leu	Glu	Phe	Met	Ile	Glu	Phe	Phe	Glu	Ile	Tyr	Cys	Glu	Tyr
65			70					75						80	
Ile	Leu	Cys	Leu	Cys	Ser	Ala	Val	Pro	Glu	Leu	Lys				
			85					90							

<210> 521

<211> 352

<212> DNA

<213> Homo sapiens

<400> 521

n n n g a t g c c a c g c c g g t c t a c g g a a t c t c c a c c g g t t c g g c g c g t t g c c g c c g c c a c
 60
 a t t c c a g a a g a g a t g c g c g c g c a g a g t g c a g c t g t c c c t g g t g c g t c c c a c g c g g c c g g c
 120
 a c c g g c c c t g a g g t g g a a g a g a a g t a a t t c g c g c g c t c a t g c t g t g c g c c t a t c c a c c
 180
 c t g t g t a c c g g c c g t a c c g g c g t g c g c c c c g t g t g g t a g a a a c t t a t g c c a a g g c g c t c
 240
 a a c g c c g g c a t c g t g c c g g g g g t g c g c g a a t a c g g g t c g c t g g g c t g c t c g g c g a c t t g
 300
 g c c c c g c t g g c t c a c t g c g c c c t a g c g c t g t t g g g t g a g g g t g a g g t a c g c n
 352

<210> 522
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 522
 Xaa Asp Ala Thr Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly Ala Leu
 1 5 10 15
 Ala Arg Arg His Ile Pro Glu Glu Met Arg Ala Gln Leu Gln Leu Ser
 20 25 30
 Leu Val Arg Ser His Ala Ala Gly Thr Gly Pro Glu Val Glu Glu Glu
 35 40 45
 Val Ile Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu Cys Thr Gly
 50 55 60
 Arg Thr Gly Val Arg Pro Val Val Val Glu Thr Tyr Ala Lys Ala Leu
 65 70 75 80
 Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys
 85 90 95
 Ser Gly Asp Leu Ala Pro Leu Ala His Cys Ala Leu Ala Leu Leu Gly
 100 105 110
 Glu Gly Glu Val Arg
 115

<210> 523
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 523
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 60
 tcagagccac caagctgctg caccatctaa ggagaacatg tcccctggag gtcctgttag
 120
 aagctcctgg ttgagaaggc cctgaagctg ggtggcatca atgtccagcc tctgctgagc
 180
 atatctgttg aaaatgcttt gttgggagcc atgttctgaa gggcttcctt tcattctgag
 240
 gttgaaatgg ctgctcaggt gcctgtcact gtctggcatt ttcaggaaga ttcggagcaa
 300
 gaactccgct gattttctcc gtgtctgtgc aaccacaaca tagttcccag ggctcagatg
 360
 gtaagtcacg gtgaagttgc ggcggaattt attatttgag ctttggacag tgtttctgaa
 420
 cgaggaaaaa aacacgggtg gaaatttctc ccggaaccgc tgtgagccag ccagaatcac
 480
 ttggaatcg agtggaattt ttgcatcttc tgctttcaaa tttgatggtg tgacagcaac
 540
 tgtgacgcac acgacaacat tgggtgccttc cattggctct tgcacagaga agttgaattg
 600
 agcatcattt ccgggtcttc ctggcgtggt tcctagaatc attgcttcct aaacattatt
 660
 tgggaccatc cttcgtggag tgtgtttcca tgg
 693

<210> 524
 <211> 193
 <212> PRT
 <213> Homo sapiens

<400> 524
 Met Ile Leu Gly Asn Thr Pro Gly Gly Pro Gly Asn Asp Ala Gln Phe
 1 5 10 15
 Asn Phe Ser Val Gln Glu Pro Met Glu Gly Thr Asn Val Val Val Cys
 20 25 30
 Val Thr Val Ala Val Thr Pro Ser Asn Leu Lys Ala Glu Asp Ala Lys
 35 40 45
 Phe Pro Leu Asp Phe Gln Val Ile Leu Ala Gly Ser Gln Arg Phe Arg
 50 55 60
 Glu Lys Phe Pro Pro Val Phe Phe Ser Ser Phe Arg Asn Thr Val Gln
 65 70 75 80
 Ser Ser Asn Asn Lys Phe Arg Arg Asn Phe Thr Met Thr Tyr His Leu
 85 90 95
 Ser Pro Gly Asn Tyr Val Val Val Ala Gln Thr Arg Arg Lys Ser Ala
 100 105 110
 Glu Phe Leu Leu Arg Ile Phe Leu Lys Met Pro Asp Ser Asp Arg His
 115 120 125
 Leu Ser Ser His Phe Asn Leu Arg Met Lys Gly Ser Pro Ser Glu His
 130 135 140
 Gly Ser Gln Gln Ser Ile Phe Asn Arg Tyr Ala Gln Gln Arg Leu Asp
 145 150 155 160
 Ile Asp Ala Thr Gln Leu Gln Gly Leu Leu Asn Gln Glu Leu Leu Thr
 165 170 175
 Gly Pro Pro Gly Asp Met Phe Ser Leu Asp Gly Ala Ala Ala Trp Trp
 180 185 190
 Leu

<210> 525
 <211> 1101
 <212> DNA
 <213> Homo sapiens

<400> 525
 nggcaagttg caaagagagc ctcagaggtc cgaagagcgc tgcgctccta ctgcggttcg
 60
 cttcttcttc ttctcggttc cctactgtga aatcgagcgc acatttaca aggctccgg
 120
 gtcctaccga gaccgatccg cagcggttgg cccggtcgcg cctattgcat cgggagcccc
 180
 cgagcaccgg cgaaggactg gcgggtgggg tagggagggtg gcggcgccgg catggcgagg
 240
 ttcccgaagg cgcacctggc cgctgcagga gttatgttac ttgcccactt cttcacggac
 300
 cagtttcagt tcgccgatgg gaaacccgga gaccaaattc ttgattggca gtatggagtt
 360
 actcaggcct tcctcacac agaggaggag gtggaagttg attcacacgc gtacagccac
 420

aggtggaaaa gaaacttgga ctttctcaag gcggtagaca cgaaccgagc aagcgtcggc
 480
 caagactctc ttgagccag aagcttcaca gacctgctgc tggatgatgg gcaggacaat
 540
 aacactcaga tcgaggagga tacagaccac aattactata tatctcgaat atatggtcca
 600
 tctgattctg ccagccggga tttatgggtg aacatagacc aaatggaaaa agataaagtg
 660
 aagattcatg gaattattgtc caatactcat cggcaagctg caagagtga tctgtccttc
 720
 gattttccat tttatggcca ctctctacgt gaaatcactg tggcaaccgg gggtttcata
 780
 tacattggag aagtcgtaca tcgaatgcta acagccacac agtacatagc acctttaatg
 840
 gcaaatttcg atcccagtgt atccagaaat tcaactgtca gatattttga taatggcaca
 900
 gcacttgtgg tccagtggga ccatgtacat ctccaggata attataacct gggaagcttc
 960
 acattccagg caaccctgct catggatgga cgaatcatct ttggatacaa agaaattcct
 1020
 gtcttgggtca cacagataag ttcaaccaat catccagtga aagtcggact gtccgatgca
 1080
 tttgtcgttg tccacaggat c
 1101

<210> 526

<211> 290

<212> PRT

<213> Homo sapiens

<400> 526

Met	Ala	Arg	Phe	Pro	Lys	Ala	Asp	Leu	Ala	Ala	Gly	Val	Met	Leu
1				5				10					15	
Leu	Cys	His	Phe	Phe	Thr	Asp	Gln	Phe	Gln	Phe	Ala	Asp	Gly	Lys
			20				25					30		Pro
Gly	Asp	Gln	Ile	Leu	Asp	Trp	Gln	Tyr	Gly	Val	Thr	Gln	Ala	Phe
		35					40					45		Pro
His	Thr	Glu	Glu	Glu	Val	Glu	Val	Asp	Ser	His	Ala	Tyr	Ser	His
		50				55					60			Arg
Trp	Lys	Arg	Asn	Leu	Asp	Phe	Leu	Lys	Ala	Val	Asp	Thr	Asn	Arg
65				70				75					80	Ala
Ser	Val	Gly	Gln	Asp	Ser	Leu	Glu	Pro	Arg	Ser	Phe	Thr	Asp	Leu
			85					90					95	Leu
Leu	Asp	Asp	Gly	Gln	Asp	Asn	Asn	Thr	Gln	Ile	Glu	Glu	Asp	Thr
			100					105					110	Asp
His	Asn	Tyr	Tyr	Ile	Ser	Arg	Ile	Tyr	Gly	Pro	Ser	Asp	Ser	Ala
		115				120					125			Ser
Arg	Asp	Leu	Trp	Val	Asn	Ile	Asp	Gln	Met	Glu	Lys	Asp	Lys	Val
		130				135					140			Lys
Ile	His	Gly	Ile	Leu	Ser	Asn	Thr	His	Arg	Gln	Ala	Ala	Arg	Val
145				150						155				Asn
Leu	Ser	Phe	Asp	Phe	Pro	Phe	Tyr	Gly	His	Phe	Leu	Arg	Glu	Ile
				165				170					175	Thr
Val	Ala	Thr	Gly	Gly	Phe	Ile	Tyr	Thr	Gly	Glu	Val	Val	His	Arg
														Met

	180		185		190
Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro					
195		200		205	
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala					
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Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe Cys Asp
      740      745      750
Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly Ser Lys Ala
      755      760      765
Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met Trp Leu Glu Lys
      770      775      780
Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn Asn Gly Ser Val Arg
785      790      795      800
Thr Ala

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<210> 531

<211> 321

<212> DNA

<213> Homo sapiens

<400> 531

ngatgatgaa tcccccgca gcctcgtaa tatggggggc ttcctacccc agcaaaaggc
 60
 acggcaatac gtctcgaaca aaggtctttt gtttcgaaat aacaaggggt tagagctaag
 120
 aggaagaagc gtgaaacgct gtaggaccag cgtttcgaac gccccgagg tgaaccctcg
 180
 ggggctctg aatcaggcca gttgggcctg ggacgacagc ggttcgagcg gcagcaatgg
 240
 cgcgtgcgga tcagccttga tcgattcacg ccaggcgccg agccactcgg cgtggccttc
 300
 gttccacacc tgctgggtgca g
 321

<210> 532

<211> 96

<212> PRT

<213> Homo sapiens

<400> 532

Met	Gly	Gly	Phe	Leu	Pro	Gln	Gln	Lys	Ala	Arg	Gln	Tyr	Val	Ser	Asn
1				5				10					15		
Lys	Gly	Leu	Leu	Phe	Arg	Asn	Asn	Lys	Gly	Leu	Glu	Leu	Arg	Gly	Arg
		20					25				30				
Ser	Val	Lys	Arg	Cys	Arg	Thr	Ser	Val	Ser	Asn	Ala	Pro	Glu	Val	Asn
		35				40					45				
Pro	Arg	Gly	Arg	Leu	Asn	Gln	Ala	Ser	Trp	Ala	Trp	Asp	Asp	Ser	Gly
	50				55					60					
Cys	Ser	Gly	Ser	Asn	Gly	Ala	Cys	Gly	Ser	Ala	Leu	Ile	Asp	Ser	Arg
65				70				75					80		
Gln	Ala	Pro	Ser	His	Ser	Ala	Trp	Pro	Ser	Phe	His	Thr	Cys	Trp	Cys
			85					90					95		

<210> 533

<211> 335

<212> DNA

<213> Homo sapiens

<400> 533

nagtttccgg tgaacccgct cgcaatgcct cgtgacatcg acttcagcga agccaacagg
 60
 agcatcatcg acaacatggc aactgcctca atcccgtttt tccgaaccga caaaaactgg
 120
 gagacgtggt cgagtcaggt ccggcatttc attagccttt tacacccaaa agtcaccctc
 180
 accaacattg acaacgtcct caacaaagat cacctgcgtt ggctacactt tcttttggag
 240
 ggtcgcttgg agccaaacgt gcgcctgatt gtccagggtt actgttcgcc tggcaagctg
 300
 taccgcaagc ttgaggagct atatgccctt tctgc
 335

<210> 534
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 534
 Met Pro Arg Asp Ile Asp Phe Ser Glu Ala Asn Arg Ser Ile Ile Asp
 1 5 10 15
 Asn Met Ala Thr Ala Ser Ile Pro Leu Phe Arg Thr His Lys Asn Trp
 20 25 30
 Glu Thr Trp Ser Ser Gln Val Arg His Phe Ile Ser Leu Leu His Pro
 35 40 45
 Lys Val Thr Leu Thr Asn Ile Asp Asn Val Leu Asn Lys Asp His Leu
 50 55 60
 Arg Trp Leu His Phe Leu Leu Glu Gly Arg Leu Glu Pro Asn Val Arg
 65 70 75 80
 Leu Ile Val Gln Gly Tyr Cys Ser Pro Gly Lys Leu Tyr Arg Lys Leu
 85 90 95
 Glu Glu Leu Tyr Ala Pro Ser
 100

<210> 535
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 535
 acgcgtctct acagccggac taagcacagg ctacgccccg gtcgccatgc gccaggctc
 60
 gggtatcagc cgaggaatcc acggcgaaat gaccagtagc ggccctaata caactatgct
 120
 gccgagcagc agacgtcgag gtcgggtcat gaggatgccg acggccaccg cgaccgggta
 180
 taccacaaat gcaggaacaa ggctgatagc tagggctgac cacagagcca ggccgcctgc
 240
 cgaggaaacg cccccacct ggtgactgcc agtatcagca ccgcgcagct caacgacgtc
 300
 aacagtctcg ggattgacca accgccacgt atgcagggcc atgtggggga gaatcacccc
 360
 caacgccaat gctgtcaccg agcctcgggc taggccgccg gc
 402

<210> 536
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 536
 Met Ala Leu His Thr Trp Arg Leu Val Asn Pro Glu Thr Val Asp Val
 1 5 10 15
 Val Glu Leu Arg Gly Ala Asp Thr Gly Ser His Gln Val Gly Gly Val
 20 25 30
 Ser Ser Ala Gly Gly Leu Ala Leu Trp Ser Ala Leu Ala Ile Ser Leu

```

      35          40          45
Val Pro Ala Leu Trp Val Tyr Pro Val Ala Val Ala Val Gly Ile Leu
  50          55          60
Met Thr Arg Pro Arg Arg Leu Leu Leu Gly Ser Ile Val Val Leu Gly
  65          70          75          80
Pro Leu Leu Val Ile Ser Pro Trp Ile Pro Arg Leu Ile Thr Glu Pro
      85          90          95
Gly Arg Met Ala Thr Gly Ala Glu Pro Val Leu Ser Pro Ala Val Glu
  100          105          110
Thr Arg

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<210> 537
 <211> 404
 <212> DNA
 <213> Homo sapiens

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<400> 537
gtgcacatcg gcggcaccga cttcgacaaa caactctcgc tggctggcat gatgccgctg
  60
ttcggctacg gcagccgcat gaagagcggc gcctacatgc ccaccagcca ccacatgaac
  120
ctggcgacct ggcacacccat caactcgggtg tactcgcaaa aatcccagct ggccttgggc
  180
agcatgcgct acgacatcga agacaccggc ggcacgcacc gcctgttcaa gctgatcgaa
  240
cagcgtgctg ggcactggct tgccatggaa gtggaagaaa ccaagatcca gtcacccat
  300
caagacagcc gccacgtgcc gctggaccgc atcgaagcgg gcctgagcgt agacctgagc
  360
cgggcgctgt tcgaatcgtc catcgacaac ctgctcgaac gcgt
  404

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<210> 538
 <211> 118
 <212> PRT
 <213> Homo sapiens

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<400> 538
Met Met Pro Leu Phe Gly Tyr Gly Ser Arg Met Lys Ser Gly Ala Tyr
  1          5          10          15
Met Pro Thr Ser His His Met Asn Leu Ala Thr Trp His Thr Ile Asn
      20          25          30
Ser Val Tyr Ser Gln Lys Ser Gln Leu Ala Leu Gly Ser Met Arg Tyr
      35          40          45
Asp Ile Glu Asp Thr Gly Gly Ile Asp Arg Leu Phe Lys Leu Ile Glu
      50          55          60
Gln Arg Ala Gly His Trp Leu Ala Met Glu Val Glu Glu Thr Lys Ile
  65          70          75          80
Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
      85          90          95
Ala Gly Leu Ser Val Asp Leu Ser Arg Ala Leu Phe Glu Ser Ser Ile
  100          105          110
Asp Asn Leu Leu Glu Arg

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115

<210> 539
 <211> 534
 <212> DNA
 <213> Homo sapiens

<400> 539
 nnacgcgtga aaaagaagaa aatgaaggaa agcgaggctg acagcgagggt gaagcatcaa
 60
 ccaattttca taaaagaaag attgaagctt tttgaaatac tgaagaaaga ccatcagctc
 120
 ttacttgcca tttatggaaa aaagggggat acaagcaaca tcatcacagt aagagtggct
 180
 gatgggcaaa cagtgcagg ggaagtctgg aaaacaacgc cttaccaagt ggctgctgaa
 240
 attagtcagg aactggctga aagcacggta atagccaaag tcaatggtga actgtgggac
 300
 ctggaccgcc cattggaagg ggactcttct ctagagctgc ttacatttga taatgaggaa
 360
 gctcaagctg tgagtatttt aaaaccagac agccaaactt tgggtagtta tgttgtaaac
 420
 tacattatat aagaggccac atattgaatt cacgaatggt gagttttttg ggggtttcta
 480
 agatttaaaa tttgattatt gatgtttaat aaatatttgc ctcatgaatg ttaa
 534

<210> 540
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 540
 Xaa Arg Val Lys Lys Lys Met Lys Glu Ser Glu Ala Asp Ser Glu
 1 5 10 15
 Val Lys His Gln Pro Ile Phe Ile Lys Glu Arg Leu Lys Leu Phe Glu
 20 25 30
 Ile Leu Lys Lys Asp His Gln Leu Leu Leu Ala Ile Tyr Gly Lys Lys
 35 40 45
 Gly Asp Thr Ser Asn Ile Ile Thr Val Arg Val Ala Asp Gly Gln Thr
 50 55 60
 Val Gln Gly Glu Val Trp Lys Thr Thr Pro Tyr Gln Val Ala Ala Glu
 65 70 75 80
 Ile Ser Gln Glu Leu Ala Glu Ser Thr Val Ile Ala Lys Val Asn Gly
 85 90 95
 Glu Leu Trp Asp Leu Asp Arg Pro Leu Glu Gly Asp Ser Ser Leu Glu
 100 105 110
 Leu Leu Thr Phe Asp Asn Glu Glu Ala Gln Ala Val Ser Ile Leu Lys
 115 120 125
 Pro Asp Ser Gln Thr Leu Gly Ser Tyr Val Val Asn Tyr Ile Ile
 130 135 140

<210> 541
 <211> 551

<212> DNA

<213> Homo sapiens

<400> 541

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ggtagcgagc tgcgcgtgtg gtatgcggcc ttctatgcca agaagatgga caagcccatg
60
ctgaagcagg ccggctctgg cgtccacgct gcaggcacc cagaaaacag cgcccccggtg
120
gagtcggagc ccagccagtg ggcgtgtaaa gtgtgttctg ccaccttcct ggagctgcag
180
ctcctcaatg gtaaggagga cgtgtgggga gcccagttg taaaactcct gtgtcgattt
240
ctctctgact tacgctgtca cctgtctgcg gctgtcgggg gtgtcccaga ctttgcctcg
300
tctgccccat tgccccacaa tgtagtcgcc agaaccaagg ctttctcagg gtttaaagct
360
tctgggcagt cccgcttccc acccccgacc cctgcaggcc tcaactcctca ctctcctgg
420
ttgggaagtt gcatttcagc tgggcgcctt gactctggag cactggcagg ggccaggggc
480
caggagccag ccgtggcatg tggtgtgcac tcttgccctt gttgtctcta cttgacagcc
540
ccctcacgcg t
551

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<210> 542

<211> 168

<212> PRT

<213> Homo sapiens

<400> 542

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Met Asp Lys Pro Met Leu Lys Gln Ala Gly Ser Gly Val His Ala Ala
1      5      10      15
Gly Thr Pro Glu Asn Ser Ala Pro Val Glu Ser Glu Pro Ser Gln Trp
20     25     30
Ala Cys Lys Val Cys Ser Ala Thr Phe Leu Glu Leu Gln Leu Leu Asn
35     40     45
Gly Lys Glu Asp Val Trp Gly Ala Pro Val Val Lys Leu Leu Cys Arg
50     55     60
Phe Leu Ser Asp Leu Arg Cys His Leu Ser Ala Ala Val Gly Gly Val
65     70     75     80
Pro Asp Phe Val Leu Ser Ala Pro Leu Pro His Asn Val Val Ala Arg
85     90     95
Thr Lys Ala Phe Ser Gly Phe Lys Ala Ser Gly Gln Ser Arg Phe Pro
100    105    110
Pro Pro Thr Pro Ala Gly Leu Thr Pro His Ser Ser Trp Leu Gly Ser
115    120    125
Cys Ile Ser Ala Gly Arg Leu Asp Ser Gly Ala Leu Ala Gly Ala Arg
130    135    140
Gly Gln Glu Pro Ala Val Ala Cys Val Val His Ser Cys Leu Cys Cys
145    150    155    160
Leu Tyr Leu Thr Ala Pro Ser Arg
165

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<210> 543
 <211> 349
 <212> DNA
 <213> Homo sapiens

<400> 543
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 60
 gggggcaaag gcagccgcct ggccccgatg accgatcagg tggccaaacc agccgtgccg
 120
 tttatgggga cgtaccgcct gattgacttt tcgctgtcca acattgtcca cagcggcttg
 180
 caggacgtct ggatcattga gcaaaacctg ccccatagct taaacgagca cctggctggg
 240
 gggcgctcct gggatctgga ccgcaccgcg ggtggcctga aggtcatgcc gcccttttcc
 300
 ggccctgccg atgaggacgg tggcttttcc gaaggcaacg cacacgcgt
 349

<210> 544
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 544
 Xaa Lys Pro Asp Met Asn Thr Arg Ile Ala Gly Lys Thr Val Leu Thr
 1 5 10 15
 Ile Ile Leu Ala Gly Gly Lys Gly Ser Arg Leu Ala Pro Met Thr Asp
 20 25 30
 Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile
 35 40 45
 Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp
 50 55 60
 Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly
 65 70 75 80
 Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met
 85 90 95
 Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly
 100 105 110
 Asn Ala His Ala
 115

<210> 545
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 545
 catgatgcaa aaacagacat gcttatttca aaatataaaa gtgaaaaaga tcgttttagca
 60
 caagaaattg ttggtgtcat cacaggttct gcaatgccgg gtgggttcagc aaaccgtatc
 120
 ccaaataaag caggctcaaa tccagaaggt tctattgcaa cgcgttttat tgcagaaaca
 180

atgtataacg aactcaaaac agtggattta actattcaaa atgctggcgg tgtacgcgca
 240
 gatattttac cggggaatgt aacctttaac gatgcttata ctttcttacc ttctcggaat
 300
 acgttatata cctataaaat ggaaagtcca ttagtgaaac aagtgcctga agatgcaatg
 360
 ctatttgctt tgggtccccc ccccccccc
 390

<210> 546
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 546
 His Asp Ala Lys Thr Asp Met Leu Ile Ser Lys Tyr Lys Ser Glu Lys
 1 5 10 15
 Asp Arg Leu Ala Gln Glu Ile Val Gly Val Ile Thr Gly Ser Ala Met
 20 25 30
 Pro Gly Gly Ser Ala Asn Arg Ile Pro Asn Lys Ala Gly Ser Asn Pro
 35 40 45
 Glu Gly Ser Ile Ala Thr Arg Phe Ile Ala Glu Thr Met Tyr Asn Glu
 50 55 60
 Leu Lys Thr Val Asp Leu Thr Ile Gln Asn Ala Gly Gly Val Arg Ala
 65 70 75 80
 Asp Ile Leu Pro Gly Asn Val Thr Phe Asn Asp Ala Tyr Thr Phe Leu
 85 90 95
 Pro Phe Gly Asn Thr Leu Tyr Thr Tyr Lys Met Glu Ser Ser Leu Val
 100 105 110
 Lys Gln Val Leu Glu Asp Ala Met Leu Phe Ala Leu Gly Pro Pro Pro
 115 120 125
 Pro Pro
 130

<210> 547
 <211> 306
 <212> DNA
 <213> Homo sapiens

<400> 547
 aagcttggtt ttctgatttt tattcaaatc tctatcatgg atgaagcatg cagtttcaga
 60
 atcagttcag tgttgacaac atatcaagat attctgcagt caatctcaat gtatgttcac
 120
 gaagcctcca acatattttg tgggatacca tctttgtcag gcattgtgct aggcactgtc
 180
 cctgcagtga ataagaaaga caggatttct gtatttatgg ggcttagtac caagttgttc
 240
 tcaaaacttc atgtttgtgt atacaaatca gctgaggcct tcactaaact cnnnnnccnn
 300
 nncenn
 306

<210> 548